EvolDir

August 1, 2025

Month in Review

Foreword

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

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

Instructions for the EvolDir are listed at the end of this message.

—— / ——

Conferences

Cambridge BiodiversityGenomics Oct27-29

Extended deadline for abstract submission is fast approaching (Monday 28th July) for our conference "Understanding Life: Using Large-scale Biodiversity Reference Genomes" to be held on 27th-29th October at the Wellcome Genome Campus, near Cambridge, UK.

More information on the conference can be found here: www.bit.ly/4j3vAZ9 This conference aims to bring together researchers interested in large-scale genomics to understand the magnificent biodiversity on our planet. It will be of interest if you work on generating sequence data, developing methods or tools for genome processing, or use genomics to understand mechanisms of evolution.

This conference will have both in-person and virtual attendance. Registration deadline (In-person): 29 September Registration deadline (Virtual): 20 October

Scientific sessions will include: - Genome evolution - Symbiosis genomics - Genomics of speciation - Ecological genomics

There will also be several workshops lead by specialists in the fields bringing together working groups and consortia associated with biodiversity reference genomes: - AI and annotation - Sequencing the holobiont - how to disentangle species - Curation of assemblies - Advances in Genomic Technologies - Project Psyche Showcase - Bat1K showcase - Aquatic symbiosis genomics - Working with industry and agritech - Population genomics and conservation

Keynote speakers: Ute Hentschel Humeida - GEOMAR Helmholtz Centre for Ocean Research, Germany Arnau Sebé-Pedrós - Centre for Genomic Regulation, Spain

Confirmed session speakers: Aoife McLysaght - Trinity College Dublin, Ireland Niklas Wahlberg - Lund University, Sweden Claire Mérot - University of Rennes, France

Posters sessions will provide opportunities to present research findings or get feedback on ongoing research.

Hope to see you in Cambridge in October!

Peter Mulhair, on behalf of the Organising Committee

peter.mulhair@liverpool.ac.uk

"Mulhair, Peter" <Peter.Mulhair@liverpool.ac.uk>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Crete AdaptiveMinds Oct27-30

The Brain Conference: Principles of the Adaptive Mind - Towards an integrated understanding of the dynamics of mental health and stress resilience as adaptation to uncertainty across multiple nested timescales

This conference will bring together a unique and interdisciplinary group of internationally recognised experts in evolutionary biology, computational cognitive neuroscience, developmental psychology, systems neuroscience, genetics/epigenetics and clinical psychiatry, to promote synthesis and synergy between the computational, social and life sciences to advance knowledge about the adaptive mind.

The conference features an evolutionary biology component in the programme, including among others lectures from: Alexandra Rosati - The evolution and development of complex cognition across primates Willem Frankenhuis - The evolution and development of plasticity Christopher Kuzawa - Food for thought: The energetic costs of brain development and the evolution of the human life history

Mental health depends on our ability to adapt our brain, mind and decisions flexibly to the uncertainty of our constantly changing environment. Such adaptation occurs over several nested timescales: within an individual's lifetime through both rapid learning and longer-term developmental plasticity, and between generations through the transfer of adaptive traits. Yet we have little understanding of the basic principles of healthy adaptation to uncertainty for stress resilience.

Attendees can expect engaging lectures from outstanding scientists, poster sessions with abstracts submitted by participants, and lively social events.

If you're interested in learning more about the adaptive mind while connecting with international leaders and peers from an array of disciplines, the upcoming Brain Conference is the place to be!

Find everything you need to know about the upcoming Brain Conference here: https://www.fens.org/news-activities/fens-and-societies-calendar/meeting-event/principles-of-the-adaptive-mind Contact: brain@fens.org

Andreea Marginean Programme Officer -The Brain Conferences FENS- Federation of European Neuroscience Societies 11 Rue d'Egmont, 1000 - Brussels, Belgium T:+32 2 545 04 55 E:brain@fens.org

Andreea Marginean <andreea.marginean@fens.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

London UK OrganismalResilience Nov20

Dear all,

Join us at the Linnean Society in London for a hybrid (in-person and online) one-day symposium focused on the mechanisms and consequences of variation in organismal resilience.

The mechanisms that allow organisms to both buffer system function from perturbation, and dynamically respond to change are the foundation of organismal resilience. Understanding these mechanisms and how they evolve is one the most pressing challenges in modern biology. Meeting this challenge will require perspectives that span all levels of biological organization, from genes to populations to ecosystems, and collaboration and integration across many different biological disciplines. Organisms are the nexus that unites lower-level genetic, cellular, and physiological processes that underlie resilience to concepts of resilience at the population, community, and ecosystem levels. Why are some individuals and taxa more resilient than others? And how does individual and species-level variation in resilience relate to the resilience of populations, communities, and entire ecosystems? This symposium will address these and related questions to advance our understanding of organismal resilience, and its potential to buffer organisms in a rapidly changing world.

This is a hybrid day meeting, offering the option of both in-person tickets or online attendance.

Confirmed speakers: Patricia Schulte (University of British Columbia, Canada) Christopher Wheat (Stockholm University, Sweden) Rose Thorogood (University of Helsinki, Finland) Luis-Miguel Chevin (Centre d'Ecologie Fonctionnelle et Evolutive, CNRS Montpellier, France) Shane Campbell-Staton (Princeton University, USA) Glenn Yannic (Université Savoie Mont Blanc & Laboratoire d'Ecologie Alpine, France) Chloe Haberkorn (Stockholm University, Sweden)

We will host a poster session, and short talks (˜15 minutes) will also be selected from submitted abstracts, with an emphasis on early-career researchers. These short talks can be presented remotely for online attendees. If you would like to contribute a poster or submit an abstract for consideration for a short talk, please submit a title and abstract (max 200 words), with lead author affiliation and career stage, to evojlinnsoc@linnean.org by 17.00 (BST) Friday 5 September 2025.

Date: 20 November 2025

Venue: Linnean Society of London, Piccadilly London W1J 0BF, United Kingdom

Registration and abstract submission deadline: 5 September 2025

Further details and registration information can be found here: https://members.linnean.org/events/6862a9bfe5e1810008367c26/description General questions can be directed to Zac Cheviron (zac.cheviron@umt.edu).

This event is supported by Oxford University Press and the Company of Biologists.

Hope to see you in London, Zac Cheviron and Karen Sears (organizers)

ZACHARY CHEVIRON

PROFESSOR DIVISION OF BIOLOGICAL SCIENCES ECOLOGY AND EVOLUTION WILDLIFE BIOLOGY PROGRAM

FACULTY DIRECTOR PHILIP L. WRIGHT ZOOLOGICAL MUSEUM

Interdisciplinary Science Building 317 | Missoula MT ph: 406-243-4496 | web: chevironlab.org | e: zac.cheviron@umt.edu

UNIVERSITYOFMONTANA

“Cheviron, Zac” <zac.cheviron@mso.umt.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Montpellier Primates July2026

Dear all,

We are pleased to announce the 11th meeting of the European Federation for Primatology < https://www.efp-primatology.com/ > (EFP) that will take place in *Montpellier, Southern France, from Monday 29th June to Friday 3rd July 2026.*

We invite you to present your work on human and non-human primates at this event. The preliminary programme, along with other practical information, is already available on the conference website < https://www.alphavisa.com/efp/2026/ >.

A variety of professional development opportunities will be offered to early-career researchers and students, including an interactive pre-conference workshop as well as networking and mentoring sessions. We are also preparing a special Equity, Diversity and Inclusion (EDI) program around the theme *“Gender in Primatology.”* Further details will be announced soon. We are also launching an initiative to support colleagues who may not be fully comfortable with written or spoken English, by helping them prepare their abstracts, posters, and/or oral presentations. Please do not hesitate to contact us! More information is available on the website (see here < https://www.alphavisa.com/efp/2026/language-accessibility.php >).

To promote inclusivity and facilitate the participation of non-European colleagues who may face lengthy administrative procedures to obtain a visa to enter France, we are announcing that all submitted abstracts will be accepted for presentation (as either an oral communication or a poster). We strongly recommend starting your visa application process well in advance ideally at least six months before the conference (you can request an official certificate of participation see here < https://www.alphavisa.com/efp/2026/visa.php >). Travel grants for students will be announced at a later date.

Official conference website: https://www.alphavisa.com/efp/2026/ *Follow us on Bluesky* for announcements and updates: @efp2026.bsky.social < https://bsky.app/profile/efp2026.bsky.social >

Venue: Maison des Sciences de l’Homme de Montpellier < https://www.mshsud.org/ > (MSH Sud), 71 Rue du Professeur Henri Serre, 34090 Montpellier, located in the heart of Montpellier’s historical centre !

Contact emails:

Administrative enquiries: efp@alphavisa.com

Scientific enquiries *ONLY*: efp2026montpellier@gmail.com

Key dates:

Symposium proposals: September-October 2025

Abstract submission: mid-November 2025 to mid-March 2026

Early bird registration: mid-November 2025 to end of February 2026

We very much look forward to welcoming you to Montpellier in the summer of 2026!

Warm regards,

Alice Baniel, Marie Charpentier & Elise Huchard (on behalf of the Organising Committee)

“alice.baniel@gmail.com” <alice.baniel@gmail.com>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

NHM London Protistology Sep4-5

We are pleased to announce the 2025 Protistology-UK Autumn meeting at the prestigious Natural History Museum, London. This meeting is vitally important to attend, as it will explore the purpose (and fate) of local protistology societies. We especially encourage younger members to attend - travel bursaries of 100 are available!

Meeting structure (two half days):

- through a plenary and an associated workshop, we will explore the purpose, sustainability and 'what you want from the Society' of Protistology-UK and the role of similar scholarly societies

- through your talks and posters we will explore the breadth and depth of protistology research

- through social events (coffee, drinks, conference dinner, museum tours) we will foster collegiality and discussions.

Location: Natural History Museum, London.

Dates and times: 11:00 on Thursday 4th September 2025 - 14:00 on Friday 5th September 2025.

Details can be found on the Protistology-UK website (https://www.protistology.org.uk) where you can register for the conference (https://www.protistology.org.uk/autumn-meeting-2025-registration) and learn how to submit your abstract (https://www.protistology.org.uk/autumn-meeting-2025).

Key Date: Deadline for early bird registration and bursary application 23rd July 2025

Dr. Martin Carr P-UK Treasurer Protistology-UK http://www.protistology.org.uk Martin Carr <martcarr74@gmail.com>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

SMBE Houston AntiMicrobialPeptides Oct13-15

Announcing the last call for applications to attend the SMBE Satellite Meeting: Evolutionary Biochemistry of Insect Antimicrobial Peptides

The SMBE Satellite Meeting on Evolutionary Biochemistry of Insect Antimicrobial Peptides will be held at the University of Houston (Texas, USA) on Oct 13-15, 2025. The Meeting is FREE to attend, but attendance requires admission following review of your application. The first round of application review will complete on July 14, 2025. Applications from Early Career Researchers and scholars from diverse research areas are highly encouraged. Travel awards are available to support attendance for early career scholars.

Please visit the meeting website for more information, including application, registration, and travel award links: https://uh.edu/nsm/biology-biochemistry/news-events/smbe-meeting/ Additional information:

Microbes that cause disease to humans, livestock, crops, and wild species are incredibly diverse and rapidly evolve resistance to existing antibiotic drugs. Naturally occurring insect antimicrobial peptides have tremendous promise to help address the challenge of antibiotic resistance, but realizing this potential requires transdisciplinary collaboration across disciplines including genomics, microbiology, biochemistry, data science, and engineering. The conference will promote growth in this area by bringing together researchers from a variety of disciplines and career stages to understand modes of action and potential applications of insect AMPs as novel antibiotic agents.

Research areas covered by this conference will include: - Phylogenetic and comparative genomics of arthropod antimicrobial peptides - Novel antimicrobials, biomimetics design, and peptide biochemistry - Microbiology, in vitro and in vivo experimentation - Machine learning and data science - Translational research

There will be multiple breakout sessions at the conference, which we intend to use to develop at least one white paper on Insect Antimicrobial Peptides and Antibiotic Drug Design.

Are you interested in the meeting but cannot attend in person? Please consider attending online (also free). Online attendees will be eligible to give talks and will be invited to participate in discussions.

Richard Meisel rpmeisel@uh.edu

"Meisel, Richard P" <rpmeisel@Central.UH.EDU>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Valencia Spain EvolBiol Jan21-23

Dear evoldir members,

Next January: 21st to 23rd, we will host the Biennial Meeting of the Spanish Society of Evolutionary Biology in Valencia (Spain).

The X Meeting of the Spanish Society for Evolutionary Biology, SESBE 2026, will feature a diverse array of topics in evolutionary biology, including population genetics, molecular evolution, evolutionary developmental biology, phylogenetics and phylogenomics, evolutionary ecology and palaeobiology, among others. The meeting will bring together leading keynote speakers from various fields, both emerging and established, and will include contributed scientific presentations (oral and poster). It will provide an excellent setting for networking and discussions with fellow researchers, as well as an opportunity to explore the vibrant city of Valencia.

Preeliminar program with confirmed keynote speakers: https://sesbe2026.es/programme/ Abstract submission until September 15th https://sesbe2026.es/abstract/

On Behalf of the organizing committee.

Mireia Coscollï¿½, PhD.

http://www.mireiacoscolla.com/ Head of PathoGenOmics at I2SYSBIO

https://www.i2sysbio.es/groups/23/ Mireia Coscolla <mireia.coscolla@uv.es>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

GradStudentPositions

Barcelona ChromatinEvolution

Pre-Doc/PhD position in Evolutionary Chromatin Biology

The role

We are looking to hire a pre-doctoral student, those finishing or have finished their Master's studies and are eventually interested in pursuing a PhD, to explore the evolution of eukaryotic chromatin states and components. Chromatin modifications are conserved across eukaryotes, but their combinatorial function across genomes are dependent on a diverse crosstalk among chromatin readers and writers. A successful candidate will initially work closely with a postdoc in the lab to identify and characterize chromatin proteins using either phylogenetic, proteomic, genomic, or biochemical methods, depending on the candidate's strengths. As a PhD student, further investigations with orthogonal methods are expected. This work is an extension of recent work on eukaryotic chromatin evolution in the lab:

https://www.biorxiv.org/content/10.1101/2025.03.17.643675v1 https://www.nature.com/articles/s41559-022-01771-6 Whom would we like to hire?

This highly interdisciplinary project will span molecular phylogenetics, chromatin profiling, proteomics, and biochemistry across a wide array of eukaryotic species. An ideal candidate would have experience in at least one of these fields and a willingness to acquire complementary skills.

Proficiency in English is a must, as are solid communication and interpersonal skills.

The offer

We offer an initial paid internship contract for 6 months, followed by a fully funded PhD position for 4 years, dependant upon favourable review. The target start date is October 2025.

About the lab

The Sebé-Pedrós lab studies the evolution of cell type programs and genome regulation, combining single-cell genomics, chromatin profiling, and comparative genomics methods in a phylogenetically diverse array of eukaryotes. For more details about the lab, visit the lab website: https://www.sebepedroslab.org/ The institute

The CRG in Barcelona is one of the leading molecular biology research institutes in Europe, hosting over 400 researchers from 44 countries. We provide a highly stimulating environment with state-of-the-art infrastructures, and unique professional career development opportunities.

Application

Submit your application by September 10 2025 here: https://recruitment.crg.eu/content/jobs/position/-research-trainee-evolutionary-chromatin-biology Please, describe what topics/questions motivate you, what is your past experience in research (if any), and why you are interested in working on chromatin evolution.

For more information, you can get in touch with Arnau Sebe-Pedros (arnau.sebe [at] crg.eu) and Sean Montgomery (sean.montgomery [at] crg.eu).

Arnau Sebe Pedros <arnau.sebe@crg.eu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

KULeuven Belgium:EvolutionaryBiology

PhD Position in Evolutionary and Molecular Ecology Link to apply: https://www.kuleuven.be/personeel/-jobsite/jobs/60500112 Project Overview We are excited to offer a fully funded PhD position focused on the ecology, evolution, and molecular mechanisms of plasticity and adaptation in Daphnia, with a particular emphasis on melanistic Daphnia zschokkei from alpine lakes. The project combines fieldwork, genomics, transcriptomics, and functional experiments to answer fundamental questions in evolutionary biology.

Suggested research questions (RQs):

* RQ1: Evolution and taxonomic status of Daphnia zschokkei Several Daphnia species and ecotypes display melanization, yet the evolutionary history of this adaptive phenotype remains largely unresolved. Daphnia zschokkei, a melanized taxon inhabiting alpine lakes, was originally described as a distinct species but is currently treated as an ecotype of D. longispina, based on single-locus and microsatellite data. However, preliminary whole-genome analyses suggest that these melanized populations may form a distinct genetic cluster. This project aims to determine whether melanization evolved once and spread across the Alps, or arose repeatedly from local D. longispina populations. Whole-genome sequencing of melanized "zschokkei" and non-melanized D. longispina across a wide geographic range will be used to resolve phylogenetic relationships, clarify taxonomic status, and reconstruct the evolutionary origins of this trait. Including other melanized populations from the D. longispina complex will allow broader inferences about the evolution of melanization.

* RQ2: Quantifying variation in melanization Melanization can be constitutively expressed or environmentally induced. To better understand variation in this trait, we will collect clonal lineages from multiple D. zschokkei populations (as part of RQ1), measure melanization levels in the field, and rear the clones under standardized lab conditions for several generations. This will allow us to determine baseline levels of constitutive expression. After baseline quantification, clones will be exposed to UV treatments to assess plastic responses. Environmental data from each site (UV exposure, turbidity, depth, nutrient levels, predator abundance) will be integrated to assess which factors best explain phenotypic variation.

* RQ3: Genetic basis and regulatory architecture of melanin expression Initial findings suggest that melanization in D. zschokkei is largely plastic, implicating regulatory mechanisms. By integrating whole-genome data (RQ1) and phenotypic data (RQ2), we will perform genome-wide association studies, outlier detection, and selection scans to identify candidate genes and regulatory elements involved in melanization. In selected populations, we will conduct controlled induction experiments and collect samples for RNA-seq and ATAC-seq to identify expression patterns and accessible chromatin regions linked to regulatory variation. This integrative approach will help distinguish between constitutive and inducible components of melanization and test whether adaptation occurred through parallel evolution or a shared genetic innovation. Promising regulatory elements will be functionally validated using CRISPR/Cas9 in collaboration with partner labs.

* RQ4: Comparative genomics of melanin regulation in Daphnia Melanized forms are also found in several species within the D. pulex complex, such as D. melanica, D. tenebrosa, and D. middendorfiana. Using the approaches developed in RQ3, we will identify candidate

genes and regulatory elements in these taxa and compare them to findings from the D. longispina complex. This comparative framework will illuminate whether similar genetic mechanisms underlie melanization across Daphnia lineages.

Candidate Profile We are looking for a highly motivated PhD candidate with:

* A strong academic track record * Enthusiasm for evolutionary ecology, population genetics and functional genomics * Bioinformatics skills * Excellent command of written and spoken English

This is a full-time position initially offered for one year, with the possibility of extension up to four years.

Research Environment You will be jointly supervised by Prof. Steven Van Belleghem at KU Leuven (Belgium) and Prof. Markus Moest at the Research Institute for Limnology, University of Innsbruck (Austria), located on the shores of Lake Mondsee.

* The research group of Steven Van Belleghem (KU Leuven) focuses on eco-evolutionary and functional genomics in a variety of systems. Website: https://bio.kuleuven.be/eeb/sv * The research group of Markus Moest (Mondsee) specializes in the ecology and evolution of the D. longispina group. The institute provides state-of-the-art infrastructure for Daphnia fieldwork,

— / —

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

---

LouisianaStateU ComputationalPhylo

PhD position opportunity in Computational Phylogenetics Department of Biological Sciences, Louisiana State University (LSU) United States of America

Potential start dates: January 2026 or September 2026 (flexible)

Research focus

The Mendes Lab develops, evaluates, and applies cutting-edge computational methods to study species evolution. Our research addresses questions such as:

(i) Where, when, and how often species originate and go extinct, (ii) Why species have the genotypes and phenotypes they do, and how these are interconnected, (iii) How species distributions evolve over space and time, (iv) How within-species processes influence or bias phylogenetic inferences related to these questions.

Work in the Mendes lab is cross-disciplinary, combining biology, computer science, and statistics, and often involves collaborations with researchers both within LSU and internationally.

Opportunities for the student

Students will be able to:

(a) Develop a deep understanding of computational methods and statistical models in evolutionary biology by engaging with recent literature. They will participate in discussions with local experts, and identify open questions from both empirical and methodological perspectives. Students will design an independent research project aligned with the lab's goals and the graduate program requirements;

(b) Gain hands-on experience with the inner workings of widely used scientific software, including BEAST 2, RevBayes, and various R and Python libraries. Students will develop coding skills, statistical modeling expertise, and may explore Bayesian inference, machine learning, and related methods depending on the focus of their research;

(c) Access world-class biological collections and expertise through the LSU Museum of Natural Science (https://www.lsu.edu/mns/index.php) and the Shirley C. Tucker Herbarium (https://www.lsu.edu/herbarium/index.php). This access will provide unique opportunities for integrating computational methods with empirical data.

Qualifications

Any and all applications that meet minimum qualifications will be considered (but see more details below on how to apply).

Minimum requirements: 1. A bachelor's degree (BSc) or master's degree (MSc) in biology, evolution, computer science, statistics, mathematics, or related field, 2. strong interest in both organismal biology and computational methods, 3. eligibility for admission to LSU's graduate programs.

Competitive applicants will have: 4. Experience with programming in R, Python, or similar languages, and/or 5. background in mathematical modeling, statistical inference, and machine learning, and/or 6. experience with large datasets and/or computational biology methods, and/or 7. strong written and oral communication skills (English), and/or 8. interest in interdisciplinary and collaborative work.

About the principal investigator (PI)

Dr. Fabio K. Mendes is an Assistant Professor in the Department of Biological Sciences at LSU. He has over a decade of experience developing and using computational methods for evolutionary biology. His research has appeared in top journals including Systematic Biology, eLife, Molecular Biology and Evolution, and Methods in Ecology and Evolution. Dr. Mendes also serves on the editorial board of Systematic Biology.

About the department and LSU

The Department of Biological Sciences (https://tinyurl.com/4drjwv97) at LSU is nationally recognized for its strength in evolutionary biology, systematics, and biodiversity science. Several faculty members are closely affiliated with the LSU Museum of Natural Science, one of the premier natural history museums in the U.S. Graduate students benefit from a collaborative and interdisciplinary environment, with opportunities to engage in cutting-edge research across a wide range of biological disciplines.

LSU is Louisiana's flagship public university, offering excellent research facilities, strong support for graduate students, and a welcoming, diverse community. LSU is also renowned for its top-tier athletics - its teams are among the most successful in the nation, and sporting events are massive, energetic, and a major part of campus life. For students looking to stay active, the university's recreation center offers state-of-the-art facilities for fitness, swimming, climbing, and more.

LSU is located in Baton Rouge, a vibrant city known for its history, culture, and affordability. Students will also be just over an hour from New Orleans, one of the most unique and culturally rich cities in the United States, known for its music scene, incredible food, and world-class festivals like Mardi Gras and Jazz Fest.

How to apply

The application process involves two steps: (i) an initial inquiry

— / —

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

Madrid FossilRecordImageAnalysis

PhD in Image Recognition Algorithms Applied to the Fossil Record

The Departments of Biology (Palaeontology Unit) and Electronic Technology & Communications at the Universidad Autï¿½noma de Madrid (UAM) are seeking a highly motivated PhD candidate to apply for an FPI-UAM Fellowship, with estimated start date of September 1st, 2025.

We are looking for a student with a strong academic background in programming and a genuine interest in Natural History and Evolution. Project Description This four-year PhD project aims to develop AI algorithms for fossil image recognition of the renowned fossil site of Las Hoyas (Lower Cretaceous, Cuenca, Spain; https://www.lyellcollection.org/doi/full/10.1144/jgs2022-079), applied to both museum collections (https://mupaclm.es) and in situ (fieldwork).

The successful candidate must demonstrate: - Strong programming skills in Python. Good knowledge of Machine Learning techniques and visualization. Excellent communication and academic writing skills. -Proficiency in working with Linux-based systems will be considered an asset. A strong understanding of Deep Learning methods and frameworks, such as TensorFlow or PyTorch, will also be advantageous. - A well-justified interest in Natural History and Evolution - A willingness to engage actively in: Annual excavation campaigns Independent research with the fossil collections at the Museum of Palaeontology of Castilla-La Mancha (MUPA)

Research will be carried out at the Universidad Autï¿½noma de Madrid, under the supervision of Profs. J. C. San Miguel-Avedillo (https://portalcientifico.uam.es/en/ipublic/researcher/261249) and J. Marugï¿½n-Lobï¿½n (https://aighol.wixsite.com/jmarugan). Eligibility Requirements

- Applicants should hold a Bachelor's degree in Engineering or a science- related field, along with a Master's degree related to Information and Communication Technologies. A strong academic background is expected in mathematics, programming in a high-level language, and machine learning - Academic record with an average grade > 7 (on a 10-point scale) - Proven skills in programming

Application Materials 1. Full Curriculum Vitae 2. A brief reference letter/Email from a recommender 3. Certified copies of academic transcripts and degree certificates 4. A motivation letter explaining your suitability for this position

Applications will be assessed strictly based on eligibility and fit. Final decisions will be made after an online interview. IMPORTANT: Please consider the short time to apply (there will be time to fix errors after deadline, but CV must be presented and it will NOT be possible to alter any original content, only format).

Key Dates - Application deadline: 13/07/2025: PLEASE CONSIDER OFFICIAL IS 23:59h July 15th 2025 - Fellowship duration: 48 months - Expected start date: September 1st 2025

Submission Please send your application as a single PDF file to: - Prof. J. C. San Miguel-Avedillo juancarlos.sanmiguel@uam.es - Prof. J. Marugï¿½n-Lobï¿½n: jesus.marugan@uam.es

For more information on FPI-UAM grants (Spanish): https://www.uam.es/uam/investigacion/oferta-empleo/contrato-predoctoral-ia-2025 Jesus Marugan Lobon <jesus.marugan@uam.es>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

MartinLutherU Halle-Wittenberg Two Symbiosis

The Faculty of Natural Sciences I - Biosciences, Institute of Biology, at Martin Luther University Halle-Wittenberg is seeking a part-time (65 %)

Research Assistant/ PhD Student (m-f-d)

for a fixed term of 3 years, starting from 01.10.2025 or at earliest convenience.

Remuneration will be determined based on job duties and responsibilities and will be aligned with the fulfill ment of listed personal requirements, up to pay grade E13 under the TV-L (Tarifvertrag für den Öffentlichen Dienst der Länder 'German Public Service Pay Agreement for the Federal States'.

The group "Evolution and Biodiversity" at MLU works on symbioses of insects, using various model systems and methodological approaches. In this DFG funded project, the aim is to comprehensively and comparatively characterize the microbial symbiont communities of psyllids (jumping plant lice). This includes genomic and metabolic approaches that will highlight host-symbiont coevolution. A particular focus will be the impact of shifts in feeding on symbiont communities.

Job Responsibilities: - Planning and implementation of collection trips in Germany and abroad - Morphological and molecular identification of jumping plant lice species - Genomic characterisation of bacterial symbiont communities - Metabolomic characterisation of psyllid host plants - Bioinformatic and statistical analysis of the data obtained - Coordination of the project with project partners in Germany and abroad - Presentation of the results in the form of scientific conference contributions and publications

Requirements: - M.Sc. in Biology or similar discipline - Proven experience in at least one of the following areas: molecular biology (e.g. DNA extractions, PCRs, qPCRs), bioinformatics (e.g. genome assembly, read mapping, working in a UNIX environment), entomology (e.g. taxonomic knowledge of jumping plant lice or other insect groups, experience in collecting trips) - Interest in the ecology and evolution of insect symbiosis - Very good command of written and spoken English - Ability to work in a team, initiative and communication skills

We offer: - an inclusive, respectful, and collaborative work group in which diversity is an essential component of everyones success - an exciting project with varied methodological approaches, and lots of room for developing as a person and scientist - public service employment with remuneration according to the Tarifvertrag der Länder (TV-L) (Collective Agreement for the Public Service) including an annual special payment and a company pension - 30 days of annual vacation plus additional days off on December 24 and 31 - a family-friendly, diversity-oriented, and intercultural work environment at a certified family-oriented uni versity, including holiday childcare, a health management framework to promote and maintain good health, as well as a broad university sports program - the opportunity to participate in diverse social communities (e.g. university sports teams, university choir or university orchestra) - reduced-price meals in the cafeterias of the Studentenwerk (Student Services) Halle

Applications from disabled persons, including those of equal status (as certified by the Bundesagentur für Arbeit / Federal Employment Agency), will be given preferential consideration if they are equally suitable and qualified. Women are strongly encouraged to apply. Applications from individuals of all nationalities are explicitly welcome. Applicants with a degree that was not obtained at a German university must submit a Statement of Comparability for Foreign Higher Education Qualifications from the Central Office for Foreign Education (ZAB) (https://www.kmk.org/zab/central-office-for-foreign-education) as proof of equivalence upon conclusion of the employment contract. You can find ways to apply for a financial grant for this under: https://www.anerkennung-in-deutschland.de/html/de/pro/anerkennungszuschuss.php# . If you have any questions, please contact Jun.-Prof. Dr. Michael Gerth, Email: michael.gerth@zoologie.uni-halle.de.

Please send your application, including Reg. No.: 5-7588/25-D, with a CV and letter of motivation until 18.08.2025 via email to Prof. Dr. Michael Gerth, Email: michael.gerth@zoologie.uni-halle.de

This job posting is subject to potential budgetary restrictions. Application costs will not be reimbursed by Martin Luther University. Application documents will only be returned if a sufficiently stamped envelope is enclosed. Electronic applications are welcome.

—

The Faculty of Natural Sciences I - Biosciences, Institute of Biology, at Martin Luther University Halle-Wittenberg is seeking a part-time (65 %)

PhD Student (m-f-d)

— / —

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

---

MontanaStateU SwiftFoxGenomics

MSc Assistantship ÂC Genetics and Movement Ecology of Swift Fox Following Establishment of a Translocated Population.

Department of Ecology, Montana State University

Smithsonian Institution National Zoo and Conservation Biology Institute

Fort Belknap Fish and Wildlife Department

We are seeking one MasterÂÂs student to work in collaboration with Montana State University, Smithsonian Institution National Zoo and Conservation Biology Institute, and Fort Belknap Fish and Wildlife Department on a research project investigating the genetics and movement ecology of swift foxes located on the Fort Belknap Indian Reservation in northern Montana. This project aims to assess genetic diversity, gene flow, kinship, dispersal, and home ranges of a newly established population of swift foxes reintroduced to the study site following translocation efforts during 2020-2023. Fieldwork is expected to include camera-based surveys to detect foxes, combined with live-trapping efforts to collect genetic samples and deploy tracking collars. The study site consists of a remote grassland habitat primarily occurring on lands owned and managed by the Fort Belknap Indian Community.

The student will begin by September 1, 2025 as an intern with the SmithsonianÂÂs Great Plains Science Program in order to gain experience with the study system and survey protocols from other ecologists assisting with the project. The student will start classes on campus at Montana State University (Bozeman, MT) in Spring 2026. The student will be supported by a combination of internship stipends, Research Assistantships, and Teaching Assistantships. This will include a stipend of ~$2,000/month during the Fall 2025 internship phase and a stipend of ~$2,400/month, plus tuition, tuition fees, and health insurance once the student is enrolled at Montana State University starting January 2026. Housing will be provided while in the field. The student will pursue a 2-3 year MSc at Montana State University in the Department of Ecology (https://www.montana.edu/ecology/), co-advised by Dr. Justine Becker (https://www.beckerecologylab.org/) and Dr. Ethan Linck (https://elinck.org/). The student will also work in close collaboration with Smithsonian Research Biologist/Ecologist Dr. Nucharin Songsasen and Jesse Boulerice, as well as members of the Fort Belknap Indian Community.

Required Qualifications: - B.S. in wildlife science, ecology, zoology, or closely related field - Average GPA of 3.0 in biology courses; 3.0 average in courses taken during the junior and senior years; and 2.5 average in chemistry, physics and mathematics courses - A strong work ethic, drive, and motivation to succeed - Aptitude for modelling and quantitative ecology / evolutionary biology - Aptitude or interest in scientific programming and bioinformatics - Strong verbal and written communication skills - Experience in field-based wildlife research, preferably in remote grassland ecosystems. - Experience in basic laboratory techniques. - Ability to work independently and as a productive member of a research team

Preferred Qualifications: - Experience programming in R and conducting statistical analyses - Background or interest in conservation, population, or evolutionary genetics / genomics, movement ecology, and animal behavior - Experience working and communicating with wildlife management agencies, tribal organizations, and the public - Experience trapping and handling small to medium-sized mammals - Experience in a wet lab environment and/or with the handling and processing of biological samples - Experience in leadership roles, especially associated with leading field crews

Start Date: September 1, 2025

Application Deadline: July 15th 2025.

To Apply: Please send the following materials via email with ÂÂ°Swift Fox MSc AssistantshipÂÂ± as the subject line to Justine Becker (justine.becker1@montana.edu) and Ethan Linck (ethan.linck@montana.edu): (1) cover letter describing the applicants qualifications, career goals, and academic interests, (2) resume/CV with contact information for references, and (3) unofficial copies of transcripts.

Ethan Linck, Ph.D. Assistant Professor Department of Ecology Montana State University https://elinck.org/ “Linck, Ethan” <ethan.linck@montana.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

NTNU Trondheim Norway PopulationBiology

Phd position in Population Biology A fully-funded PhD position in Population Biology is available at the GjÃrevoll Centre for Biodiversity Foresight Analyses (https://www.ntnu.edu/gjaerevoll) at the Norwegian University of Science and Technology (NTNU).

The PhD position is associated with the Advanced Grant project “Eco-Evolutionary Rescue of Fragmented Populations” funded by the European Research Council and NTNU, with an overall aim of providing new understanding of factors affecting the viability of small populations in nature. The primary focus of the PhD will be to analyse and parameterize models describing the ecological and evolutionary dynamics of small and fragmented populations, and how the risk of extinction is affected by changes in the environment such as expected alterations of the climate and loss of critical habitat types. The primary model system for examining the validity of the models will be a unique long-term individual-based data set on house sparrows at the coast of Helgeland in Northern Norway.

The PhD position provides an exciting opportunity to gain broad basic research experience and expertise in evolutionary ecology under a conservation biology context, while working in an interdisciplinary research environment. The successful candidate will acquire broad training in the necessary research skills, and the position will suit a candidate who is motivated to undertake high-level research in the interface between different research disciplines. The three-year position includes research time as well as course components corresponding to half a year of studies. There will also be opportunities to contribute to fieldwork in beautiful nature.

The position will be hosted within a dynamic research group based at NTNU, with strong collaborative links to many internationally leading research groups nationally and abroad. There will be opportunities for international mobility to the collaborating groups, and for conference and workshop participation.

The main supervisor will be Professor Bernt-Erik SÃther (GjÃrevoll Centre, NTNU), and co-supervisors will be Dr Yimen Araya-Ajoy (Department of Biology, NTNU) and Professor Henrik Jensen (Department of Biology, NTNU).

Application deadline is August 15th.

Read more about the position and how to apply here: https://www.jobbnorge.no/en/available-jobs/-job/281322/phd-position-in-population-biology Dr. Henrik Jensen Professor, Deputy of Research Department of Biology and the GjÃrevoll Centre NTNU NO-7491 Trondheim NORWAY

E-mail: Henrik.Jensen@ntnu.no Mobile: +47 91897064

Personal web: https://www.ntnu.edu/employees/-henrik.jensen Centre web: https://www.ntnu.edu/web/-cbd/english Henrik Jensen <henrik.jensen@ntnu.no>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Paris NematodeGeneticAssimilation

A PhD position is open in the Teotónio lab at the Institut de Biologie de l'Ãcole Normale Supérieure (IBENS), in Paris, France (https://www.ibens.bio.ens.psl.eu/-?rubrique28); as part of a collaborative research project between the host lab and that of Christian Braendle at the Institut de Biologie de Valrose in Nice, France (http://ibv.unice.fr/research-team/braendle/).

Genetic assimilation describes the evolutionary process during which an environmentally-induced phenotype becomes a genetically encoded phenotype. This important concept remains controversial because the molecular mechanisms of genetic assimilation are rarely understood. This project will characterize genetic assimilation of environmentally induced egg retention in the nematode Caenorhabditis elegans at the molecular level.

We will use genome-wide association mapping to identify molecular variants involved in genetic assimilation during experimental evolution. To study the functional consequences of these variants on egg laying, we will employ CRISPR-Cas9 gene editing, tissue-specific reporter genes, and mosaic analysis. The evolutionary history of identified variants will be tracked across replicate populations over 100 generations of experimental evolution. Finally, we will extend our molecular analyses from experimental to natural populations to understand how these variants influence the environmental sensitivity of the egg-laying circuit in wild C. elegans.

Candidates are expected to have a master's degree or equivalent in evolutionary biology and an excellent understanding of the fundamental problems of quantitative genetics and population genetics, including QTL and GWAS mapping. Candidates with experience in model organism handling, computer programming, experimental evolution and statistical analysis of large data sets are preferred. The PhD project may involve the use of genetic transformation methods, so experience with molecular and developmental biology techniques is a plus. The PhD student will be expected to conduct full-time independent research in the Teotónio lab.

The PhD position, including social benefits, is funded by the National Agency of French Research (ANR MolAssim) for three years, with a potential one-year extension. Successful applicants can start their PhD as soon as November 2025.

To apply, please send a single PDF file containing your CV, a letter of motivation, and the contact information of two referees to Henrique Teotónio (teotonio@bio.ens.psl.eu). Use the subject line: PhD_MolAssim_YOURNAME. Informal inquiries are welcome. Applications will be accepted until 19 September 2025, and shortlisted candidates will be interviewed (in person or online) during the week of 29 September - 3 October.

Relevant background findings: Dey et al. 2016. doi:10.1371/journal.pbio.1002388.s008 Noble et al. 2017. doi: 10.1534/genetics.117.300406 Teotónio et al. 2017. doi: 10.1534/genetics.115.186288 Vigne et al. 2021. doi: 10.1126/sciadv.abd9941 Mignerot et al. 2023. doi:10.7554/elife.88253 Fausett et al. 2023. doi:10.1038/s41467-023-38527-0

Henrique Teotónio, Professor Experimental Evolutionary Genetics Institut de Biologie de l'ENS 46 Rue d'Ulm 75005 Paris, France https://www.ibens.ens.fr/?rubrique28 Henrique Teotónio <teotonio@bio.ens.psl.eu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

TrentU PlantEvolution

PhD project - Eco-evolutionary and conservation dynamics of desert succulents (Lithops spp.) from southern Africa

The Integrative Wildlife Conservation lab at Trent University, in collaboration with the Lithops Research and Conservation Foundation, is offering a unique PhD project on the eco-evolutionary and conservation dynamics of Lithops spp., a genus of small succulent plants occurring in isolated colonies across desert landscapes in southern Africa. In the wild, Lithops are susceptible to human collection, habitat loss, and climate change, with many populations and species currently subject to high extinction risk. There are important knowledge gaps related to Lithops phylogeny and ecology that are currently impacting rigorous conservation status assessment and protection. Trent University is among only a handful of facilities worldwide housing Lithops plants and seeds originating from wild colonies, providing a truly unique opportunity to address integrative questions related to evolution, population genetics, and conservation biology in a controlled, rigorous and impactful context. The PhD project may include investigations related to genome sequencing, phylogenetics, evolutionary divergence and linkage analysis, and adaptation to harsh environmental conditions, and the candidate will have the opportunity to develop specific research questions based on their interest and expertise.

Successful candidates MUST have an MSc in Biology, Genetics, Conservation, or related field, demonstrated evidence of peer-reviewed publications, strong lab and field skills, and an interest in working collaboratively within a large and diverse research group. Additional desirable qualifications include DNA sequencing, bioinformatics and GIS skills.

To apply, send a cover letter, curriculum vitae, unofficial academic transcript, and contact information for 3 references to: Dennis Murray (dennismurray@trentu.ca).

For additional details, see www.dennismurray.caand www.lithopsfoundation.com . The position will be filled as soon as a suitable candidate is found.

Dennis Murray CRC in Integrative Wildlife Conservation, Bioinformatics, and Ecological Modeling Director, Bioenvironmental Monitoring and Assessment graduate program Trent University Peterborough, ON CANADA

www.dennismurray.ca dennis murray <dennismurray@trentu.ca>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UArkansas ArthropodBiodiversityEvolution

PhD position in Arthropod Biodiversity & Evolution University of Arkansas, Fayetteville, Arkansas, USA

The Forest Ecology & Health Lab at the University of Arkansas is seeking a student interested in pursuing a PhD studying arthropod biodiversity, evolution, and forest ecosystem function. The focal project will be to sample arthropods from high-elevation sites in the Ouachita Mountains of Arkansas and Oklahoma, employ high-throughput DNA barcoding methods to uncover biodiversity patterns, and relate those patterns to environmental variables and ecosystem function. Prospective applicants should have research interests in entomology, ecology, and evolutionary biology, and should have strong field, lab, and analytical skills. Applicants with previous experience using molecular techniques (e.g., PCR, NGS library preparation, metabarcoding, etc.) and bioinformatics are preferred. Experience with GIS and/or R is also desirable.

Financial support will be provided through a combination of teaching and research assistantships. Assistantships come with a full tuition (not fees) waiver and 67% of the student health insurance paid for by the university. The selected applicant would need to be admitted to a PhD program at the University of Arkansas for the Spring 2026 semester, which begins January 12, 2026. Students admitted to a PhD program may also be eligible for a U of A Doctoral Fellowship that adds to their assistantship stipend for 4 years. More information about these fellowships can be found at: https://graduate-students.uark.edu/cost-and-funding/index.php .Note that applications for these fellowships require the GRE General Test even if it is not required for admission to a graduate program. Applicants who would be competitive for a doctoral fellowship will be viewed favorably. Continued support will be contingent on satisfactory performance and progress.

Research in the Forest Ecology & Health Lab uses field experiments and naturally occurring environmental gradients to examine how biogeochemistry and nutrients impact community structure and trophic interactions among soil arthropods and ant species primarily in forest ecosystems. This project is in collaboration with Dr. Donald Shepard in the University of Arkansas, Department of Biological Sciences, and Dr. Ashley Dowling in the University of Arkansas, Department of Entomology and Plant Pathology. More information about their research and labs can be found at: https://shepardlab.wixsite.com/home and https://adowling.hosted.uark.edu/index.html. Information about the PhD in Entomology program and its requirements is provided here: https://enpl.uark.edu/-programs/phd-program.php. Depending on their interests and goals, the selected applicant may have the option to apply through the PhD in Biology program: https://biology.uark.edu/academics/graduate/-index.php . To apply, send an email to Dr. Natalie Clay (nclay@uark.edu) that includes as attachments: 1) a cover letter expressing your interest and highlighting your qualifications for the position as well as your future career goals, 2) your curriculum vitae, 3) an unofficial copy of your college transcripts, and 4) names and contact information for three professional references. To receive full consideration, submit your application by August 1, 2025; however, applications will be considered until the position is filled. Note: the selected applicant will still need to apply to and be accepted into a PhD program at the University of Arkansas. The application deadline for Spring 2026 admission is September 1 for Entomology and October 1 for Biology. Please email Dr.

Clay (nclay@uark.edu) with any questions or concerns about the project/position.

Natalie A. Clay Associate Professor Department of Entomology and Plant Pathology University of Arkansas Fayetteville, AR 72701, USA Email: nclay@uark.edu Lab website: https://natalieclay.weebly.com/ Don Sheppard <dshep@uark.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UGoettingen 11 EvolGenomics

At the University of Gï¿½ttingen -Public Law Foundation-, GRK 2984 Evolutionï¿½re Genomik: Folgen biodiverser Fortpflanzungssysteme, there are 11 positions as

Doctoral Researchers in Evolutionary Genomics (all genders welcome) Entgeltgruppe 13 TV-L/65%

to be filled. Starting date is 1/1/2026. The positions are limited to 31.12.2028.

These are qualification positions for junior researchers pursuing a PhD degree for three years, with a possible prolongation until 31.12.2029. The goal of our research training group is to analyze the evolution of genomes in sexual and asexual organisms in animals, plants, fungi, and microorganisms. Our collaborative efforts will provide a better understanding of the "paradox of sex" in nature. We will study the evolution of nuclear genomes to test hypotheses of genome erosion and functional changes with asexuality, the interaction of nuclear-organelle genomes under different modes of reproduction, and horizontal gene transfer via viruses between prokaryotes and prokaryotes-eukaryotes. We will further include projects to develop new methods for analysis of chromosome architecture and models for genome analysis under different mutation-selection scenarios.

Please see further details on the PhD projects at our homepage: https://uni-goettingen.de/de/687607.html. Please regard only the PhD 2 positions (1st positions filled) and indicate your preferred project(s) (up to three, in order of preference) in your motivation letter.

Successful candidates will have - an outstanding Master's degree (or equivalent) in Biology, with a focus on evolutionary genomics, - experience in molecular lab work and/or in bioinformatics and statistical genomics methods - proven background in theory related to evolution of reproductive systems, - excellent command of scientific English (oral and written, min. equivalent to C1). We also expect successful candidates to be active team players in the RTG.

Your application must include a letter of motivation, CV, lists of publications, transcripts of your Master's degree or equivalent, and certificates of English language proficiency as pdf files.

We offer an excellent research team on the Gï¿½ttingen Campus, including a Center for National High Performance computing and an AI service center. Our training concept includes seminar and conference presentations, methods courses and workshops, and teaching. Experience with innovative methods, networking and publishing within the RTG team will be gained.

The University of Gï¿½ttingen is an equal opportunities employer and places particular emphasis on fostering career opportunities for women. Qualified women are therefore strongly encouraged to apply in fields in which they are underrepresented. The university has committed itself to being a family-friendly institution and supports their employees in balancing work and family life. The University is particularly committed to the professional participation of severely disabled employees and therefore welcomes applications from severely disabled people. In the case of equal qualifications, applications from people with severe disabilities will be given preference. A disability or equality is to be included in the application in order to protect the interests of the applicant.

Please upload your application in one pdf file including the usual documents until 1/9/2025 on the application portal of the university using this link: http://obp.uni-goettingen.de/de-de/OBF/Index/75985. For more information get in touch with Elvira Hï¿½randl directly via E-Mail: elvira.hoerandl@biologie.uni-goettingen.de, Tel. +49 551 39 28540 .

Please note: With submission of your application, you accept the processing of your applicant data in terms of data-protection law. Further information on the legal basis and data usage is provided in the Information General Data Protection Regulation (GDPR)

"Menster, Antje" <antje.menster@uni-goettingen.de>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

ULeiden InsectGenomics ClimateChange

PhD position: Genomics and Functional Genetics of Temperature-dependent Egg Development Time in Insects **Application deadline: July 8, 2025**

What? 4-year full-time PhD position at Leiden University, the Netherlands, with the goal to identify universal genes involved in the temperature sensitivity of insect egg development. To be able to predict which wild insect populations harbor sufficient genetic variation to effectively respond to selection by climate change.

Preferred start date: 1 October 2025

Why? Insect species that overwinter as eggs are particularly vulnerable to climate change, as egg development time strongly depends on temperature. However, the genetic underpinning of egg development time in insects is poorly known, making it difficult to assess population adaptive potential.

Who? You will address this knowledge gap in the group of Maurijn van der Zee at Leiden University, the Netherlands, as part of an NWO ENW M2 grant funded in collaboration with the Department of Animal Ecology at the Netherlands Institute of Ecology (NIOO-KNAW).

How? You will use functional genetics approaches (RNAi, CRISPR/Cas9) and genomics approaches (RNAseq, WGS) - in both the model system Tribolium castaneum and in wild populations from 12 different insect species (bugs, butterflies, and grasshoppers) - to find universal genes involved in the temperature sensitivity of egg development across insects.

Requirements MSc in Biology or related field Experience or affinity with analyses of genomic and transcriptomic sequencing data Wet-lab experience with, or eager to learn, molecular biological techniques such as molecular cloning, qPCR, RNAi, and CRISPR/Cas9 Interested to work with insects Strong interest in ecology and evolutionary developmental biology (evo-devo) Ability to work independently, but also to collaborate in an academic research team Skills to communicate scientific data in spoken and written English

Apply now! For a full description of the position and how to apply, see: https://www.universiteitleiden.nl/-vacatures/2025-nl/q2/15758phd-genomics-and-functional-genetics-of-temperature-dependent-egg-development-time-in-insects Or contact Dr. Maurijn van der Zee (m.van.der.zee@biology.leidenuniv.nl) for more information.

"Van Dis, Natalie E" <natalie.vandis@helsinki.fi>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UMontpellier WheatGenetics

PhD Project Proposal: From root to field: unraveling the ecological and genetic bases of genotype interactions to design resilient durum wheat variety mixtures

Keywords: Durum wheat, variety mixtures, root architecture, plant-plant interactions, functional ecology, quantitative genetics, QTL, climate resilience, drought stress

Abstract: Durum wheat is a key crop in Mediterranean regions, increasingly affected by drought stress due to climate change. This PhD project aims to understand how root system architecture, particularly root branching intensity, shapes interactions between genotypes and determines the performance of durum wheat variety mixtures.

By combining functional ecology and quantitative genetics, the project will identify the genetic basis of root traits and develop predictive tools to design more resilient and productive varietal mixtures.

Context: Durum wheat plays a critical role in global agricultural systems, particularly in semi-arid regions, due to its adaptability, economic significance, and contribution to food security (Sissons 2016). Like other crops from these regions, durum wheat is already experiencing yield reductions caused by increased temperatures and reduced water availability (Rao 2011). Diversifying durum wheat fields by introducing mixtures of varieties instead of mono-genotypic stands could be a solution to improve resource use efficiency through positive interactions between varieties (Barot et al. 2017). Our group has identified several Quantitative Trait Loci (QTLs) associated with Root Branching Intensity (RBI) in durum wheat (Triticum turgidum ssp. durum). Our preliminary data indicate that these candidate QTLs associate with varietal mixture performance under contrasted environmental conditions, suggesting that RBI genes could be involved in plant-plant interactions and could thus be used as a predictive tool to design varietal mixtures. However, optimizing varietal mixture composition remains a major scientific challenge (Borg et al. 2018; Wuest et al. 2021), primarily because the mechanisms underlying varietal interactions are poorly known.

Objective: The overarching objective of this thesis is to use plant-plant interactions to enhance the resilience of durum wheat to adverse abiotic conditions, especially drought. More specifically, we aim to develop a better understanding of how plants interact belowground to design assembly rules for varietal mixtures with optimal composition to face water limitations.

Methods: In this PhD project, we will combine functional ecology and quantitative genetics to uncover the genetic determinants of root architectural traits and assess their effect on mixture performance. In contrast to previous trait-based approach, our interdisciplinary approach will allow scale down to the genetic levels, potentially leading to a better understanding of the mechanisms underlying varietal interactions under contrasted resource conditions, and providing direct outputs for plant breeding such as molecular markers that could be used to design climate-resilient and genetically diverse durum wheat varieties.

This work will be organized in three major tasks:

- Detailed root phenotyping on a panel of 180 durum wheat genotypes, conducted under both controlled conditions and in the field, with a specific focus on root branching.

- Genetic analyses (GWAS) to identify the QTLs involved in root system architecture and their interaction with water availability.

- Variety mixture experiments under different water availability scenarios to assess agronomic performance and decipher the ecological mechanisms (complementarity, competition) related to root traits.

To conduct the experiment, the partners will benefit from the collaboration and the expertise of the “Terrain d’Expérience” experimental platform from UMR CEFE for the greenhouse and the “UE DIASCOPE” form the INRAE for the field experiment.

Expected results:

The first expected result is a dataset of root traits and root trait plasticity in response to water stress, measured using standardized protocols in a wide range of durum wheat varieties. Such high-quality dataset will fill the gap in the low representation of root traits in currently available crop trait databases (e.g., CropTraits). This dataset will be used to study root trait diversity and trait covariations between the above and belowground compartments, and how these are affected by resource availability, which will be published in the first scientific article.

The second result will be a characterization of the genetic architecture of architectural root traits in durum wheat and an exploration of the interaction between these genetic factors and durum wheat growth environment, notably through water availability management.

The last result will be the experimental assessment of the benefits of varietal mixtures, especially under low water availability

— / —

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

---

UNottingham HarvestMouseConservationGenetics

MRes Opportunity

Conservation genetics of the UK Harvest Mouse

Supervisors:Dr. Ylenia Chiari, University of Nottingham, School of Life Sciences

Collaborator:Prof. Matyas Liptovszky, University of Nottingham, School of Veterinary Medicine and Science

Start date:February 2026

We are offering an MRes research opportunity to join a collaborative project investigating the genetic health of the UK’s native harvest mouse (Micromys minutus), a species of high conservation concern. This work is part of a broader initiative aimed at informing the conservation and management of both wild and captive populations.

In this project, the MRes student will:

- Work with various sample types (hair, faeces, tissue from museum specimens, blood) preserved under different conditions to identify the best sample type and preservation method for DNA analyses, and provide guidelines for handling different tissue types. - Analyse mitochondrial DNA (and if there is time microsatellite data too) from wild and captive populations across the UK.

The student will benefit from working within an interdisciplinary team that includes evolutionary biologists, zoo veterinarians, and conservation professionals. Supervision will be provided in conservation genetics and wildlife health, with opportunities to contribute to a scientific publication.

We are seeking a highly motivated student with a BSc (2:1 or above) in biology, zoology, genetics, or a related discipline, a strong interest in conservation and molecular biology, and a willingness to work both independently and as part of a team. Some lab experience is desirable, but full training will be provided.

The position is open to National and International students. However, tuition fees are different for home or international students.

The Chiari Lab (www.yleniachiari.it) works on causes and consequences of morphological and physiological variation in reptiles and on conservation biology.The Lab is committed to promoting and supporting diversity and a multicultural environment and we encourage underrepresented students to apply.

This is a self-funded MRes. Prospective students should send a brief description of their research interests and past experience (max 500 words), along with their CV (including the names of two references), to Dr. Ylenia Chiari at Ylenia.Chiari@nottingham.ac.uk.

Ylenia Chiari, PhD

Associate Professor

My name is pronounced

EE-len-ee-ah Kee-AH-ree

(hear name)

EYlenia.Chiari@nottingham.ac.uk

University of Nottingham,

School of Life Sciences Life Sciences Building

University Park Nottingham

UK

www.yleniachiari.it ChiariLab - YouTube

Ylenia Chiari <Ylenia.Chiari@nottingham.ac.uk>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

USheffield AnimalSignals

Fully-funded PhD opportunity for UK students at the University of Sheffield: deadline 15 Sept 2025

Perceptual bias and the evolution of organism communication signals https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=186190 Project overview:

The natural world is full of visually striking organism communication signals, from the vibrant colours of fish and butterflies to the elaborate courtship displays of birds and other animals. Over decades biologists have made excellent progress in understanding the communicative functions of such signals (e.g. attracting mates, defending territories or warning predators), but explaining the specific design of signalling traits (i.e. the arrangement of a signal's component features) has proved frustratingly difficult.

A key hypothesis that could explain these observations is that biases in the perceptual systems used by animals (including humans) to detect and process sensory information have played an important role in shaping communication signal evolution. In particular, it has been argued that evolution should favour signal designs that can be processed efficiently i.e. with minimal metabolic cost by the perceptual systems of other organisms. This idea, referred to as 'processing bias', implies that animal signal evolution and perhaps even human aesthetic preferences for certain organismal signals may both be better understood by studying signal evolution through the lens of information processing by signal receivers.

This PhD project will test fundamental predictions for the role of processing biases in shaping organism visual signal evolution and human aesthetic preferences for them using birds as a model system. Capitalising on recent advances in computational neuroscience and machine learning, specific objectives are to (1) quantify common design features of avian visual communication signal features, (2) use computational models to estimate visual processing efficiency of avian signalling vs. non-signalling traits and (3) investigate connections between visual processing efficiency and human aesthetic judgements of avian visual phenotypes.

Supervisors:

Dr Chris Cooney (Sheffield), Prof Gavin Thomas (Sheffield), Dr Julien Renoult (CNRS Montpellier). Lab website: https://www.cooneylab.co.uk/ . What we're looking for:

We welcome applications from candidates from any relevant background (e.g. ecology, evolution, computer science, neuroscience) to tackle this novel and exciting opportunity. Training will be provided in specific analysis techniques and the successful applicant will acquire advanced computational and communication skills that are highly transferable. The student can expect to work closely with all supervisors, as well as other project team members including a PDRA and research technician. In addition to the objectives outlined above, there will be ample opportunity for the student to develop their own research questions over the course of the project.

The student will join a vibrant community of academic staff and postgraduate students within the Ecology and Evolutionary Biology cluster within the School of Biosciences at the University of Sheffield, where extensive PhD training and development are available. There will also be opportunities to engage with the public at large to disseminate the student's research, for example via exhibitions at local (Weston Park Museum) and national (Natural History Museum, London) museums with which the supervisory team already have strong links.

Funding and eligibility:

Fully funded PhD position (3.5 years) via a Leverhulme Trust Research Project Grant. Funding covers stipend (UKRI 2025/26 rate 20,780), tuition fees (UKRI 2025/26 rate 5,006) and research support and training grant (RTSG). Only UK students are eligible to apply.

Apply:

To apply, please submit an application via the University of Sheffield's application portal: https://www.sheffield.ac.uk/postgraduate/phd/apply/applying. Informal enquiries are welcome, please contact: c.cooney@sheffield.ac.uk.

NERC Research Fellow School of Biosciences University of Sheffield www.cooneylab.co.uk Chris Cooney <c.cooney@sheffield.ac.uk>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UWesternAustralia MidwaterBiodiversity

Hello Colleagues,

Please help us get the word out about several PhD opportunities at the University of Western Australia dealing with midwater biodiversity and sensory biology.

https://researchdegrees.uwa.edu.au/scholarships/18x834/discovery-in-the-largest-frontier-advance-imaging-and-genomics-of-open-ocean-animals
https://researchdegrees.uwa.edu.au/scholarships/18xyw3/termite-sensory-systems-and-neurophysiology

Many thanks for telling your highly qualified masters and honors students, Karen

Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 osbornk@si.edu http://orcid.org/0000-0002-4226-9257 Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012, Washington, D.C. 20013-7012 USA

Courier Address: Smithsonian Institution, MR 0163, Natural History, West Loading Dock, 10th and Constitution Ave NW, Washington, D.C. 20560

** Due to my schedule, you may get an email outside of your normal working hours. Please do not feel that you need to respond outside of your normal working hours. **

"Osborn, Karen" <OsbornK@si.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Vigo Spain SalmonGenomics

"We are looking for a predoctoral researcher with an interest in Evolution, Archaeology and Artificial Intelligence (AI) to join the OLDSALMO (https://oldsalmo.csic.es) group at the ACUABIOTEC Laboratory of the Institute of Marine Research (IIM-CSIC) in Vigo (Spain). OLDSALMO is an interdisciplinary project on long term genomic changes in exploited salmon populations using ancient and environmental DNA, funded by the ATRAE programme.

We use Atlantic salmon as a study species to develop novel approaches to assess the role of overfishing and climate change in natural population declines. This new position seeks to expand the objectives of the project by developing species identification methods based on image analysis using AI, which will be combined with metabarcoding analysis to test hypotheses related to the long-term temporal changes of exploited fish populations. The project has a close collaboration with Swansea University, the University of Cantabria (International Institute of Prehistoric Research of Cantabria and Evoadapta Group), Harvard University (David Reich's Lab), the Norwegian Institute for Nature Research (NINA) and Environmental Management of Navarra.

What we offer:

A 3-year fully funded PhD contract, starting mid-November or early December 2025Access to cutting-edge facilities and an international research networkInterdisciplinary training at the crossroads of molecular ecology, archaeology, and AIThe chance to contribute to conservation science with real-world applications

What we're looking for:

A BSc and MSc in Biology, Archaeology, or related fields-Basic experience in molecular biology, bioinformatics, and/or AIProgramming skills in R or PythonA collaborative mindset and enthusiasm for interdisciplinary research

How to apply:

Application deadline: September 8th, 2025

Interviews will take place the 12th or 15th of September

The selected candidate will enrol in the Doctoral Program at the University of Vigo in October 2025

For general enquiries contact Sofía Consuegra: sconsuegra@iim.csic.es."

dgarciasouto <dgarciasouto@iim.csic.es>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Jobs

BielefeldU EvolutionAnimalBehaviour

A full-time scientific assistant position (salary scale E13) is available in the Department of Animal Behaviour at Bielefeld University from March 1st 2026 or soon thereafter. The position is available for six (3+3) years, with a possible extension in exceptional cases for another four years. The position is comparable to a Lecturer position in the UK or an Assistant Professor position in the US.

We seek a bright and highly motivated postdoctoral researcher who ideally has several years of postdoc experience in a relevant topic (e.g. animal behaviour, behavioural ecology, population ecology, evolutionary ecology). Extensive experience with genetic and genomic approaches to behaviour and/or tracking data will be a distinct advantage. The scientific assistant will be responsible for developing his or her own research agenda while also significantly contributing to one of the three core model systems of the department (zebra finches in the lab, birds of prey in the field, sea lions in the field). It is expected that he/she will be able to obtain significant third-party research funding. The ideal candidate will be able to work both independently and as part of a multidisciplinary team. The teaching duties of a scientific assistant are 4 hours per week during semesters or 120 hours per annum. In addition, the successful candidate is expected to contribute to the running of the Department of Animal Behaviour which is headed by Oliver Krï¿½ger.

The successful candidate will be based at the Department of Animal Behaviour at Bielefeld University (www.uni-bielefeld.de/fakultaeten/biologie/-forschung/arbeitsgruppen/behaviour). The department is the oldest of its kind in Germany. It offers a stimulating international environment and an excellent research infrastructure including a brand-new building (to be completed in 2025) with state-of-the-art laboratories and offices. The working language of the Department is English. Together with the Evolutionary Population Genetics (Joe Hoffman), Behavioural Ecology (Barbara Caspers) and Evolution (Klaus Reinhold) research groups housed in the same building, there are over 70 scientists and PhD students from a dozen different countries working on related topics in behaviour, ecology and evolution.

Bielefeld is a city of 325,000 inhabitants with an attractive historical centre and easy access to the Teutoburger Wald for hiking and other outdoor pursuits. It offers a high standard of living and is well connected to most major European cities.

To apply for the position, please provide: (i) a letter of motivation including a 3-5-page statement of your research interests, how you would contribute to the core model systems in the department, relevant skills and experience; (ii) a CV including publication list; (iii) names and contact details of three referees willing to write confidential letters of recommendation. All materials should be emailed as a single PDF file to: oliver.krueger@uni-bielefeld.de.

The application deadline is September 10th 2025 and interviews will take place in September/October 2025. The preferred start date is March 1st 2026 but is flexible and will depend on the timeframe of the most qualified applicant. For further information, please browse the webpage of the department or contact Oliver Krï¿½ger via email (oliver.krueger@uni-bielefeld.de) with any informal inquiries.

The University of Bielefeld is an equal opportunity employer. We particularly welcome applications from women and handicapped people. Given equal suitability, qualifications and professional achievement, women or handicapped people will be given preference, unless particular circumstances apply.

“Chakarov, Nayden” <nayden.chakarov@uni-bielefeld.de>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

ClaremontMcKennaC MolecularEvolution

Dear all,

The Kravis Department of Integrated Sciences (KDIS) at Claremont McKenna College (CMC) invites applications for a tenure-track Assistant or Associate Professorship in Biology. We seek candidates whose research uses experimental methods in areas such as cell and molecular biology, molecular genetics, genomics, molecular physiology, and molecular evolution. Techniques of particular interest include gene editing and other genetic engineering methods, 3-D tissue and organoid systems, and single cell -omics.

The position will begin on July 1, 2026. The successful candidate is expected to have completed a Ph.D. in Biology or related areas and postdoctoral training by the time of the appointment. Candidates should also have experience teaching and/or mentoring undergraduate students.

KDIS offers an innovative and transformational Integrated Sciences program that is organized around three challenges: Health (Genomics, Systems Biology, and Health), Brain (Brain, Learning, and Decision Sciences), and our Planet (Climate, Energy, and the Environment). The KDIS faculty have a key role in developing and implementing a program that serves as an incubator for new approaches and fosters a culture of inclusion, creativity, and continuous improvement. The department is housed in the new Robert Day Sciences Center.

The candidate must demonstrate potential for establishing an active research program that involves undergraduate students, as evidenced by a track record of high-quality scholarship and a research statement that outlines a clear plan for their research effort at CMC. The candidate must also demonstrate potential for excellence in teaching through a thoughtful teaching statement and supporting evidence from prior teaching experiences.

The teaching load at CMC is two courses per semester. The candidate will help develop and teach a foundational biology curriculum that will be taken by all Integrated Sciences majors and will include integration with the foundational curriculum in chemistry, physics, and computation. Additional teaching will include upper-division courses in cell biology, genetics, physiology, and/or molecular biology, and other upper-division electives in the candidate's area of expertise in support of the department's three themes, and/or a natural science general education course taken by all CMC students.

Given the College's commitment to cultivating an inclusive educational environment, we seek candidates who can demonstrate a commitment to teaching, mentoring, and inspiring students representing a broad range of socioeconomic backgrounds, political opinions, genders, races, ethnicities, nationalities, sexual orientations, and religions. Moreover, as part of its commitment to? https://www.cmc.edu/the-open-academy, the College values freedom of expression, viewpoint diversity, and constructive dialogue.

Anticipated Annual Salary Range:

$115,000 - $150,000 per year

Applications should include a cover letter; curriculum vitae; research statement; teaching statement that addresses the candidate's ability to teach, mentor, and inspire students representing a broad range of backgrounds (optionally, this can be addressed in a separate diversity statement); evidence of teaching effectiveness such as course evaluations; and three representative peer-reviewed publications (either submitted as part of the application materials or links provided from the CV). Applicants must also submit the names and e-mail addresses of three references; an email request will be automatically sent to them with a link to upload their confidential recommendation letter.

Review of complete applications will commence on September 15 and will continue until the position is filled. Preliminary interviews will be conducted via Zoom.

Claremont McKenna College is a highly selective undergraduate institution ranked among the top liberal arts colleges nationally. It is part of The Claremont Colleges, which also includes Pomona College, Scripps College, Harvey Mudd College, Pitzer College, Claremont Graduate University, and Keck Graduate Institute. The Claremont Colleges consortium constitutes an academic community of more than 9,000 students. Claremont is located 35 miles east of downtown Los Angeles.

Claremont McKenna College is an equal opportunity employer. In a continuing effort to enrich its academic environment and provide equal educational and employment opportunities, the College actively encourages applications from members of historically under-represented groups in higher education.

Apply here: https://webapps.cmc.edu/jobs/faculty/-faculty_opening_detail.php?PostingID=17075 Lars Schmitz, Kravis Professor of Integrated Sciences Email: lschmitz@cmc.edu

Lars.Schmitz@ClaremontMcKenna.edu

(to subscribe/unsubscribe the EvolDir send mail to

— / —

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

---

ClemsonU LabManager MolecularGeneticist

Molecular Lab Manager/Molecular Geneticist (staff position) The Clemson University Genomics and Bioinformatics Facility (CUGBF) Clemson, South Carolina, USA

JOB SUMMARY: A molecular geneticist who will manage the daily operations of the genomics/molecular biology aspect of the CUGBF, including ordering and billing. Plans, oversees staff laboratory personnel, supervises and train students and postdoctoral researchers. Perform other duties as assigned.

JOB DUTIES: 55% - Essential - Research Activities: Designs, performs technical molecular biology experiments, including but not limited to: DNA/RNA isolation, cDNA prep, RNA/DNA library preparation, Illumina short-read NGS, qPCR, PCR, etc. Performs basic bioinformatics tasks such as de-multiplexing, trimming NGS reads, etc. Monitors quality control of data generation and oversees/ runs the all equipment in the NGS sequencing pipeline. 25% - Essential - Lab Management: Manages lab ordering, invoicing, accounting/budgeting, record keeping and generation of quotes. Assists in maintaining regulatory compliance. Manages lab inventory and records. Maintains/updates social media/website and helps organize seminars/workshops. Oversees day-to-day maintenance of lab space, facilities, and equipment. 20% - Essential - Personnel Oversight and training: Supervises CUGBF molecular biology personnel, and trains students, staff, and faculty to carry out genomic and molecular biology experiments and protocols. Conducts in-service workshops on how to carry out genome level molecular biology

MINIMUM REQUIREMENTS: Education - Bachelor's Degree - Microbiology or medical technology and experience in a laboratory setting related to the area of employment; or a bachelor's degree in the natural sciences with academic credits in biology and experience in a laboratory setting related to the area of employment. A doctorate in microbiology may be substituted for the required work experience.

Work Experience 0+ years

PREFERRED REQUIREMENTS: Education - Doctoral / Professional Degree - Biology or related field (Chemistry, Microbiology, Biochemistry, Genome Science)

Work Experience 4+ years of high level genomics and molecular biology work including next generation library preparation and basic computer skills

WORK SCHEDULE: Standard Hours: 37.5

COMPENSATION INFORMATION: Anticipated Salary Range: $57,334 - $61,000

APPLICATION DEADLINE: July 23, 2025 at 11:59pm EST

APPLICATIONS: https://jobs.clemson.edu/psc/ps/JOBS/EXT/c/HRS_HRAM_FL.HRS_CG_SEARCH_FL.GBL?Page=HRS_APP_JBPST_FL&Action=U&FOCUS=Applicant&SiteId=1&JobOpeningId=109786&PostingSeq=1 Inquiries about this position may be directed to: Dr. Christopher Parkinson, Director, Clemson University Genomics and Bioinformatics Facility viper@clemson.edu

Rooksana Noorai <rooksan@clemson.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

Ecuador 6mnth BiodiversityConservation

Call for Applications:

Evolutionary Genetics for Biodiversity Conservation.

The National Institute of Biological Resources of Korea (NIBR) invites applications for a highly motivated and experienced researcher to contribute to the project entitled "Establishment of the National Data Bank of Biodiversity in Ecuador". This position presents an exciting opportunity to contribute to advanced evolutionary and biodiversity conservation research through genetic resource data analysis, within a dynamic national research network in Ecuador, South America.

Position: Researcher in evolutionary genetics for biodiversity conservation.

Location: National Institute of Biological Resources of Ecuador (INABIO), Quito, and 7 additional regional partner institutions (Urcuqui, Sangolgui, Tena, Loja, Santa Elena, Pichincha, Galapagos). Ecuador

Duration: Six months

Salary & Benefits:

- The total salary is KRW 31,680,000 (6 months, approx. USD 22,107).

- Accommodation and other expenses are subject to separate negotiation.

- The final amount may vary with exchange rate fluctuations.

- Additional benefits will be discussed if applicable.

Responsibilities:

- Lead and contribute to research projects focused on evolutionary genetic resource data analysis using metagenomic approaches.

- Transfer knowledge, capacities and training to local researchers at INABIO and several associated research institutions.

- Develop and implement bioinformatics pipelines to process, analyze, and interpret genetic resource data for biodiversity conservation.

- Contribute to the development of biodiversity conservation strategies for Ecuador through genetic resource data analysis.

- Participate in biodiversity monitoring and genetic resource data analysis processes.

- Collaborate with a network of universities and research institutes across Ecuador.

- Prepare and present research findings in scientific publications and conferences.

- Contribute to the training and mentoring of students and technicians.

Qualifications:

- Ph.D. in Bioinformatics, Computational Biology, genetics, Microbial Ecology, environmental DNA study or a related field.

- A Master's degree or higher in bioinformatics, biology, genetics, molecular biology, or biodiversity-related fields.

- At least 8 years of research (including research as a graduate student) or professional experience in the field of biodiversity.

- Proven experience in bioinformatics research, including metagenomic analysis.

- Minimum of two (2) years of postdoctoral or equivalent research experience in genetic resource data analysis.

- Strong expertise in bioinformatics tools and programming languages (e.g., R, Python, Perl).

- Excellent communication skills in English (both written and oral).

- Demonstrated ability to work independently and collaboratively in a team environment.

- Strong publication record in peer-reviewed journals.

Desired Skills:

- Experience in developing biodiversity conservation guidelines based on genetic resource data.

- Knowledge of Ecuadorian biodiversity and genetic resources.

- Familiarity with biodiversity monitoring and genetic resource data analysis protocols.

- Experience in handling and analyzing large-scale genetic resource datasets.

Proposed Tasks and Products:

- Development of biodiversity conservation strategies for Ecuador through genetic resource data analysis in an evolutionary context.

- Implementation of biodiversity monitoring processes.

- Development of robust bioinformatics pipelines for genetic resource data analysis.

- Publications in high-impact scientific journals.

- Presentations at national and international conferences.

- Technical reports and data summaries.

Working Environment:

The successful candidate will join a vibrant research team at INABIO and collaborate with a network of leading universities and research institutes in Ecuador. This position provides access to a small DNA sequencing laboratory, including Oxford Nanopore technology.

Application Process:

Interested candidates should submit the following documents in English:

- Cover letter outlining research interests and relevant experience.

- Curriculum vitae (CV) including a list of publications, Research Achievements, Degree Certificates (Certified copies of diplomas).

- Recommendation Letters (Three signed letters of recommendation from professional or academic referees) and Contact information for three professional references.

- A short research plan (max. 2 pages) for biodiversity conservation research in Ecuador using genetic resource data analysis in Ecuador.

Applications should be sent electronically to [nibroda@korea.kr] with the subject line " Researcher - Soil Microbiome Bioinformatics."

Deadline for Applications: [July 31, 2025]

Pablo Jarrín Experto Dirección de Gestión de la Innovación Instituto Nacional de Biodiversidad

"Pablo Jarrín-V." <pablo.jarrin@biodiversidad.gob.ec>

— / —

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

---

EuracResInst LabTech AncientDNA

Eurac Research is looking for a Lab-Technician for laboratory and bioinformatics analysis

We are looking for a Lab-Technician with specialization in laboratory analysis and in bioinformatics in the field of ancient DNA. The candidate must have technical laboratory experience with knowledge of how to develop analysis protocols with some experience in the genetic analyses of ancient remains and in the computational and statistical analyses of genomic data. The candidate will work closely with the scientific staff of Eurac Research, Institute for Mummy Studies.

Our Institute is internationally renowned for its research on the Iceman and other mummified and skeletal human remains of different periods from all over the world. The position will be in the framework of the project FESR1060-MummyLabs 2.0 founded by Autonomous Province of Bolzano- South Tyrol and co-funded by the European Union with the duration until 2027. One of the main aims of the project regards the optimization of a protocol for the "service" from external requests (e.g. museums, colleagues from other institutions) that includes laboratory and basic bioinformatic analyses of the generated genetic data. The candidate will work on these topics closely with the scientific staff of Eurac Research, Institute for Mummy Studies.

Tasks * Plan and perform laboratory analyses * Perform computational and bioinformatic analyses * Working with the research team in service design

Requirements: * Master degree in Biology * Computational and statistical skills with expertise in ancient DNA analyses. * Good problem-solving skills and the ability to work both independently and collaboratively. * Proficiency in spoken and written English.

We offer: We offer a one-year 75% part-time Lab-Technician position, starting in September 2025. The candidate will have the opportunity to work in a stimulating multidisciplinary team composed of researchers from different fields and countries and, moreover, to collaborate with scientists from other national and international institutions.

How to apply: Interested candidates should submit their application (CV, cover letter and further relevant documents) here https://eurac.onboard.org/-mummies_lab_tech_22072025_evoldir by 06.08.2025

The project FESR1060-MummyLabs 2.0 has been funded by the Autonomous Province of Bolzano/ Bozen South Tyrol and co-funded by the European Union (European Regional Development Fund, FESR 2021-2027 second call -priority 1 Smart of the Autonomous Province of Bolzano- South Tyrol, CUP: D53C24002530009).

Cassar Renate <Renate.Cassar@eurac.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

KunmingInstZool Biodiversity ClusterHire

Senior Principal Investigator, Junior Principal Investigator, and Postdoctoral Positions at the Kunming Institute of Zoology, Chinese Academy of Sciences (KIZ, CAS) Kunming, China; Competitive Salary + Benefits Packages

The Kunming Institute of Zoology in Kunming, China is recruiting Senior and Junior PIs and postdoctoral fellows across all its research fields, which include evolution, genetics, ecology, and conservation.

We have particular interest in recruiting a senior PI to develop scalable biodiversity monitoring, for both basic and applied science.

Kunming is a very liveable city with the ideal climate combination of high altitude (1900 m) in the subtropics. KIZ has no undergraduate teaching.

We will begin assessing applications on 12 August 2025.

To make informal queries regarding applications at the Senior and Junior PI levels, especially from non-Chinese nationals, please feel free to email me at dougwyu@mac.com.

I will post this announcement multiple times before the deadline. The formal announcement is below.

Douglas Yu

About the KIZ

The Kunming Institute of Zoology (KIZ) is directly affiliated to the Chinese Academy of Sciences (CAS). Located at the head of the Indo-Burma biodiversity hotspot, KIZ is dedicated to research in the fields of evolution, genetics, human disease mechanisms, ecology, and biodiversity conservation.

KIZ provides a fertile environment for scientific innovation and vibrant interactions, offering competitive remuneration packages and high-quality training programmes for graduate students and postdoctoral fellows. The Institute currently has 40 research groups and attracts postgraduate students from around the world. It is home to several major research platforms, including the State Key Laboratory of Genetic Evolution & Animal Models, the National Research Facility for Phenotypic and Genotypic Analysis of Model Animals (our primate facility), and the Kunming National High-level Biosafety Primate Research Centre (Level-3 Lab). For more information, see www.kiz.ac.cn or english.kiz.ac.cn

KIZ welcomes applications for (1) Senior Principal Investigators, (2) Junior Principal Investigators, and (3) Postdoctoral Fellows from interested individuals of all nationalities and ethnicities.

Positions: 1. Senior Principal Investigators (Level 2)

To lead large research teams that tackle high-risk/high-reward questions in one or more of the research fields listed above. Level 2 PIs are equivalent to Full Professors in the western academic system. Qualifications: Candidates should have made significant contributions in one or more of the research fields listed above. Candidates should have shown the ability to independently fund and lead a research team. Candidates should have demonstrated a high degree of scientific integrity and interest in collaborative research. Support: Senior PIs will receive full support from KIZ to establish a research team of research technicians, postdoctoral fellows, and graduate students. In addition, KIZ will provide excellent research facilities, attractive start-up funding, and competitive salary, benefits, and housing subsidy.

2. Junior Principal Investigators (Level 4)

To establish independent research programmes in one or more of the research fields listed above. Level 4 PIs are equivalent to Assistant Professors in the western academic system. Qualifications: Candidates should have a PhD degree in a relevant field. Candidates should have excellent scholastic achievements and exhibit the potential to develop into an independent scientist. Candidates should demonstrate a strong team spirit and a high degree of scientific integrity. Support: Junior PIs will be supported with the resources necessary to establish an independent research programme, including start-up funds, laboratory space, and a salary and benefits, and housing subsidy. A mentorship committee of three senior PIs will provide guidance in research direction and laboratory management.

3. Postdoctoral Fellows

To join one of the well-funded research laboratories in KIZ, contributing your expertise in evolutionary biology, genetics, molecular and cell biology, ecology, bioinformatics, and/or statistics. Qualifications: Candidates should have a PhD degree in a relevant field. How to Apply (send to kizfsc@mail.kiz.ac.cn) Cover letter (please specify your target position) CV (include birthdate, nationality, and full publication list) Contact information for 3 references Deadline: We will begin assessing applications on 12 August 2025. Explore: www.kiz.ac.cn The first step to success in life is to get the macroeconomics right.

Douglas W. Yu, Ph.D. Professor of Ecology, University of East Anglia (BIO, Bldg 6/0.57), UK Principal Investigator, Kunming Institute of Zoology, China Co-Founder, NatureMetrics Google Scholar

— / —

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

---

LavalU ColdEcosystemConservation

Canada Excellence research chair in cold ecosystems conservation Posting date: 27 June 2025 Application deadline: 15 September 2025

The Department of Biology of the Faculty of Science and Engineering at Laval University is accepting applications for a Canada Excellence Research Chair (CERC) in cold ecosystems conservation. The CERC Program enables Laval University to recruit world-class researchers in line with the government of Canada's priorities in science, technology, and innovation.

The CERC in Cold Ecosystem Conservation aims to transform our understanding of how cold ecosystems function in a changing world and to propose relevant management and mitigation solutions. The Chairholder and the research group they assemble will pursue an ambitious research program to elucidate the key ecological and evolutionary processes of cold ecosystems. The approach should include exploiting exceptional field data acquired over several decades by Universitï¿½ Laval researchers and the use of models to address open questions in Cold Ecosystem Conservation to inform environmental policy. We seek to recruit an individual with proven leadership experience in integrating ecological and climate science. We are looking for a candidate whose expertise will enrich existing Universitï¿½ Laval centers and institutes and create synergies within the University strengths in cold region ecology. This will foster a dynamic and collaborative research environment within our institution.

The Department of Biology at Universitï¿½ Laval is an ideal place for training and research in fundamental fields of biology, from cellular and molecular biology to genomics, physiology, and animal, marine, freshwater, and plant ecology, as well as conservation and evolution. The Department currently has an enrollment of 435 undergraduate students, 135 graduate students in Masters and PhD programs, and 22 professors. The Department is a leader in northern research, with recognized centers of excellence in non-human genomics, ecology and evolution, and oceanography. This research is supported by major infrastructure at Universitï¿½ Laval, including the new scientific complex Institut nordique du Quï¿½bec, the Institute of Integrative Biology and Systems, NGCC Amundsen research icebreaker and 11 research stations in Nunavik and Nunavut under the stewardship of the Centre for Northern Studies. These stations include weather stations that have been maintained for 30-40 years and cover a latitudinal gradient of 3,000 km.

According to the Times Higher Education 2024 Impact Ranking, based on the 17 United Nations Sustainable Development Goals, Laval University ranks 19th in the world and first among French-speaking universities. Laval is also the top Canadian university and one of the top international universities in Arctic and subarctic sciences. The total student enrollment stands at 55,000 with 1,700 professors.

The person selected by the Nomination Committee must successfully pass an internal selection process at Universitï¿½ Laval as well as the national selection as part of the Canada Excellence Research Chair competition.

The successful candidate will receive:

* A tenured full-time full professor position.

* A competitive salary package including a chair bonus of up to 30% of union negotiated salary.

* $8 million over 8 years ($1 million/year, including salary) in funding from the CERC Program.

* A partial exemption from teaching duties for the duration of the chair.

* An allocation of $800,000 from the Canada Foundation for Innovation (CFI) for major laboratory equipment that can be leveraged to $2M.

* Access to state-of-the-art laboratories in the INQ's new science complex, including laboratories for simulating cold conditions and a logistics center for mission preparation.

* Competitive and attractive start-up funds.

Click here to access the full call for applications https://www.services-recherche.ulaval.ca/system/files/public/documents/financement/CERC/CERC_COLD_ECO_CONS_final.pdf BIO Directeur de Biologie <directeur@bio.ulaval.ca>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

MichiganStateU FishFacilityManager

Fish Facility Manager Job at Michigan State University

The Fish Evo Devo Geno Lab (PI Ingo Braasch) at Michigan State University, Department of Integrative Biology [https://www.fishevodevogeno.org/], is seeking a new Fish Facility Manager for our Ancient Fish Facility to start as soon as possible.

This 2,000 sq feet, world-wide unique aquatic facility keeps spotted gar (Lepisosteus oculatus) and other non-teleost and teleost fish species as models for vertebrate comparative biology, evolution, development, and genomics.

We are looking for a candidate with a B.S. in biology or a related field with experience in aquaculture, husbandry, and/or spawning of fishes or other aquatic organisms in a professional setting. The Ancient Fish Facility Manager will be in charge of the daily operations of fish rooms, including food preparation and feeding, fish health assessment, water quality management, tank cleaning, fish stock management, and aquatic system set-up, maintenance, and management. The facility manager will keep the rooms in compliance with animal use and environmental health and safety protocols and works as a liaison with the MSU IACUC, EHS, and CAR units.

Experience with lab management, molecular methods (e.g., DNA/RNA extraction, PCR, gel electrophoresis, sequencing), and/or developmental biology is desired, but is not essential. A personal vehicle is required to reach the facility.

A formal job posting will soon be available on https://careers.msu.edu/ . If you are interested or know a great candidate, please get in touch with Ingo Braasch via email [braasch@msu.edu].

—

Dr. Ingo Braasch | Associate Professor Department of Integrative Biology | College of Natural Science | Michigan State University

braasch@msu.edu | phone: +1 (517) 432 3484

https://www.fishevodevogeno.org/ | fishevodevogeno.bsky.social < https://bsky.app/profile/fishevodevogeno.bsky.social >

braasch@msu.edu

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

MNHN Paris IntegrativeTaxonomy

Dear colleagues,

Applications are welcome for a Junior Professorship (Chaire de Professeur Junior) available at the Muséum national d'Histoire naturelle (Paris, France), in the field:

Integrative taxonomy to describe biological diversity and understand evolutionary and adaptive processes.

The possible Research Units (all based in Paris, *National Museum of Natural History*) of assignment are: BOREA - Biology of aquatic organisms and ecosystems CR2P - Palaeontology Research Centre - Paris ISYEB - Institute of Systematics, Evolution and Biodiversity MCAM - Communication and Adaptation Molecules of Microorganisms MECADEV - Adaptive Mechanisms and Evolution

The advertisement can be consulted on the ODYSSEE recruitment portal: https://odyssee.enseignementsup-recherche.gouv.fr/procedures/recrutement-ec/offres-poste/fiche-offre-poste/253142 Applications must be submitted via this portal, by accessing the ODYSSEE platform, between 8 July and 8 September 2025.

Auditions will take place in October, with a contract starting no later than 1 December 2025.

You will find the detailed profile online (English version: https://filesender.renater.fr/?s=download&token=-627c10bb-cec9-4a43-8137-a293760085f0).

Please pass on this opportunity to your colleagues who are looking for a very attractive position, with substantial support and accelerated career development, in a leading institution in the field, while remaining on a human scale.

Thank you in advance.

Best regards,

Pierre-Yves HENRY Professeur, Directeur +33 (0)1 40 79 36 60 +33 (0)7 78 03 89 56

MUSÃUM NATIONAL D'HISTOIRE NATURELLE Département Adaptations du Vivant (Adaptations of living organisms) Maison Buffon, 36 rue Geoffroy St Hilaire - CP 41 - 75005 Paris - France < http://www.mnhn.fr > https://www.mnhn.fr/fr/adaptations-du-vivant Centre de Recherches sur la Biologie des Populations d'Oiseaux (France Bird Ringing Scheme) https://crbpo.mnhn.fr/ Pierre-Yves HENRY <pierre-yves.henry@mnhn.fr>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

MonashU Genomics

Lecturer / Senior Lecturer in Genomics - Monash University (Melbourne, Australia)

The School of Biological Sciences at Monash University is seeking an academic to join our team as a Lecturer or Senior Lecturer in Genomics. This is a tenured-equivalent position under the Australian academic system (ongoing, subject to probation).

In this role, you will contribute to innovative research and teaching in genomics and play a key role in advancing our School's profile in this rapidly evolving field.

We welcome applicants employing genomic tools and methods in diverse biological contexts, from functional genomics to evolutionary and ecological genomics. While we will consider candidates working on any system, including model organisms or humans, we particularly encourage applications from researchers working with plants.

Diversity is one of our greatest strengths at Monash. We encourage applications from Aboriginal and Torres Strait Islander people, culturally and linguistically diverse people, people with disabilities, neurodivergent people, and people of all genders, sexualities, and age groups.

Visa sponsorship for successful international candidates is available.

Remuneration:

* Level B: $118,974 - $141,283 AUD per annum

* Level C: $145,740 - $168,049 AUD per annum (plus 17% employer superannuation)

Applications Close:—Thursday 7 August 2025, 11:55pm AEST

More info and application portal: https://-careers.pageuppeople.com/513/cw/en/job/679703/-senior-lecturer-lecturer-in-genomics *Enquiries:* Professor Anne Peters, Deputy Head of School Anne.Peters@monash.edu

"anne.peters@monash.edu" <anne.peters@monash.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

Montpellier 36mnth ResEngineer EcoEvolution

Dear all,

A 'research engineer' position (36-month fixed-term CNRS contract, based at CEFE in Montpellier) is open within the framework of the ECO-EVO BIODIV project (Eco-evolution: an overarching framework to make sense of biodiversity dynamics) to both manage this project (30% time) and conduct scientific work in ecology and evolution (70%). For more information on this position and the application, see https://emploi.cnrs.fr/Offres/CDD/UMR5175-PHIJAR-001/Default.aspx (French and English version).

Applications will be received until October 15, 2025 for a position in early 2026.

For any information request, please contact me.

Have a good day.

Philippe Jarne

UMR Cefe - campus CNRS

1919 route de Mende

34 293 Montpellier France

06 32 99 51 46

https://www.cefe.cnrs.fr/

Philippe JARNE <philippe.jarne@cefe.cnrs.fr>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

QueenMaryLondon EvolutionaryGenomics

The Department of Biology at Queen Mary University of London has an open research-focussed faculty position at the Reader (Associate Professor) level.

The successful candidate will have a demonstrated ability to contribute to the field of Evolutionary Genomics, broadly defined. The new faculty member will join our research Centre for Evolutionary and Functional Genomics https://www.seresearch.qmul.ac.uk/cefg/ .

This a tenure-track position suitable for a motivated individual with a strong interest in growing their research programme in one of the most inclusive universities in the UK.

The job advert and application process are available at: https://qmul-jobs.tal.net/vx/appcentre-ext/brand-4/candidate/so/pm/1/pl/3/opp/6534-Reader/en-GB and will close on August 17th.

Informal inquires can be addressed to: Matteo Fumagalli (Head of Department) m.fumagalli@qmul.ac.uk Chema Martin (Head of Research Centre) chema.martin@qmul.ac.uk

m.fumagalli@qmul.ac.uk

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Rennes France StudyOfBiodiversity

Dear All,

A junior professorship position will open at the Ecobio Lab, University of Rennes, France on quantitative and computational approaches to the study of biodiversity (https://www.univ-rennes.fr/recrutement-des-enseignantes-chercheures). Applications will be accepted on the French national platform Odyssee, job offer NÂ^o 253071 < https://odyssee.enseignementsup-recherche.gouv.fr/procedures/recrutement-ec/offres-poste/fiche-offre-poste/253071 >, from August 18 to September 18. Interviews will then take place in October, with the contract starting no later than December 15, 2025. The profile is detailed below.

Best regards,

Sylvain Glémin

Quantitative and computational approaches to the study of biodiversity

Detailed description of research activities: One of today's challenges is to understand the responses of species and communities to anthropogenic pressures and global change, in order to predict their evolution in the near future. The availability of large datasets and high-performance analysis methods enables new approaches to meet this challenge. ECOBIO has strong expertise in experimental and field ecology, including long-term monitoring, and in multi-omics data production and analysis, and is looking to strengthen skills in complex and heterogeneous data analysis, modelling, meta-analysis, as well as the development of quantitative and predictive approaches. The person recruited will develop research based on computational approaches (e.g. modelling, simulations, advanced statistics, AI, meta-analyses) and the analysis of "massive data" in ecology and/or evolutionary biology, available in public databases, within research observatories and/or the laboratory (e.g. inventories, habitats, traits, surveys, participatory science data, multi-omics data). The project must fit in with one or more of the UMR's themes, but is open in terms of biological models already considered within the UMR, ecosystems or territories studied, and spatial and temporal scales. The successful candidate must also be able to respond to major national and European calls for research projects. Desired skills: - Background in ecology and/or evolutionary biology - Management and integration of complex and heterogeneous data - Statistics and data analysis - Modelling, simulations Research laboratory: ECOBIO UMR 6553, Rennes https://ecobio.univ-rennes.fr Contact: Julien Pétillon: julien.petillon@univ-rennes.fr

Detailed description of teaching duties: The person recruited will strengthen the B2E department team by teaching: - in evolution, both on micro and macro evolutionary aspects. In particular, he/she will be involved in teaching population genetics, phylogeny... and/or - community and population ecology, functional ecology. He/she may also be involved in statistics courses. and/or - complex data analysis, modelling and meta-analysis, particularly in the context of new courses to be developed in our training offer.

These courses will be taught in particular in the Organismal Biology Bachelors program and in the Biodiversity-Ecology-Evolution (BEE) Masters program. Teaching will take the form of lectures, tutorials and practical work. The person recruited will be expected to take on teaching responsibilities and be involved in developing new teaching approaches.

Expected skills in the use of online teaching resources. The person recruited is expected to participate in the international dimension of the school and to develop his/her teaching activities in this direction. The person recruited will therefore be encouraged to teach all or part of his/her course in English, and to participate in the University's European and international openness, notably through physical and/or virtual teaching mobility, and the development of courses in collaboration with teachers and teacher-researchers from member universities of the EDUC European University. Teaching component: Biology, Ecology and Ethology Department https://sve.univ-rennes.fr Contact: Jean-Christophe Sangleboeuf: jean-christophe.sangleboeuf@univ-rennes.fr

Application procedure and timetable : Application via the ODYSSEE application: from 18/08/2025 to 18/09/2025 https://odyssee.enseignementsup-recherche.gouv.fr Sylvain Glemin <sylvain.glemin@univ-rennes.fr>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

RostockU Germany PopGenomics

Dear All,

A full-time group leader/scientific assistant position, salary scale E13 is available in the Population Genetics Department at the University of Rostock, Germany from October 1st 2025 or soon thereafter. The position is permanent and comparable to a Lecturer position in the UK or an Assistant Professor position in the US.

*** About the lab *** The Population Genetics group at the University of Rostock is a newly established chair led by Prof. Dr. Mathilde Cordellier, with a focus on evolutionary research, mainly with invertebrate species. Our work is at the interface of evolution and ecology. Our goal is to understand rapid adaption through hybridization processes by studying the genomes of invertebrate species such as Daphnia. Working on these species offer the unique opportunity to look back in time by using resting stages, and planned projects include the genomic analysis of sediment cores. Further, the group is working on genome and sex chromosome evolution in spiders. We make use of a broad range of techniques: life history experiments, transcriptomics, genome sequencing, bioinformatics are all contributing to our understanding of species' evolution.

Research topics and lab resources can be consulted here: https://www.populationsgenetik.uni-rostock.de/en/ *** Your tasks *** We are looking for an enthusiastic researcher who is keen to contribute to the research topics in the group, such as (1) Recombination and Hybridization in a Daphnia species complex (2) Population genomics through time with resting egg banks (3) Interspecific variation in gene expression in hybridizing Daphnia species (4) Genome and sex chromosome evolution in spiders.

- Research in the field of population genetics and genetics of invertebrates, with topics closely related to the research profile of the chair and with the aim of establishing your own line of research.

- Publication of research results and acquisition of third-party funding.

- Scientific, research-based teaching comprising 8 SWS in the areas of genetics/population genetics in the Bachelor's and Master's programmes as well as in the teacher training programmes.

- Participation in field research, including the supervision of practical field courses.

- Participation in the further development of the Master's programme in Integrative Zoology.

- Supervision of Bachelor's and Master's theses.

- Design, preparation, implementation and correction of student examinations

- Support with scientific and teaching organizational tasks (study organization, committee work)

*** This makes you a good fit *** - Completed university degree (state exam, diploma, master's degree or comparable degree) in Biology or comparable discipline - Completed PhD degree in Biology or comparable discipline at the time the contract starts - Experience working with high-throughput sequencing data for genomic and/or transcriptomic studies, for example for variant analysis and gene expression profiling (RNAseq/ATACseq/scRNAseq) - Successful publication of research results in peer reviewed journals is required - Teaching experience for Bachelor and/or Master degrees in a university setting is required - Confident knowledge of german and english language, both written and spoken - 1 - 2 years of relevant professional experience as postdoc is required - Experience working with non-model species is advantageous - Experience in applying for third-party funding for research projects is a plus - Very good ability to work on schedule, communication skills for presenting research results and ability to work in a team and with international partners

*** How to apply? *** Please send your application via the university application portal using this link, as email applications will not be accepted https://jobs.uni-rostock.de/jobposting/cd190b697c99f8b1b61de1879e1ff57b207301e70?ref=homepage Application should comprise a cover letter, resume with a publication list and contact information for at least two references, diploma with indication of final grade, summary of previous research experience and exciting projects you want to conduct (max 2 pages) all combined in one single file.

The application deadline is August 11th 2025 and interviews will take place in September 2025. The preferred start date is October 2025 but is flexible and will depend on the timeframe of the most qualified applicant.

Further information about the position can be obtained from mathilde.cordellier@uni-rostock.de

Prof. Dr. Mathilde Cordellier Institute of Biological Sciences Chair of Genetics - Population genetics and Biodiversity Research University of Rostock Albert-Einstein-Strasse 3 D-18059 Rostock, Germany

Email: mathilde.cordellier@uni-rostock.de Pronouns: She/her

— / —

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

---

SmithCollege EvolCellBiology

The Department of Biological Sciences at Smith College is inviting applications for a tenure track Assistant Professor position in Cell Biology to begin July 1, 2026. The position description and application information for the Assistant Professor-Cell Biology position can be found at: apply.interfolio.com/170354

Teaching responsibilities will include the introductory Molecules, Cells, and Systems course, a foundational biochemistry course, and intermediate/advanced cell biology courses in the candidate's area of expertise. A PhD is expected by the date of appointment; strong candidates will have postdoctoral experience. We seek applicants who are committed to inclusive undergraduate education and to developing an active research program that incorporates undergraduate researchers.

Located in Northampton, MA, Smith College is the largest women's college in the country and is dedicated to excellence in teaching and research across the liberal arts. A faculty of outstanding scholars interact with students in small classes, as advisors, and through student-faculty research projects. Smith College offers opportunities to foster faculty success at every career stage, such as those listed here. Smith College offers state-of-the-art resources including the Centers for Microscopy & Imaging, Mass Spectrometry, and Molecular

Biology, along with a research greenhouse, Botanic Garden, an accredited animal care facility (with mammalian, amphibian, zebrafish and marine systems in place), and a high performance computing center.

We seek applicants whose research interests complement and broaden the existing expertise in the Department of Biological Sciences and Program in Biochemistry. The new faculty member will also have opportunities to collaborate with Smith College's programs in Neuroscience, Exercise and Sport Studies, Engineering, and Statistics and Data Sciences. In addition, the Five College Consortium (comprising Smith, Amherst, Mount Holyoke, and Hampshire Colleges and the University of Massachusetts at Amherst) provides a rich intellectual and cultural life for faculty and students, as well as opportunities for collaborative research and mentoring of doctoral students.

Laura Katz <lkatz@smith.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UCopenhagen 30mnth Bioinformatics

Bioinformatician in population genomics We are looking for a highly motivated and dynamic person for a 2.5-year position as bioinformatician (staff scientist) at the Villum Center for Global Mountain Biodiversity at the GLOBE Institute to commence 1 September 2025 or as soon as possible thereafter.

The position will be based at the Globe Institute. The Institute's main purpose is to address basic and applied scientific questions through interdisciplinary approaches. The institute operates at the intersection of natural and medical sciences and the humanities. Information on the institute can be found at www.globe.ku.dk . The research will be conducted at the Center for Global Mountain Biodiversity, a Villum Center of excellence led by Professor Carsten Rahbek. Thec enter comprises 20 scientific staff, technicians and students focused on understanding how mountains shape the distribution and diversity of life on Earth, with particular attention to tropical mountain biodiversity. Inspired by natural history knowledge, we engage in rigorous fieldwork around the world to build and improve an assemblage of biological data sets on species' distributions and traits. We use a range of tools from novel macroecological process-based and null models to cutting-edge DNA, genomic techniques and powerful bioinformatic tools. This holistic approach strengthens our ability to address fundamental questions about the distribution and diversity of life on Earth.

The Villum Center for Global Mountain Biodiversity is housed within the Center for Macroecology, Evolution and Climate (CMEC; www.macroecology.ku.dk) and the Section for Biodiversity at the Globe Institute, University of Copenhagen. CMEC is a leading center of excellence with a cross-disciplinary research program addressing fundamental questions on the origin, maintenance, conservation and future of life and biological diversity on Earth. Our team of 40+ researchers representing over 14 nationalities juxtaposes faculty staff scientists from the fields of macroecology, historical biogeography, oceanography, evolutionary biology, community ecology, population biology, climate change research, conservation biology and environmental economics.

We prioritize teamwork and close collaboration both within the Center and across our global research network. Our group culture is supportive, inclusive, and driven by mutual respect, where diverse skills and experiences are valued. We are committed to fostering not only scientific excellence, but also professional growth and career development at every stage.

Job description We are offering a 2Â½ year bioinformatician position with Professor Carsten Rahbek. In collaboration with also Associated Prof Rute Andreia Rodrigues da Fonseca, Associated Prof. Peter Hosner and Assistant Prof Anna Brüniche-Olsen, you will work with whole genome data to understanding the spatio-temporal dynamics of two aspects: 1) how species with current small populations and limited geographical ranges have been impacted by climate changes through glacial and interglacial periods during the Quaternary period and since the last glaciation period (with additional impact of humans), and 2) how species with very small population sizes persist at extremely low densities for centuries to perhaps 10,000s of years. According to conventional knowledge, long-term persistence at species with extremely low population sizes with apparently very little geneflow should not be likely due to stochastic factors. For our Andean work we have population genomic data of 700 specimens of 24 bird species of og High Andean Polylepis forests. We also have genomic data for 5000 bird species (being part of the B10k program aiming at sequencing all bird species in the world).

Your job. As a bioinformatician, your role will be as a staff scientist to develop, implement, and maintain computational tools and workflows to support the genomic research on our Andean bird project and broader avian genomic datasets. You will process and analyze whole-genome sequencing data (both low and high depth of coverage), assist in managing large-scale genomic databases, and provide technical expertise to researchers working on evolutionary, ecological, and environmental questions. You will work closely with faculty, postdocs, and students to ensure efficient, reproducible analysis pipelines primarily using, e.g., Python, R, Bash, and workflow managers such as Snakemake on high-performance computing clusters. Your contributions will be essential to enabling cutting-edge research through scalable and well-documented bioinformatics solutions.

Profile We are looking for a highly motivated and enthusiastic scientist with the following skills and experience:

Essential experience and skills.

We seek an internationally competitive candidate with:

- A PhD in bioinformatics, biology or related field.

— / —

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

---

UInnsbruck TechAssist EcoEvo

TA position Research Department for Limnology, Mondsee of the University of Innsbruck:

A Technical Assistant position is available within an Austrian Science Fund (FWF) START project on eco-evolutionary dynamics and admixture at the University of Innsbruck. We investigate admixture in an aquatic keystone grazer and study the consequences of admixture on eco-evolutionary dynamics in the context of global change on the population, species, community, and ecosystem level. The position is funded for 3 yrs at ~50% employment with possibilities of full and/or extended employment. The workplace is the Universities Research Department for Limnology located in Mondsee (Upper Austria) close to Salzburg (https://www.uibk.ac.at/limno/index.html.en).

Your responsibilities The TA will be will be responsible for maintaining Daphnia and algae cultures. Moreover, the TA will be involved in with phenotyping assays, molecular lab and mesocosm experiments.

Your skills The planned work requires a high degree of independence and the ability to work in a team. Prior experience in any of the following areas will be an advantage but is not strictly required: (i) molecular lab work (DNA extractions, PCRs, library prep), (ii) cultivation of animals and/or microorganisms, (iii) lab management. Any education as BMA/CTA/BTA/MTA/TA or a BSc or MSc degree in science will be of advantage. The work with an international and diverse team and several international collaborators will require some English and/or German skills.

What the position offers The monthly gross salary is depending on the qualification and falls between EURO 2.500 und EURO 3.300 (14x per year) for a 50% employment (alternative arrangements are possible). The contract includes health insurance and 5 weeks of holidays per year. Furthermore, the university has numerous attractive offers: https://www.uibk.ac.at/universitaet/zusatzleistungen/index.html.en We aim to ensure an excellent working environment in which everyone can contribute their experience, ideas and ways of thinking and we offer and support professional training. Moreover, I strive for cultural and gender equity, diversity, and inclusion for anyone to be involved in this project. Candidates with a broad range of backgrounds, perspectives, and ideas will be welcomed and are encouraged to apply. For more information on the position, the project, the group, or the University, please do not hesitate to contact Markus.Moest@uibk.ac.at.

How to apply I am looking forward to receiving your application. Please send a single pdf file including a short letter of motivation and curriculum vitae and contact details of previous employers (if any) to Markus.Moest@uibk.ac.at. Applications should be written in English or German. We are seeking to fill the position as soon as possible and will review applications on a rolling basis.

MOEST Markus, PhD Research Department for Limnology, Mondsee University of Innsbruck Mondseestrasse 9 A-5310 Mondsee Markus.Moest@uibk.ac.at

“Möst, Markus Hartmann” <Markus.Moest@uibk.ac.at>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UlmGermany EvolutionaryEcology OneHealth

The Faculty of Natural Sciences of Ulm University seeks to appoint a W3-Professorship for Functional Biodiversity (m/f/d) at the Institute for Evolutionary Ecology and Conservation Genomics at the earliest possible date.

The Institute's research under the direction of Prof. Sommer operates at the interface of evolutionary ecology, genetics (immune genes, microbiome) and ecosystem resilience in a OneHealth frame work. The overall aim is to understand the ecological, behavioral, genetic and health-related processes that promote or restrict adaptive evolutionary processes to maintain the health of wild animals and ecosystem functions. We seek an internationally recognized scientist with exceptional qualifications in functional biodiversity research with a zoological focus. The successful candidate will investigate the impact of anthropogenic stressors on ecological processes, infection resistance, and ecosystem services in a OneHealth context. The professorship collaborates with other institutes of the Biology Department to advance its research focus "Stress Response and Resilience of Biological Systems". Active participation in the faculty's academic self-governance is required. The professorship also involves German and English teaching in the bachelor and master programs of the Biology Department, covering topics such as evolutionary ecology, zoology(e.g., animal evolution and biodiversity, functional biodiversity), biostatistics, scientific integrity, as well as data analysis and management. Instruction will include lectures, seminars, practical exercises, and field trips. Employment requirements are completed university studies as well as teaching aptitude, a doctoral degree and further pertinent scientific achievements (ç 47 LHG).

For more information and to apply, use the link below; Prof. Simone Sommer (Simone.sommer@uni-ulm.de) can also be contacted for additional information.

https://stellenangebote.uni-ulm.de/jobposting/8eab77b137ae0e285b2909a6d6b86c722299a09aï¿¼

Prof. Dr. Lena Wilfert University of Ulm Institute of Evolutionary Ecology and Conservation Genomics Albert-Einstein Allee 11 D-89069 Ulm Germany Tel.: 0049-731-5030615 Fax: 0049-731-5022683

email: lena.wilfert@uni-ulm.de Website: https://www.uni-ulm.de/nawi/evolutionary-ecology-and-conservation-genomics/prof-dr-lena-wilfert Honorary Professor University of Exeter email: lena.wilfert@ex.ac.uk

please note my new address from 1.9. 2025 University of Regensburg Institute of Zoology Universitätstrasse 31, D-93053 Regensburg Germany

Email: lena.wilfert@ur.de

"lena.wilfert@uni-ulm.de" <lena.wilfert@uni-ulm.de>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

Uppsala Sweden Three Bioinformaticians

Dear all,

National Bioinformatics Infrastructure Sweden (NBIS), a part of SciLifeLab, have several bioinformatician positions out in Uppsala, Sweden. These are permanent staff scientist positions focusing on support to Swedish researchers. They are NOT post doc positions. Please see the links below for more information and how to apply. We only accept applications through the application system, not in email.

1-2 positions focusing on spatial transcriptomics and/or biostatistics/machine learning: https://www.uu.se/en/about-uu/join-us/jobs-and-vacancies/job-details?query=838183 Deadline Aug 29.

1 position focusing on scripting/development/pipelines, placed in the Evolution and Biodiversity team: https://www.uu.se/en/about-uu/join-us/jobs-and-vacancies/job-details?query=838223 Note that you need to supply a link to a GitHub repo with own-developed scripts/pipelines for this position. Deadline Aug 18.

Best regards, Henrik

Henrik Lantz Support manager, NBIS/SciLifeLab Uppsala, Sweden

Nï¿½r du har kontakt med oss pï¿½ Uppsala universitet med e-post sï¿½ innebï¿½r det att vi behandlar dina personuppgifter. Fï¿½r att lï¿½sa mer om hur vi gï¿½r det kan du lï¿½sa hï¿½r: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: http://www.uu.se/en/about-uu/data-protection-policy Henrik Lantz <henrik.lantz@imbim.uu.se>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

USalzburg Austria EvolEcol

New professorship “Zoological EvolEcol” available at the University of Salzburg Austria. More information here: https://www.plus.ac.at/personalwesen/-stellenmarkt-en/universitatsprofessuren-en/tenured-full-professorship-in-zoological-ecology/?lang=en Rüdiger Jens <jens.ruediger@plus.ac.at> Rüdiger Jens <jens.ruediger@plus.ac.at>

USaoPaulo MetazoanPhylogenomics-Bioinformatics

Dear colleagues,

The Institute of Biosciences of the University of Sāo Paulo (IB-USP) invites applications for one full-time faculty position at the rank of Professor Doutor (equivalent to Tenure TRack Assistant Professor) in the Department of Zoology (DZ).

Bioinformatics and Phylogenomics are fundamental to advancing scientific research by integrating genomic data and computational tools to address complex scientific questions. This interdisciplinary field is essential for unraveling evolutionary relationships, understanding biodiversity, and exploring biological processes at a molecular level. In this context, the Department of Zoology (DZ) is seeking a highly qualified candidate with demonstrated expertise in this area. The selected candidate will be expected to contribute to original research, teaching, and outreach activities. This includes working collaboratively, fostering interdisciplinary initiatives within and outside the department, and actively pursuing research funding. The candidate is expected to strengthen current research lines, ensure the consistent quality of core undergraduate and graduate courses, propose new curricular offerings, and contribute to the formation of highly qualified human resources. This strategic hire aims to address a critical departmental need, reinforce the Institute's leadership, and strengthen the long-term commitment to academic excellence in the life sciences, particularly given the department's foundational role in systematics and phylogenetics.

Further information can be found at the website: https://academica.ib.usp.br/concursos/zoologia/-edital-19-2025 Please contact Prof. Dr. Daniel J. G. Lahr, Department Head, with further inquiries.

Daniel J. G. Lahr PhD habil., Associate Prof. Department Head, Zoology Inst of Biological Sciences, Univ. of Sao Paulo, Brazil Office number: + 55 (11) 3091 0948 http://lahr.ib.usp.br Dan Lahr <dlahr@ib.usp.br>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UTennessee Knoxville EvolGenomics

Evolutionary Genomics, Assistant Professor, Ecology & Evolutionary Biology, Fall 2026

*

Dept of Ecology & Evolutionary Biology

*

The University of Tennessee Knoxville

Description

The Department of Ecology & Evolutionary Biology (EEB) at the University of Tennessee, Knoxville, seeks applications for a tenure-track Assistant Professor position in Evolutionary Genomics. We invite applicants whose research leverages modern genomic tools and statistical approaches to address fundamental questions in evolutionary biology. We are particularly interested in candidates working on functional and evolutionary genomics in any system plant, microbe, or animal (including humans) who bring innovative, integrative approaches to large-scale genomic data analysis.

Successful candidates will complement and expand existing departmental strengths in ecology, evolution, animal behavior, genetics, and/or quantitative biology. We seek individuals with strong interdisciplinary backgrounds spanning biology, bioinformatics, statistics, and computational methods, who are eager to collaborate across EEB and the broader Division of Biology, including opportunities at the National Institute for Modeling Biological Systems (NIMBioS) and data science initiatives on campus, as well as at the nearby Oak Ridge National Laboratory. Applicants could also integrate our nearby field resources (including Great Smoky Mountains National Park, national forests, and natural areas), extensive biodiversity collections, and advanced computational and sequencing facilities into their research program.

We are dedicated to expanding access to educational opportunities, striving to remove barriers, and making academic pursuits more affordable. Consistent with the University's commitment to high academic standards, student achievement, and the preparation of responsible citizens, we believe that engaging with individuals from all backgrounds and perspectives fosters a vibrant learning environment that enhances critical thinking and intellectual growth. Our collective strengths make us stronger, and we are committed to promoting an atmosphere where all members of the University community feel welcome, can thrive, and achieve success.

The University is beginning a next-level initiative aimed both at substantially elevating the University's national reputation for impactful research, scholarship, and creative activity and at assembling a roster of faculty committed to delivering one of the nation's best educational experiences for undergraduate and graduate students. Qualifications

Required

Candidates must hold a Ph.D. in Biology, Genetics, Evolutionary Biology, Genomics, Bioinformatics, or a related field at the time of appointment and should demonstrate a strong record of scientific accomplishment, including peer-reviewed publications. Excellent communication skills and a commitment to effective and modern teaching practices are required.

Preferred

Postdoctoral or comparable research experience is preferred, as is a record of or potential for securing external research funding. UTK is a land-grant university and values engaged forms of research/scholarship/creative activity, teaching and service, and considers evidence of these commitments in the records of applicants. Application Instructions

Applications will be reviewed beginning September 19, 2025, and will continue until the position is filled. This position has an anticipated start date of August 1, 2026.

Interested applicants should submit via Interfolio (https://apply.interfolio.com/170735) a cover letter, curriculum vitae, two-page statement of research accomplishment and plans, two-page description of teaching experiences and interests, and contact information of at least three individuals who could write letters of reference.

Please direct any questions to the search chair, Dr. Elizabeth Derryberry (ederryb1@utk.edu).

– Michael A. Gilchrist, Ph.D. (He/Him) Associate Professor Ecology & Evolutionary Biology University of Tennesse Knoxville

"Gilchrist, Michael" <mikeg@utk.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Other

BiodiversityGenomics Survey

Dear colleagues,

We are conducting an international research study at Arizona State University to understand scientific practices and interests related to biodiversity and genomics. We are reaching out to experts working with biospecimens, biosamples or data from any species across the tree of life for their valuable insights.

The survey will take approximately 10-15 minutes to complete and it is available in English and Spanish. Your participation would be incredibly valuable to this research and help shape a better understanding of the current landscape of biodiversity efforts and genomics.

The survey is anonymous, and all responses will be confidential. All the participants must be 18 years or older. There is also an optional randomized drawing where participants could enter and win one of our six $100 gift card.

If you're willing to participate, please click the link below to access the survey: https://asu.co1.qualtrics.com/jfe/form/SV_6P48DHfOgelZ6Yu Please feel free to share with your networks and other colleagues. Your input will contribute directly to advancing knowledge in this area of study.

Thank you very much for considering this request. If you have any questions or need additional information, please do not hesitate to contact Jocelyn Chee-Santiago via e-mail: jcheesan@asu.edu. Your contribution is greatly appreciated!

Thanks, Beckett Sterner School of Life Sciences, Arizona State University

EvolutionMeetings Survey

Dear EvolDir subscribers,

The Evolution Meetings organizers are seeking input on likely challenges to future meeting attendance. Even if you did not attend the most recent Evolution Meetings in Athens, GA or the associated virtual meeting, you are invited to fill out this survey on meeting attendance: https://qualtricsxmv7fq7w2f6.qualtrics.com/jfe/form/SV_eeW7FbwhncO0XMq Sincerely,

The Evolution Meeting Organizers

This email contains links to content or websites. Always be cautious when opening external links or attachments.

Please visit https://carleton.ca/its/help-centre/report-phishing/ for information on reporting phishing messages.

When in doubt, the ITS Service Desk can provide assistance. https://carleton.ca/its/chat Alex Wong <AlexWong@cunet.carleton.ca>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Galapagos 2FieldAssist SeaLions

Field assistant position

We are looking for 2 field assistants to participate in the upcoming field season of the Sea Lion Project Galapagos to assist with our research on animal behaviour and personality, population dynamics and foraging strategies in Galápagos sea lions (Zalophus wollebaeki) in the research group of Oliver Krüger at the Department of Animal Behaviour at Bielefeld University, Germany.

(https://www.uni-bielefeld.de/fakultaeten/biologie/forschung/arbeitsgruppen/behaviour/)

Field work will take place from mid/end of October until mid December on Caamaño, a small island near Puerto Ayora in the centre of the Galápagos archipelago. We have studied Galápagos sea lions there since 2003 with most animals being individually marked. Work on Caamaño includes daily census rounds, a variety of behavioural response tests, behavioural observations, and captures of animals for tagging, growth assessment, biologging deployment, and sample collection. Previous work experience with animals and these type of activities is an advantage.

The field site is a small islet (300m diameter), isolated from civilisation, and has no facilities, so an ability to work under truly primitive conditions is essential. Participants have to live in a tent the entire time and share all camp duties (cooking, cleaning, daily data entry). No sanitary facilities are available and we have fresh water only for drinking and cooking. Field work will be physically and mentally demanding. All gear has to be transported onto the island via a difficult landing and camp conditions are primitive, including a basic diet based primarily on dried and tinned foods. Due to the long duration of the field season and the tough conditions field assistants need to be physically capable. Previous experience with working in an outdoor environment and with handling wild animals is highly preferable.

The duration of the field season is 2 months. The positions are unpaid, however travel expenses to the Galapagos Islands as well as all food while on Caamaño and accommodation while in town (before and after the field season) will be covered by the project. Additionally, there might be a possibility to continue with the project for a PhD if funding becomes available. We encourage people who are interested in pursuing a PhD to apply. Ecuadorian nationals are especially encouraged to apply.

Applications open until July 27th.

Please send applications in English (letter of motivation and curriculum vitae) to the following address:

svenja.stoehr@uni-bielefeld.de

alexandra.childs@uni-bielefeld.de

Summary:

Field Assistant Position - Sea Lion Project Galápagos When: mid October - mid December Where: Caamaño Island, Galápagos

Institution: Bielefeld University, Dept. of Animal Behaviour

Project Focus

Galápagos sea lion behaviour, personality, population, and foraging Tasks: daily censuses, behavioural tests, animal captures (tagging, sampling)

Applicant Requirements

Physically fit and mentally resilient Willing to live in a tent under primitive conditions & carry out manual camp duties Experience with wild animals, fieldwork, behavioural studies Ecuadorian nationals especially encouraged to apply Unpaid, but travel, food, and accommodation (pre/post fieldwork) covered Possible PhD opportunity if funding allows

Apply by July 27

“Stöhr, Svenja” <svenja.stoehr@uni-bielefeld.de>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

RequestInfo ImproveGraduateStdWellbeing

Dear Colleagues,

We are a group of biologists and biology education researchers conducting a collaborative research project to create and evaluate educational resources showcasing biologists' hobbies outside of science with the end goal of supporting graduate student well being and preventing burnout. This project is an expansion of the Beyond the Bench blog (https://thelattinlab.com/-beyond-the-bench) that Christine Lattin at LSU started in a scientific writing class for graduate students. We are looking to recruit instructors interested in implementing an activity in their graduate-level courses that features scientist profiles and asks students to make their own scientist profile (https://drive.google.com/file/d/-1MyCSugTrKete-f546oMtwvGIQ8AWuGQ-/view). For more information about this study, please visit our FAQ page.

For instructors interested in participating in our study and in learning more, please fill out this brief form (https://sunybuffalo.qualtrics.com/jfe/form/-SV_cHXvm1qtxrazcLc) to express your interest and provide us with more information about the courses you teach.

We ask that you please forward this message to all biology faculty at your university who teach introductory graduate courses (i.e., Introduction to Graduate School, Science Communication, Scientific Writing).

Thank you for helping with our efforts to improve graduate education and well being, and please reach out with any questions (robincos@buffalo.edu).

Cheers,

Robin Costello, Assistant Professor, University at Buffalo

Christine Lattin, Associate Professor, Louisiana State University

Melissa Kjelvik, Research Specialist, Michigan State University

Margaret Adams, Graduate Student, University at Buffalo

Robin A. Costello, PhD (she/her) Assistant Professor Department of Biological Sciences University at Buffalo (SUNY) Office: 641 Cooke Hall www.costello-lab.com Robin Costello <robincos@buffalo.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

SSE InternationalEventGrants

The Society for the Study of Evolution (SSE) International Committee invites applications for the International Event Grants, which provide funding for international symposia, workshops, courses, and other events within the field of evolutionary biology, including virtual events. Our priority is to support events that benefit emerging communities in the field of evolutionary biology. The diversity of participants and invited speakers will be considered as a criterion for selection.

Application deadline: September 15, 2024

More information: https://rb.gy/76fgi SSE Communications <communications@evolutionsociety.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

SSE Lifetime Achievement Award

The Society for the Study of Evolution (SSE) invites nominations for the Lifetime Achievement Award, which recognizes individuals who have made substantial contributions to the study of evolution through conceptual advances, impactful publications, and/or outreach/education. Individuals who have demonstrated outstanding mentorship of trainees, provided noteworthy service to the evolution community, and/or contributed to the diversity and inclusion of the field will also be recognized.

The awardee will be presented at the 2026 Evolution meeting (https://www.evolutionmeetings.org/). Recipients of this award are also invited to submit an accompanying article to Evolution (https://academic.oup.com/evolut) (primary research, review, insight or commentary, fast-tracked through review and made freely available) within two months of the conference. Published articles would highlight the award obtained.

Nomination Instructions:

Complete the form below with your name, the nominee's name, and two short descriptions of the nominee's contributions to the field and community. You will also be asked if you would be willing to provide a longer and more detailed nomination letter at a later date. SSE values the contributions of diverse researchers and encourages nominators to consider all potential mentors and colleagues. Self-nominations are welcome.

Nomination form: https://docs.google.com/forms/d/e/1FAIpQLSc4Fpif6vDjgAM5mZc0HNTVy4BJauwg1tK9k9cBaDebxDZL
viewform?usp=header Deadline: September 30, 2025

View past recipients of the award: http://www.evolutionsociety.org/society-awards-and-prizes/lifetime-achievement-award.html Learn more about SSE: http://www.evolutionsociety.org/ *Kati Moore*she/her *Communications Manager* *Society for the Study of Evolution* communications@evolutionsociety.org www.evolutionsociety.org SSE Communications <communications@evolutionsociety.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Survey FederalPolicySentiment

Dear Colleagues, Given the critical situation researchers in the United States are facing, we believe it's essential to measure the consequences of government actions not only on research but also on a personal level, particularly for those of us who depend on work visas to conduct science in this country.

For this reason, I'm sharing a survey led by my colleagues at LSU to quantify these impacts. The survey takes 15-20 minutes and covers research-related challenges as well as the emotional toll of recent policy pressures. The survey will not collect any identifiers.

We'd greatly appreciate your participation and insights. You can access the survey here: https://lsu.qualtrics.com/jfe/form/SV_8k17859vbCURCvk Please feel free to share the link within your colleagues and institutions.

Thank you so much for your time and support! Best regards, Ana

Ana Salgado, Ph. D. (she/her/ella) Postdoctoral Associate & Program Coordinator Department of Biological Science Louisiana State University Baton Rouge, LA 70803

Ana Lucia Salgado <amald@lsu.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

PostDocs

Austria UScitizens EvolBiol

DEADLINE: 27.7.25

Austria is offering special funding for promising postdocs to pursue their research at an Austrian university.

The Vetmeduni could offer one of these Postdoc fellowships, which cover 4 years of funding (125k euro /year), which includes salary and consumables. While candidates interested in population genetics and polygenic adaptation are most likely to benefit from the scientific environment at the Vetmed, we are open to other topics related to evolutionary biology.

The application material (CV and a short statement of research interests) must be received by myself by July 27 to be considered-which is very soon!

The eligibility criteria are: - completed PhD - affiliation with a US university (at least until 1.1.25) - no citizenship restrictions - start within 6 months after nomination (which corresponds to approx. March 26)

The selection process is quite unusual to allow for rapid decisions: the position will be awarded to the best candidate applying to the Vetmed-this implies they are only competing among candidates for the Vetmeduni not across all universities in Austria!

please feel free to distribute this information in your local network!

many thanks,

Christian

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe

Zoom: https://bokuvienna.zoom.us/j/-99886139039?pwd=dnZXUHZlK2dkWVBxU1NXQ2NCRXhwUT09 phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://www.vetmeduni.ac.at/en/population-genetics/ Vienna Graduate School of Population Genetics http://www.popgen-vienna.at christian.schloetterer@vetmeduni.ac.at

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

ChicagoFieldMuseum PopGeneticsLichenSymbioses

https://www.fieldmuseum.org/about/careers Postdoctoral Research Associate in Comparative and Population Genomics of Lichen Symbioses

Our Mission:Since the 1893 World Columbian Exposition, our organization has aimed to connect people to the natural environment and human history.

Join our team and enjoy a benefits package that truly supports your well-being and lifestyle:

Comprehensive Health Coverage: Including medical, dental, vision plans, and even pet insurance.Financial Security: Life and disability benefits plus a 403(b) savings plan to help you plan for the future.Work-Life Balance: Generous paid time off, paid sick leave, and paid holidays to ensure you have time to recharge and spend with loved ones.Exclusive Perks: Enjoy great employee discounts and complimentary general admission to participating cultural institutions.

We're dedicated to enhancing your life both at work and beyond!

The Grainger Bioinformatics Center of the Collections, Conservation, and Research Division at the Field Museum is seeking a highly motivated and skilled Postdoctoral Research Associate for a full-time, two-year position, with the possibility of extension.

This privately funded (non-government) position focuses on advancing research in the comparative genomics and population genomics/phylogenomics of lichen symbioses, particularly involving non-model organisms and complex symbiotic systems.

Project Scope

This position offers an exciting opportunity to explore evolutionary diversification, population structure, and genomic adaptation in lichens, with an emphasis on fungal symbionts and their interactions with algal and bacterial partners. The research leverages whole-genome sequencing, target enrichment, and RADseq to investigate co-evolution, genomic convergence, and ecological specialization across taxonomic and geographic scales.

Duties and Responsibilities:

Analyze genomic datasets, including assembly, annotation, and comparative analysis of symbiont genomes.Develop and apply workflows for phylogenomic inference, population structure analysis, and species delimitation.Collaborate on sequencing, data integration, and interpretation of multi-omic datasets.Contribute to manuscript writing, presentations, and broader dissemination of research outcomes.Participate in mentoring and training undergraduate students, particularly those from underrepresented groups in STEM fields.

Qualifications:

PhD in bioinformatics, computational biology, evolutionary biology, or a related discipline.Proven experience in genomic data analysis, especially in comparative or population genomics.Proficiency in one or more scripting languages (e.g., Python, R, Perl, Bash).Familiarity with standard bioinformatics pipelines for sequence analysis, genome assembly, and variant analysis.Strong written and verbal communication skills.Ability to work both independently and in a collaborative, interdisciplinary environment.

Preferred Qualifications

- Experience with RADseq, target enrichment, or metagenomic sequencing approaches.

- Background in fungal biology, lichenology, or symbiotic systems.

- Interest in molecular evolution, non-model organisms, and integrative evolutionary analysis.

Mentorship and Expectations

The position includes support and career development under a formal Postdoctoral Mentoring Plan.The postdoctoral researcher is expected to publish at least one lead-author manuscript per year and to contribute to collaborative publications.The position is based at The Field Museum in Chicago, and active on-site participation is expected.

Pay: 48,000/Annually

Apply online at:

https://www.fieldmuseum.org/about/careers Review of applications will begin on July 15, 2025, and will continue until the position is filled.

PLEASE READ: *When you apply for multiple positions, please make sure to delete your previous resume and cover letter and upload the latest version of your resume and cover letter that is relevant to the job you are applying for, every time you apply. This will help our hiring managers access the correct documents. Please note that removing the resume and cover letter will not delete any previously submitted resumes and cover letters.

The Field Museum is an equal-opportunity employer. We are committed to providing a workplace free from discrimination, embracing diversity, and fostering mutual respect. We value the unique perspectives each team member brings, which empowers our ability to innovate and overcome challenges.

At the Field Museum, we are dedicated to making our career website and recruitment process accessible to everyone. If you encounter any difficulty when using or accessing our online application, or if you need a reasonable accommodation for completing your application, participating in interviews, or any other part of the selection process,

— / —

This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.-

mcmaster.ca/~brian/evoldir.html

MNHN Paris BioinformaticsTaxonomy

MNHN_Paris_France.Bioinformatics.Taxonomy

Postdoctoral Position (24 months): Researcher in Bioinformatics Applied to Integrative Taxonomy.

Detailed offer and application: https://recrutement.mnhn.fr/front-jobs-detail.html?id_job=1294&id_origin=0 Description Context: This position is a 24-month postdoctoral research contract. Each year, over 20,000 new species are described worldwide (approximately one every 30 minutes). It is estimated that the planet hosts at least ten million species, which means it would take several more centuries to complete a full inventory. To accelerate the global cataloging of life, our team is developing free, user-friendly, ergonomic, and accessible digital tools for all systematics researchers. These tools include standalone applications (iTaxoTools) and online analysis workflows (SPART Explorer). Covering the full spectrum of taxonomy (from species delimitation to their description and diagnosis) these tools allow the integration of diverse data types: DNA sequences, morphological traits, geographic coordinates, etc. They aim to formalize the definition of taxonomic hypotheses while promoting open, collaborative, and faster science in the service of biodiversity knowledge and conservation.

Missions: The main mission of the recruited candidate will be to develop new software solutions tailored to the needs of research in integrative taxonomy (with a priority on a multigene version of ASAP, as well as possibly other complementary applications dealing with geographic or morphological data). As part of the project, the candidate will also be responsible for presenting the project's progress to various partners.

Evaluation Criteria and Expected Deliverables: The recruited researcher will work in close collaboration with supervisors and other project partners to ensure precise monitoring of progress. Expected deliverables include: - Design and development of new digital tools for research in integrative taxonomy. - Writing and publishing scientific papers in peer-reviewed international journals. - Contribution to outreach and dissemination of scientific knowledge.

Supervision The recruited researcher will work closely with specialists in systematics and bioinformatics under the supervision of: - Aurélien MIRALLES (Junior Professor, MNHN) - main supervisor - Nicolas PUILLANDRE (Associate Professor, MNHN) - Paul ZAHARIAS (Associate Professor, MNHN) - Guillaume ACHAZ (Professor, Collège de France / Université Paris Cité)

The position will be under the primary responsibility of Aurélien MIRALLES.

Professional Environment and Recruitment Context Internal: The recruited candidate will join the Institut de Systématique, Ãvolution et Biodiversité (ISYEB - UMR 7205) at the Muséum national d'Histoire naturelle (MNHN). The institute brings together more than 90 researchers and nearly 70 PhD students and postdocs. Its work spans a wide range of topics primarily related to systematics, evolutionary biology, ecology, biogeography, and macroecology, focusing on a diverse array of non-model organisms. The MNHN is equipped with cutting-edge platforms for data acquisition and analysis, which the candidate will be encouraged to use and where they will interact with engineers and technicians responsible for these platforms.

External: The recruited candidate will also collaborate closely with bioinformatics partners at the Collège de France.

Required Skills and Qualifications The ideal candidate should: - Hold a PhD in Computer Science, Bioinformatics, or Software Engineering - Have a general understanding of the technological and scientific communities in this domain. Familiarity with the tools and methods used in integrative taxonomy would be a valued asset. - Have strong skills in algorithms and programming, with experience in analyzing and processing complex biological data (especially with a genetic component) - Be able to communicate results clearly and work collaboratively within multidisciplinary teams composed of biologists and other specialists - Be sensitive to user experience and usability, as one of the key success factors for these tools is the development of intuitive and user-friendly graphical interfaces

Essential competencies and knowledge - Proficient in programming languages (e.g., Python, C, C++, etc.) - Experience in scientific writing - Interest in evolutionary science and biodiversity - Interest in evolutionary modeling - Fluency in English, both written and spoken - Strong teamwork skills - Willingness to contribute to scientific outreach and community activities

Working Hours and Conditions - Working time: 35 hours and 35 minutes per week - Annual leave: 44 paid vacation days per year

Workplace Muséum national d'Histoire naturelle (MNHN), Institut de Systématique,

— / —

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

Montpellier MusselGenomics

Eighteen-month Postdoc Position: Haplotype-Resolved Assembly and Structural Variation of Polyploid Genomes in Transmissible Cancers of the Blue Mussel (M/F)

Announcement here: https://euraxess.ec.europa.eu/jobs/333894 We are seeking a highly motivated postdoctoral researcher to join the ERC project HyperCan: Mechanisms and evolutionary significance of hyperploidy variations in blue mussel transmissible cancer. The postdoc's main task will be to produce high-quality reference genomes of MtrBTN transmissible cancers in blue mussels. They will process and assemble long-read sequencing data (PacBio, ONT and Hi-C) to generate haplotype-resolved assemblies of these polyploid genomes, as outlined in the HyperCan project plan. Obtaining such reference genomes is a critical step for the continuation of the project, as well as for the broader scientific community working on this topic. The researcher will also analyse nucleotide and structural variants identified in these genomes.

Application Process: https://euraxess.ec.europa.eu/jobs/333894 Contacts: erika.burioli@umontpellier.fr ; nicolas.bierne@umontpellier.fr

Nicolas Bierne <nicolas.bierne@umontpellier.fr>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

NIH Bethesda ViralEvolution

NIH Postdoctoral Fellow

Computational Biologist (Postdoctoral Fellow)

Organization

National Library of Medicine, Bethesda, MD and surrounding area

Join a dynamic and interdisciplinary team pushing the frontiers of genomics and pandemic virus research under the leadership of Dr. Martha Nelson in the Division of Intramural Research (DIR) at the National Library of Medicine (NLM).

About the position

The NLM is one of the 27 institutes at the National Institutes of Health (NIH). The NLM is the world's largest biomedical library and a leader in research, development, and training in biomedical informatics and health information technology. The DIR within the NLM has two primary research areas: computational health research and computational biology. In computational health research, our efforts center on natural language processing (NLP), clinical image analysis, biomedical ontologies, information modeling, and clinical data analytics. In computational biology, we emphasize transcriptional regulation, chromatin and network biology, structural and functional analysis, sequence statistics, and evolutionary genomics. The post-doctoral scholar will study how rapidly evolving RNA viruses (e.g., H5N1 avian influenza, coronavirus) transmit and evolve at the human-animal interface, using advanced Bayesian phylodynamic approaches and large-scale genomic data. This project is part of a longstanding government-academic partnership spanning multiple Federal agencies and academic institutions to study disease spillover between humans, wildlife, and livestock and identify successful intervention strategies to break transmission in real-world settings. Specific tasks and responsibilities include:

Phylodynamic analysis of virus genome data Writing papers for publication in peer-reviewed journals Presenting data at conferences and seminars Leading projects involving international collaborators Working collaboratively with other lab members

Position Overview: This is a full-time postdoctoral fellow position. The initial appointment will be for one year, and is renewable on a yearly basis, with extensions up to 5 years total. The NIH offers a competitive salary (based on postdoctoral experience, see stipend tables:https://www.training.nih.gov/stipends/) and comprehensive health insurance. The NIH is dedicated to the continued education and career development of all its research staff. Candidates are subject to a background investigation. Additional information about NIH postdoctoral fellowships:https://www.training.nih.gov/research-training/pd/ Apply for this vacancy

What you'll need to apply

Prospective candidates should include "Computational Biologist (Postdoctoral Fellow)" and their last name in the email subject line. Applicants must submit the following materials to Martha Nelson atnelsonma@mail.nih.gov:

Updated CV Statement of research interest Contact information for 3 references (please include the full name with titles, institute, email address and phone number of each reference).

Application Deadline: Applications will be accepted until the position is filled.

Contact name

Martha Nelson

Contact email

nelsonma@mail.nih.gov

Qualifications

Candidates should have or be close to obtaining a Ph.D. or equivalent degree in computational biology, computer science, bioinformatics, molecular biology, or a closely related field. Candidates with a background in Bayesian approaches to phylodynamic analysis of virus populations are particularly encouraged to apply. Programming skills (e.g., R, python) and an ability to learn how to use new software and quickly apply it to genomic data are essential. Experience developing new software for genomic analysis Applicants must possess good communication skills and be prepared to work collaboratively on a fast-paced team of international scientists to inform time-sensitive outbreak responses.

Disclaimer/Fine Print

U.S. citizens and permanent residents are eligible to apply. NIH welcomes foreign nationals with the exception of individuals from this list.

– Martha Nelson, PhD Staff Scientist Division of Intramural Research National Library of Medicine National Institutes of Health Building 38A, Room 6N609C 301-480-6924 Martha.Nelson@nih.gov

"Nelson, Martha (NIH/NLM) [E]" <nelsonma@mail.nih.gov>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

NTNU Taiwan EvolutionStagBeetleWeapons

A Postdoc Position in Evolution of Stag Beetle's Weapons & Fighting Behaviors (NTNU, Taipei, Taiwan)

A 3-year postdoc is available in the Department of Life Science at the National Taiwan Normal University (NTNU), Taipei, Taiwan, starting on August 1, 2025 for an innovative and motivated person to work on research topics related to the evolution of weapons & fighting behaviors in stag beetles and related insects. The position is funded by the NSTC (National Science & Technology Council, Taiwan) grants.

Project: Evolutionarily innovative traits represent one of the most exciting topics of modern biological research in understanding adaptive diversification. Males of many animal species use weapons in direct physical combats with rival males over access to resources critical for survival and reproduction, such as food, females and breeding sites. Animal weapons exhibit a remarkable diversity in forms and often evolve to reach extreme size and attain elaborate shapes. Equipped with exaggerated mandibular weapons, the stag beetle (Lucanidae) is one of the insect groups with the most diverse weapon forms. The project will investigate the evolution of weapon forms, fighting behavior and fighting assessment strategy in Odontolabis stag beetles, which exhibit a diverse polymorphism of distinct male morphs with unique weapon forms.

References: 1. Nasif B. S., R. J A Guilani, S. Ramezanpour, A. Toofani, S. H Eraghi, G. Goss, C-P. Lin, S. Gorb and H. Rajabi(2025) Engineering the battle: Design-specific analysis of stag beetle mandibles for combat efficiency. PNAS Nexuspgaf205, (accepted) doi.org/10.1093/pnasnexus/pgaf205

2. Chen H., S-P. Huang, C-P. Lin, Z-Y. Chen and Y. Hsu(2024) Energetically costly weaponry in the large morph of male stag beetles. Journal of Zoology324: 277-286 doi.org/10.1111/jzo.13222

3. Weber, J. N., W. Kojima, R. P. Boisseau, T. Niimi, S. Morita, S. Shigenobu, H. Gotoh, K. Araya, C-P. Lin, C. Thomas-Bulle, C. E. Allen, W. Tong, L. C. Lavine, B. O. Swanson and D. J. Emlen(2023) Evolution of horn length and lifting strength in the Japanese rhinoceros beetleTrypoxylus dichotomus. Current Biology33: 1-13

doi.org/10.1016/j.cub.2023.08.066

4. Chen, Z-Y., C-P. Lin and Y. Hsu(2022) Stag beetleCyclommatus mniszechiemploys both mutual- and self-assessment strategies in male-male combat. Behavioural Processes22: 104750 doi.org/10.1016/j.beproc.2022.104750

5. Chen, Z-Y., Y. Hsu and C-P. Lin(2020) Allometry and fighting behaviour of a dimorphic stag beetleCyclommatus mniszechi(Coleoptera: Lucanidae). Insects11(2), 81 January 23 2020 doi.org:10.3390/insects11020081

Requirement: 1. The postdoctoral fellow will be responsible for either leading hypothesis-driven field/laboratory experiments, or the analyses of genomic-scale DNA sequence data sets. The applicant is also encouraged to develop an independent project based on applicant's expertise and the study systems.

2. The successful applicant must have demonstrated expertise in field research, behavioral ecology, behavioral studies, population genetics, phylogenetics, genomics, or computational statistics and modeling.

3. Preference will be given to candidates with: (1) Background in behavioral ecology & behavioral studies, (2) Experience of high performance computing, (2) The ability to develop and apply statistical or computational methods to solve biological problems, (3) Expertise in research on adaptation, theoretical models of evolution, or trait divergence.

Application: To apply, please contact Prof. Chung-Ping Lin by e-mail (treehopper@ntnu.edu.tw), with a message title "postdoc application 2025", and attach a single PDF file containing: 1) a cover letter, 2) a CV, 3) a brief 2-page statement of research interests, and how your research skills can contribute to project objectives, and 4) contact information for three references.

Salary & Deadline: The position will be available from 2025/08/01 to 2028/07/31 (re-newable based on the performance). The exact starting date is negotiable.

A monthly post-doc salary of ~ $65,000 NTD ($2,200 USD) will be offered, including retirement plan, health benefits, and a year-ending bonus of 1.5-month salary. The average living cost in Taipei, Taiwan is about 1/2 of that in major cities of the USA.

The deadline for application is 2025/08/01. The position will remain open until a suitable candidate is found.

More information: Prof. Chung Ping Lin's lab: http://arachsociety.tw/systevo/index.php?page=home&lang=en Department of Life Science in NTNU: https://www.biol.ntnu.edu.tw/index.php/en/home_en/ National Taiwan Normal University (NTNU): https://en.ntnu.edu.tw/ Treehopper <treehopper@ntnu.edu.tw>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

SantaFeInst Complexity

APPLY HERE < https://apply-sfi.smapply.org/prog/complexity_postdoctoral_fellowship_/ >

Complexity Postdoctoral Fellowship at Santa Fe Institute (apply by October 1st, 2025) An utterly unique opportunity to work on fundamental questions at the intersection of disciplines.

The fellowship offers:

freedom to pursue your own research agenda without boundaries up to three years in residence at the Santa Fe Institute dedicated funds for research and collaboration a structured leadership training program competitive salary and paid family leave opportunities for transdisciplinary collaboration with leading researchers worldwide TO APPLY: http://www.santafe.edu/sfifellowship For questions please contact sfifellowship@santafe.edu

Hilary Skolnik Program Manager Postdoctoral Fellows Santa Fe Institute hilary@santafe.edu

Hilary Skolnik <hilary@santafe.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

SunYat-senU VertEvoDevo MutliOmics

Postdoctoral Research Scientist in Vertebrate Evolutionary Morphology and Bioinformatics

Overview: The Koyabu Lab at Sun Yat-sen University (SYSU) is an international, multidisciplinary team investigating the evolution of the mammalian cranium through an integrative approach that combines paleontology, comparative anatomy, embryology, molecular developmental biology, and multi-omics. Our methodologies include x-ray microtomography, synchrotron imaging, geometric morphometrics, 3D histology, in situ hybridization, single-cell RNA sequencing, spatial transcriptomics, and light sheet fluorescence microscopy. We are recruiting five postdoctoral research scientists in the areas of evolutionary morphology (Position A), geometric morphometrics (Position B), evolutionary genomics (Position C), evolutionary developmental biology (Position D), morpho-informatics (Position E) to start in January 2026.

Sun Yat-sen University (SYSU) is a rapidly rising research-intensive university ranked #13 in the most recent Nature Index 2024 (https://www.nature.com/nature-index/research-leaders/2024/institution/all/all/global). The School of Ecology at SYSU is China's top-ranked institution in ecology and evolution, renowned for its research and academic excellence. Located in Shenzhen, China's innovation capital at the heart of the "Greater Bay Area" encompassing Hong Kong and Macau, the School represents SYSU's commitment to addressing pressing environmental challenges through cutting-edge research and interdisciplinary collaboration.

Qualifications for all positions: Ph.D. in vertebrate morphology, developmental biology, paleontology, evolutionary genomics, bioinformatics or related fields, and demonstrated record of productivity and publications. Obtained their Ph.D. within the past 36 months at the time of application.

Minimal responsibilities for all positions: To collaborate within a multidisciplinary team taking responsibility for research progress and research reporting, presentations at lab meetings and scientific meetings. To write grants, co-supervise students and assistants.

Position A (Evolutionary Morphology): Conduct comparative anatomical and developmental investigations of the bat cranium, with a particular focus on the inner ear and larynx. The research will utilize advanced 3D histological techniques to characterize morphological patterns associated with distinct echolocation behaviors. Qualifications: background in anatomy or paleontology with collection-based research

Position B (Geometric Morphometrics): Main Responsibilities: To reconstruct 3D models from histological sections and micro-/nano-CT data, and to conduct comparative analyses of cranial growth trajectories and modularity patterns in mammals using semi-landmark-based geometric morphometrics. Qualifications: advanced proficiency in geometric morphometrics

Position C (Evolutionary Genomics): Main Responsibilities: To perform evolutionary bioinformatics analyses, including comparative genome alignments, time-series bulk RNA-seq, time-series snRNA-seq, and time-series spatial transcriptomics of bats and closely related mammals. Qualifications: proficiency in bioinformatics

Position D (Evolutionary Developmental Biology): Main Responsibilities: To study cranial development in key mammalian orders using experimental developmental biology approaches, histological techniques, light sheet fluorescence microscopy, and time-series spatial transcriptomics. Qualifications: proficiency in wet lab and histology techniques

Position E (Morpho-informatics): Main Responsibilities: To study the relationship between prenatal time-series transcriptome data vs prenatal time-series 3D morphological shape change. Qualifications: experience in transcriptome data and proficiency in python

Salary and appointment term: This is a multi-year postdoctoral position, with an initial appointment of 24 months and the possibility of renewal for up to an additional two years. Qualified candidates may also apply for senior research positions at SYSU during their tenure. A highly competitive salary will be offered. Foreign researchers will be eligible for significant tax reductions. Those who hold Ph.D. from high-ranking universities will be eligible to receive an additional annual allowance of 120,000 RMB for three years from the Guangdong Provincial government. For details regarding the salary and allowance, do not hesitate to contact the assistant of Prof. Dai Koyabu, Ms. Yixuan Hong (675064474@qq.com).

Benefits: Postdoctoral apartments with good living conditions will be provided by SYSU. The university will facilitate admission for children of postdoctoral researchers to the affiliated schools of SYSU.

Start date and deadline: The position will be available from January 2026. The exact starting

— / —

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

---

UBritishColumbia PopGenomics

A two-year postdoctoral research position is available in the laboratory of Dr. Michael Russello at The University of British Columbia (Okanagan Campus) in the area of population and conservation genomics starting October 1, 2025. I am looking for a highly motivated individual to join our group studying the genomic basis of adaptation and vulnerability to changing environments in North American pikas. The project offers opportunities for both laboratory and field-based research, and direct collaboration with Provincial, Federal and Indigenous management agencies. Interested individuals must have strong bioinformatic and analytical skills. Prior experience with analyzing whole genome resequencing is highly desirable.

UBC is one of the world's leading universities, and is consistently ranked in the top 40. The university has two distinct campuses, one in Vancouver and one in Kelowna. UBC's Okanagan campus, located in the city of Kelowna, has over 10,000 students in seven faculties, with strong undergraduate and graduate programs. Situated in the heart of the Okanagan Valley, one of the most scenic regions in Canada, it offers an intimate learning environment and excellent opportunities for regional, national, and international scholarly activities.

The position requires a two-year commitment and comes with a completive salary that exceeds the NSERC scale as well as an excellent benefits package. To apply, e-mail your CV and contact information for three references to michael.russello@ubc.ca. Materials must be received by July 28, 2025 for full consideration, but late applications will be accepted until the position is filled. Visit the Ecological and Conservation Genomics Laboratory website (https://blogs.ubc.ca/russellolab/) for more information on our current research directions.

Dr. Michael Russello Professor, Population and Conservation Genomics The University of British Columbia, Okanagan Campus Department of Biology 3247 University Way, FIP346 Kelowna, BC Canada V1V 1V7 michael.russello@ubc.ca

"Russello, Michael" <michael.russello@ubc.ca>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

UCalifornia Berkeley HumanEvolGenetics

Post-doctoral position - University of California, Berkeley - Human Evolutionary Genetics.

Description: The Moorjani Lab (https://moorjanilab.org/) at the University of California, Berkeley uses computational and statistical methods to investigate questions in human evolutionary genetics, in particular to understand mutation rate evolution, demographic inference and archaic ancestry. A central aim in the lab is to understand the impact of evolutionary history on genetic variation and to apply this knowledge to learn about human history and disease. To this end, we use genetic data from ancient specimens and present-day species to learn about: (1) when key evolutionary events–e.g, introgression and adaptation–occurred in human history, (2) how different evolutionary processes such as mutation rate evolve across primates, and (3) how we can leverage these patterns to identify genetic variants related to human adaptation and disease. The research in the lab involves both development of new methods and large-scale genomic data analysis.

Recent publications from our lab: Kerdoncuff E*, Skov L*, Patterson N, Banerjee J, Khobragade P, , Chakrabarti SS, Chakrawarty A, Chatterjee P, Dhar M, Gupta M, John JP, Koul PA, Lehl SS, Mohanty RR, Padmaja M, Perianayagam A 12, Rajguru C, Sankhe L, Talukdar A, Varghese M, Yadati SR, Zhao W, Leung YY, Schellenberg GD, Wang YZ, Smith JA, Dey S, Ganna A , Dey AB, Kardia SLR, Lee J, Moorjani P. 50,000 years of Evolutionary History of India: Impact on Health and Disease Variation. Cell 188 (2025):13, 3389-3404.e6.

Iasi LM*, Chintalapati M*, Skov L , Mesa AB , Hajdinjak M, Peter BM, Moorjani P. Neandertal ancestry through time: Insights from genomes of ancient and present-day humans. Science 386.6727 (2024): eadq3010.

Gao Z, Zhang Y, Cramer N, Przeworski M, Moorjani P. Limited role of generation time changes in driving the evolution of the mutation spectrum in humans. eLife (2023):12, e81188.

Responsibilities: A successful candidate will develop and apply computational approaches to large genomic datasets to characterize patterns of population history and evolution. The main responsibilities include conducting research, attending regular lab meetings and journal clubs, and preparing research results for publication and presentations at scientific meetings. Opportunities may also exist for mentoring graduate and undergraduate students.

Required qualifications: Ph.D. or equivalent in genetics, genomics, computational biology or related fields and demonstrated record of productivity and publications. Experience with programming (e.g. C/C++, Python/ Perl, R or other programming languages), genomic data analysis and methods development.

Please contact Priya with your CV and a brief overview of research questions you are interested in pursuing.

Please also request three recommenders to send a letter of reference on your behalf. The position is open until filled.

Salary: This is a multi-year postdoctoral position (initial appointment is for 24 months and renewable annually up to two more years). Salary is commensurate with qualifications and experience.

Contact: Priya Moorjani Assistant Professor Department of Molecular and Cell Biology Center for Computational Biology https://moorjanilab.org/ Email: moorjani@berkeley.edu

Priya G Moorjani <moorjani@berkeley.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UCaliforniaLosAngeles ConservationScience

The 2026 UCLA La Kretz Center Postdoctoral Fellowship in California Conservation Science

The UCLA La Kretz Center for California Conservation Science invites applications for its 2026 Postdoctoral Fellowship in California Conservation Science. We seek to hire one or more postdoctoral scholars who conduct innovative biological research at the interface of applied and basic science. Our long-term goal is to help fund a cadre of innovative young scientists who will work closely with UCLA faculty, help broaden the mission of conservation science for the campus, and lead to long-term collaborations between our academic scientists and applied conservation practitioners that will direct and lead California conservation efforts.

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

The Nature Conservancy: Sophie Parker (restoration; urban conservation; invasive species)

Note: TNC has been a particularly active partner and cofunder in recent years, and we encourage applicants working with TNC mentors to consult : https://tnc.box.com/s/uetrddu6sncp3nipgn8a1hh6fi3jisgi LA Natural History Museum: Jann Vendetti (mollusk ecology and evolution; species natural history)

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

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

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

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

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

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

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

The La Kretz Fellowship is for two years, subject to review after the first year. The target start date is September 2026, but this date is quite flexible. The position offers a competitive salary, full benefits, and a research/travel allowance of $7500. Candidates who have recently completed their Ph.D. or will have completed it before their start date are encouraged to apply.

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

(i) Cover Letter: Briefly introducing yourself and your project

(ii) CV: Composed of your work and accomplishments.

(iii) Research and Management Accomplishments Statement (maximum one page)

(iv) Project Proposal: Lays out, in some detail, your project (e.g., motivation, methods, expected outcomes/results), why this work is

— / —

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

---

UCaliforniaLosAngeles MicrobiomePopGenetics

Postdoctoral research position at UCLA in microbiome / population genetics

The Garud lab is seeking a postdoc to join our group (https://garud.eeb.ucla.edu)in the Department of Ecology and Evolutionary Biology at the University of California, Los Angeles.Our lab focuses on quantifying evolutionary dynamics in natural populations, with an emphasis on the human gut microbiome. The position may be either100% in the Garud lab or joint with Kirk Lohmueller's group, also at UCLA.

The successful candidate will have substantial input in the specific nature of their research project. However, the project should broadly fit within the lab's goals of learning about evolution in natural populations.There are a wide range of projects to choose from, including developing fundamental population genetic theory, as well as application of theory and models to metagenomic data. The candidate is also welcome to work on other study systems besides human microbiomes, including Drosophila and Humans.

Candidates should have a Ph.D. in biology, genetics, computer science, bioinformatics, statistics, computational biology, or a related field. A background in population genetics/evolutionary genomics is preferred. As this is a computational position, proficiency in programming in R, Perl, or Python, and shell scripting is essential. Preference will be given to candidates with a strong publication record, evidence of substantial research productivity, and ability to successfully communicate scientific information.

Interested candidates should send to Nandita Garud atngarud@ucla.eduthe following:

- A letter describing your background and motivations pursuing a postdoc in the Garud Lab

- CV that includes a brief 1-2 sentence description of your contribution to past research projects.

- Contact information for two referees who can provide references upon request

The University of California is an equal opportunity/affirmative action employer.

–

Nandita Garud, PhD Associate Professor Department of Ecology and Evolutionary Biology Department ofHuman Genetics, DavidGeffen School of Medicine University of California, Los Angeles 621 Charles E. Young Drive South Los Angeles, CA 90095-1606

Lab website:https://garud.eeb.ucla.edu Nandita Garud <ngarud@g.ucla.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UCalifornia SantaBarbara EvolPlantPolyploids

Dear EvolDir community,

The Sharbrough lab in the EEMB Department at the University of California - Santa Barbara is recruiting a postdoctoral researcher who is broadly interested in evolutionary genomics, with an emphasis on polyploidy, to work on an NSF-funded project. The conceptual direction of the position encompasses uncovering the genetic mechanisms of cytonuclear responses to polyploidization and the phenotypic consequences of polyploidy for cellular respiration and photosynthesis. Experience in some or all of the following areas would be relevant:

analysis of NGS datasets, comparative genomics, molecular evolution, population genetics, molecular genetics, confocal microscopy, plant transformation, and plant phenotyping. The postdoctoral scholar will have primary responsibility for the collection, quality control, and analysis of single-cell RNAseq (and other 'omics) data from a diverse panel of diploid and polyploid wheat and Arabidopsis accessions. The postdoc will also be responsible for phenotyping photosynthetic and respiratory performance in diploids vs. polyploids. As part of this work the postdoc will be guided in the development of their own independent research program and contribute to lab efforts to disseminate our science to other members of the plant genomics community (e.g., by writing papers and attending conferences) and to the public at large (e.g., by participating and designing lab outreach activities).

This is a full-time position. Competitive salary and benefits commensurate with experience (salary range: $69,073 - $82,836). The initial appointment is for 2 years with the potential for an additional year based on satisfactory performance and funding availability.

The University is especially interested in candidates who can contribute to the diversity and excellence of the academic community through research, teaching, and service as appropriate to the position.

The University of California is an Equal Opportunity/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 status, protected veteran status, or any other characteristic protected by law.

Basic Qualifications (required by the time of application):

Applicants must have completed all requirements for a PhD program (or equivalent) except the dissertation in plant biology or related discipline, at the time of application.

Additional Qualifications (required at the time of start):

PhD in plant biology or related discipline

Preferred Qualifications:

2 years experience in comparative genomics/transcriptomics 1 year experience at the command line (R/Python preferred) 2 years experience with various wet-lab techniques (e.g., plant transformation, plant physiology, molecular genetics, etc.) Strong writing skills/experience Demonstrated experience working as part of a collaborative team Interest in graduate/undergraduate mentoring

The full job posting can be found here:

https://recruit.ap.ucsb.edu/JPF02986 Please feel free to forward this email and the job posting to anyone that might be interested in the position.

Thanks!

Joel

Joel Sharbrough, Ph.D. (he/his) Assistant Professor Ecology, Evolution, and Marine Biology University of California, Santa Barbara website: sharbroughlab.com email: jsharbro@ucsb.edu

Joel Sharbrough <jsharbro@ucsb.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

UCopenhagen PopulationGenomics

Postdoc in Population Genomics at the Villum Center for Global Mountain Biodiversity, Globe Institute Faculty of Health and Medical Sciences, University of Copenhagen

We are looking for a highly motivated and dynamic person for a 2 ï¿½ -year position as postdoc at the Villum Center for Global Mountain Biodiversity at the GLOBE Institute to commence after October 2025.

The position will be based at the Globe Institute. The Institute's main purpose is to address basic and applied scientific questions through interdisciplinary approaches. The institute operates at the intersection of natural and medical sciences and the humanities. Information on the institute can be found at www.globe.ku.dk . The research will be conducted at the Center for Global Mountain Biodiversity, a Villum Center of excellence led by Professor Carsten Rahbek. The center comprises 20 scientific staff, technicians and students focused on understanding how mountains shape the distribution and diversity of life on Earth, with particular attention to tropical mountain biodiversity. The Center works end-to-end. Inspired by natural history knowledge, we engage in rigorous fieldwork around the world to build and improve an assemblage of biological data sets on species' distributions and traits. We use a range of tools from novel macroecological process-based and null models to cutting-edge DNA and genomic techniques. This holistic approach strengthens our ability to address fundamental questions about the distribution and diversity of life on Earth. For an overview of our macroecological mountain research, two review papers by Rahbek et al. published in Science in 2019 offer a useful introduction to the background and scope of our work on global mountain biodiversity.

The Villum Center for Global Mountain Biodiversity is housed within the Center for Macroecology, Evolution and Climate (CMEC; www.macroecology.ku.dk) and the Section for Biodiversity at the Globe Institute, University of Copenhagen. CMEC is a leading center of excellence with a cross-disciplinary research program addressing fundamental questions on the origin, maintenance, conservation and future of life and biological diversity on Earth. Our team of 40+ researchers representing over 14 nationalities juxtaposes faculty staff scientists from the fields of macroecology, historical biogeography, oceanography, evolutionary biology, community ecology, population biology, climate change research, conservation biology and environmental economics.

We prioritize teamwork and close collaboration both within the Center and across our global research network. Our group culture is supportive, inclusive, and driven by mutual respect, where diverse skills and experiences are valued. We are committed to fostering not only scientific excellence, but also professional growth and career development at every stage

Job description We are offering a 2ï¿½ year postdoc position with Professor Carsten Rahbek. In collaboration also with Assoc. Prof Rute Andreia Rodrigues da Fonseca, Assoc Prof. Peter Hosner and Assist Prof Anna Brï¿½niche-Olsen, you will work with whole genome data to understanding the spatio-temporal dynamics of two aspects: 1) how species with current small populations and limited geographical ranges have been impacted by climate changes through glacial and interglacial periods during the Quaternary period and since the last glaciation period (with additional impact of humans), and 2) how species with very small population sizes persist at extremely low densities for centuries to perhaps 10,000s of years. According to conventional knowledge, long-term persistence at species with extremely low population sizes with apparently very little geneflow should not be likely due to stochastic factors.

Your job This position will mainly focus on Andean birds, especially those of high altitudinal Polylepis forest of the Andes but could also be expanded to other genomic data sets. Polylepis forests are today characterized by isolated fragments distributed mainly from Ecuador through Peru to Bolivia. However, evidence from pollen records indicates that these forests were much more widespread and continuous in the past, and they have likely fluctuated noticeably with periods of glaciation. Applicants are expected to engage in ongoing research projects using the center's data/resources and to contribute to further development of new projects. For the Andes, we currently have whole genome sequencing data from 700 specimens of 24 bird species inhabiting Polylepis forests. Additionally, for all the bird species we have high quality, curated distributions at ï¿½ degree spatial resolution, trait data, phylogenies, and genomic data for 5000 bird species (being part of the B10k program aiming at sequencing all bird species in the world)

— / —

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

---

UDenver PDF PhD Tech EvolSpongeImmuneSystems

Multiple Positions Available - Immunity, Symbiosis, and Evolutionary Cell Biology in Sponges

The Nichols Lab at the University of Denver is recruiting PhD students, postdoctoral researchers, and research technicians to join our team exploring the evolution of animal immune systems using the freshwater sponge Ephydatia muelleri. Our work is centered on the cellular foundations of multicellular evolution in animals, and integrates cell biology, host-microbe interactions, and evolutionary immunology. Our research program includes:

Innate immune signaling

Discovery of novel lectins and glycosidases for bacterial recognition

Structure, function, and evolution of the mucosal epithelial barrier

Experimental infections with Legionella pneumophila

Microscopy and manipulative cell biology in sponges

We are seeking motivated candidates with experience or strong interest in bench-based molecular or cell biology, host-microbe interactions, microscopy, or unconventional model systems. While computational skills are a plus, we are especially excited to hear from those with experience in wet-lab research. Prior work with sponges is not required.

These are multi-year positions and we welcome applicants at all stages - from recent undergraduates seeking research experience to postdocs ready to launch independent careers.

To apply, please email Scott Nichols (Scott.Nichols@du.edu) with a brief statement of interest, your CV, and the names of professional references.

Scott Nichols, Ph.D.

Associate Professor Department of Biological Sciences University of Denver

Office : 2101 E. Wesley Ave, 203 Mudd

SHIPPING ADDRESS: Attn: Scott Nichols Lab Biological Sciences, 288 Mudd University of Denver 4925 E. Pacific Place Denver, CO 80222

email: sa.nichols321@gmail.com lab homepage: Nichols Lab Homepage phone: 303-871-5658

Scott Nichols <sa.nichols321@gmail.com>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UFlorida SensoryEvoDevo

The McCulloch Lab is looking for a Postdoctoral Associate with up to two years of guaranteed funding to work on genetics, genomics, and cell physiology of sensory opsin-expressing cell types in the sea anemone, Nematostella vectensis.

We are an integrative and comparative lab, using multidisciplinary cutting-edge techniques and making use of phylogenetically informative species and lineages to answer major questions about the evolution of gene to phenotype relationships.

LOCATION: Main Campus (Gainesville, FL)

DEPARTMENT: BIOLOGY

MINIMUM REQUIREMENTS: PhD in Biology, Development, Molecular Biology, Genetics, Neuroscience, Evolutionary Biology or similar field. The ideal candidate should have a strong background in one or more of the following: developmental biology, genetics, molecular techniques, bioinformatics/genomics, electrophysiology, calcium imaging, microscopy/imaging, in situ hybridization/immunohistochemistry.

Demonstrated independent and critical thinking abilities, excellent communication skills, ability to take initiative and work independently.

JOB DESCRIPTION: A postdoctoral associate is available in the lab of Dr. Kyle McCulloch in the department of Biology at the University of Florida. Expected start date is flexible, but ideally the candidate will start on or near November 1, 2025.

The lab broadly seeks to understand how genes relate to phenotype in the context of visual system evolution. The lab is multidisciplinary and integrative, with genomics, evo-devo, neurophysiology, and behavior projects ongoing. Work will primarily be related to the genetics and physiology of opsin-expressing sensory cells in the lab's model system, Nematostella vectensis. Depending on expertise and interest, the successful candidate may work on one of multiple areas of focus that are available. The postdoctoral associate will be mentored and encouraged to seek extramural fellowships and develop their own project ideas, in addition to working toward the lab's research goals.

This position will be initially awarded for one year, and, contingent upon strong performance and conduct can be renewed for another year. Position is dependent on available funding after the second year.

EXPECTED SALARY: $60,000/year

REQUIRED QUALIFICATIONS: PhD in Biology or related field.

PREFERRED: Expertise in Evo-Devo methods, genetics, genomics, molecular biology, neurophysiology, microscopy, and/or behavior methods. Demonstrated ability to critically think and work independently. Strong publication record.

SPECIAL INSTRUCTIONS TO APPLICANTS: For full consideration, applications must be submitted online. Click on Apply Now at the top of this posting. A complete application includes (1) a letter (no more than one page) of application summarizing the applicant's qualifications, interests, and suitability for the position, (2) a complete curriculum vitae, and (3) the names and email addresses of three references must be provided. An email will be sent to your references, requesting them to upload their confidential letter to the submission packet.

Applications will be reviewed beginning September 15, and the position will remain open until filled. Only complete applications will be reviewed at this time.

This is a time-limited position.

Link to job application: https://explore.jobs.ufl.edu/en-us/job/536499/postdoctoral-associate Kyle J McCulloch, PhD (he/him) Assistant Professor Department of Biology University of Florida Gainesville, FL 32611

"McCulloch, Kyle" <k.mcculloch1@ufl.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UGoettingen EvolGenomics

At the University of Gï¿½ttingen -Public Law Foundation-, GRK 2984 Evolutionï¿½re Genomik: Folgen biodiverser Fortpflanzungssysteme, there is one position as

Postdoc in Evolutionary Genomics and Bioinformatics Entgeltgruppe 13 TV-L/100%

to be filled. Starting date is 1/1/2026. The position is limited to 30/06/2028.

This is position be mainly engaged to guide and coordinate synthesis papers of the research training groups, with a focus on nuclear genome evolution in eukaryotes. The goal of our research training group, including 11 subprojects, is to analyze the evolution of genomes in sexual and asexual organisms in animals, plants, fungi, and microorganisms. Our collaborative efforts will provide a better understanding of the "paradox of sex" in nature. The task of this postdoc will be to develop analysis pipelines, train PhD students in specific workshops and courses, and to develop overarching meta-analyses and joint papers, and present results in talks and at conferences. The postdoc will get ample opportunity to bring in own ideas into these joint papers, and will benefit from first authorships of these papers, from broadening methodical expertise, and by establishing scientific networks.

Please see further details on the postdoc positions at https://uni-goettingen.de/de/events/687613.html, see first postdoc position, indicate your interest in your motivation letter.

Successful candidates will have - an outstanding Doctorate/PhD in Biology, with a focus on evolutionary genomics, or in Bioinformatics/Computational Biology, with a focus on eukaryotic genomes, - experience in genomics, specifically with large genomes (also polyploids), and ample experience in statistical methods, proved by publications - proven background in theory related to evolution of reproductive systems and "paradox of sex" - excellent command of scientific English (oral and written, min. equivalent to C1), -experience in guidance and training of students in evolutionary genomics, bioinformatics and biostatistics - experience in teamwork and in writing multi-authored papers.

Your application must include a letter of motivation, CV, lists of publications, transcripts of your PhD, and certificates of English language proficiency as pdf files.

We offer an excellent research team on the Gï¿½ttingen Campus, including a Center for National High Performance computing and an AI service center. Experience with innovative methods, networking and high-impact publishing within the RTG team will be gained.

The University of Gï¿½ttingen is an equal opportunities employer and places particular emphasis on fostering career opportunities for women. Qualified women are therefore strongly encouraged to apply in fields in which they are underrepresented. The university has committed itself to being a family-friendly institution and supports their employees in balancing work and family life. The University is particularly committed to the professional participation of severely disabled employees and therefore welcomes applications from severely disabled people. In the case of equal qualifications, applications from people with severe disabilities will be given preference. A disability or equality is to be included in the application in order to protect the interests of the applicant.

Please upload your application in one pdf file including the usual documents until 20/9/2025 on the application portal of the university using this link: http://obp.uni-goettingen.de/de-de/OBF/Index/-75997. For more information get in touch with the spokesperson Elvira Hï¿½randl directly via E-Mail: elvira.hoerandl@biologie.uni-goettingen.de, Tel. +49 551 39 28540 .

Please note: With submission of your application, you accept the processing of your applicant data in terms of data-protection law. Further information on the legal basis and data usage is provided in the Information General Data Protection Regulation (GDPR)

"Menster, Antje" <antje.menster@uni-goettingen.de>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

UPennsylvania EvolGenomics MachineLearning

Post-doctoral position at the University of Pennsylvania - Machine Learning and Evolutionary Biology

The Mathieson Lab at the University of Pennsylvania (https://saramathieson.github.io/lab) is hiring a computational postdoc to join the lab. We focus on projects related to machine learning (ML), novel architectures for biological data, interpretability, and comparison of ML with traditional methods. Other projects in the lab include genetic data representation, privacy-preserving generative models, and pedigree-based methods for understanding recent evolution. Application-based projects are also possible, including to mosquito data from the MalariaGEN project as well as humans or other species.

Experience with Python and either PyTorch or TensorFlow is preferred but not required. Please email me if you have any questions or are interested in applying: smathi@sas.upenn.edu. To apply, send a CV, unofficial transcript, and names/contact of 2-3 professional references.

Sara Mathieson

Assistant Professor of Machine Learning in Biology University of Pennsylvania

https://saramathieson.github.io/lab Associate Editor for Genome Biology and Evolution (GBE)

https://academic.oup.com/gbe "Mathieson, Sara" <smathi@sas.upenn.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

USouthCarolina RadiationAndGenomicAnalysis

Postdoctoral Position(s) in Genomic Analyses of Free-Breeding Dog Populations: Chornobyl, Pacific Islands, Atomic Bomb Test Sites and Other Hot Areas

Hi Folks! We are looking for postdoctoral research scientists to help with projects using WGS data to address questions related to evolution in free-breeding dog populations around the world. Of particular interest are evolutionary responses to radiation exposure to dog populations in Ukraine (especially Chernobyl), atomic bomb test areas (e.g. Kazakhstan, the Marshall Islands), and other Pacific Islands. Many other exciting questions related to evolutionary history, effects of selection (natural and otherwise), disease, and development are also being addressed.

The ideal candidate(s) will be smart, hard-working and have some experience doing analyses with genomic and/or population genetic data. The goal will be to use modern bioinformatic approaches for analysis of WGS and related data to address fundamental evolutionary and population genetics questions related to mutation-selection balance, the relationship between genotype and phenotype, epigenetic influences on evolution, bridging genomic and quantitative genetics and other related topics. A passion for dogs and genetics would be an asset.

These projects represent an ongoing collaboration between research teams led by Tim Mousseau at the University of South Carolina and Elaine Ostrander at the NIH. See the following links for more info about the PI's:

https://irp.nih.gov/pi/elaine-ostrander https://-sc.edu/study/colleges_schools/artsandsciences/-biological_sciences/our_people/directory/-mousseau_timothy.php Successful applicants will be housed at the NIH in Bethesda, MD, and could have opportunities to engage in field work in addition to genomic and bioinformatics research if so desired. Compensation is generous. This is a unique opportunity for anyone wishing to gain experience using the latest genetic tools to address fundamental evolutionary questions as a member of one of the most productive labs in this field in the world.

Interested? Please contact mousseau@sc.edu for more information.

Tim Mousseau, PhD, FRGS, FACLS, FAAAS

Professor of Biological Sciences

University of South Carolina

Columbia, SC 29208 USA

+1-803-920-7704

mousseau@sc.edu

http://cricket.biol.sc.edu/Mousseau/Mousseau.html Google ScholarResearchGate

"Mousseau, Timothy" <MOUSSEAU@sc.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UStAndrews Phylogenetics

Post-doctoral Research Fellow in Phylogenetics

Applications are sought for a committed Post-doctoral Research Fellow to work with Dr Rui Borges conducting research for the Austrian Science Fund (FWF) funded project P37050 entitled “Inferring gene flow from phylogenies with ubiquitous genomes”. Evolutionary biologists have gathered substantial evidence showing that most species evolve while exchanging genetic material. However, the extent of these gene flow events is not yet fully understood. With new genome sequencing technologies, we now have the data to quantify these events, but we need new mathematical models and statistical methods, especially over longer time scales, where the direction and magnitude of gene flow are challenging to infer. This project aims to develop these tools, advancing our understanding of how species diverge and, ultimately, how biodiversity forms.

The successful applicant will have (or be near to completion of) a PhD and have expertise in any two of the following: (1) evolutionary biology, (2) statistical inference, (3) mathematical modelling and (4) computational biology. We also welcome applications from statisticians and mathematicians or computer scientists, even without prior knowledge from evolutionary biology, that wish to diversify their career.

Details here: https://www.vacancies.st-andrews.ac.uk/Vacancies/W/4377/0/454526/889/research-fellow Rui Pinto Borges <rb251@st-andrews.ac.uk>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UStockholm YeastEvolutionaryGenomics

Postdoctoral position in Yeast Evolutionary Genomics at the University of Stockholm, Sweden

The Stelkens Lab is hiring a highly motivated person for a 2-year fully funded postdoc position. Research topics include but are not limited to 1) test for parallel climate adaptations in yeast from Europe and South America, 2) describe the genetic architecture of thermal traits, 3) test for the evolution of pathogenicity as a by-product of thermotolerance, and 4) use data-driven predictive modelling to identify key drivers of thermal adaptation.

The selected candidate will use the powerful microbial model system budding yeast (Saccharomyces spp.), experimental evolution, and cutting-edge genomic tools to study evolutionary processes. We are looking for candidates with a strong interest in evolutionary biology, ideally with some experience in experimental evolution and/or molecular, population, and quantitative genetics. Prior training in yeast cultivation, statistics, and programming (e.g. R, Python) is a plus. Applicants should be independent thinkers, well-organized, good communicators, and happy to work in an international team.

Applicants are required to hold a PhD degree. The degree must have been completed at latest before the employment decision is made, but no more than three years before the closing date. An older degree may be acceptable under special circumstances.

The work will mostly be lab-based but may include some fieldwork. There is flexibility within the project for the postdoc to develop their own projects. The successful candidate will receive a salary and full social benefits.

Work environment: Stockholm University is located four metro stops from the centre of Stockholm, one of the most beautiful and dynamic capital cities of Europe. SU is home to a vibrant scientific community, including the Science for Life Laboratory and the Swedish Museum of Natural History. Sweden is a free and open society, and strives to be one of the worlds most innovative and research-intensive nations. We enjoy a respected system of democracy and individual rights, free health care, freedom of speech, a free press, the right to scrutinize those in power, and access to beautiful nature. Most Swedes speak English.

We recommend reading relevant literature to prepare your application (e.g. doi.org/10.1073/pnas.2423262122 < https://www.pnas.org/doi/10.1073/pnas.2423262122 >, doi.org/10.1093/molbev/msac242 < http://doi.org/10.1093/molbev/msac242 >, doi.org/10.1371/journal.pgen.1011154 < http://doi.org/10.1371/journal.pgen.1011154 >, doi.org/10.1093/evolinnean/kzae023 < http://doi.org/10.1093/evolinnean/kzae023 >).

Application: Use the official Stockholm University job portal to submit your formal application, including a statement of motivation, relevant expertise, your CV, and the contact details of at least two references. Link to application portal with more details is here: https://su.varbi.com/en/what:job/jobID:841228/ Start date: Start date October 2025 or as per agreement. Application deadline: 15. August 2025

Informal enquiries to Rike Stelkens: rike.stelkens@zoologi.su.se

Rike Stelkens Associate Professor Yeast Evolutionary Genomics Department of Zoology Stockholm University, Sweden

email: rike.stelkens@zoologi.su.se tel: +46 (0) 816 4223 lab website: stelkenslab.com

Rike Stelkens <rike.stelkens@zoologi.su.se>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UTennessee Knoxville PlantMorphologicalEvol

Subject: UTennessee.Knoxville.PlantMorphologicalEvolution

Recruiting an NSF-funded Post-Doctoral Researcher in EEB The Budke Lab in the Department of Ecology & Evolutionary Biology at the University of Tennessee (http://jmbudke.github.io/) is seeking a Post-Doctoral Research Associate to work on an NSF-funded project. This project is investigating morphological evolution in a phylogenetic context using moss plants as the experimental system.

The research responsibilities will include (1) assembling morphological datasets using the literature and herbarium specimens, (2) compiling DNA sequence datasets from publicly available resources and laboratory-based methods using herbarium specimens, and (3) combining these data to analyze the evolution of morphological structures across a phylogeny.

Opportunities will also be available to develop novel research questions focusing on the functional morphology, physiology, and evolution of the parent-offspring relationship in mosses. Supervising and mentoring undergraduate researchers in both the laboratory and herbarium will be required.

An additional aim of this project is to build awareness of and appreciation for plants and botanical natural history collections. As part of the team, the postdoc will participate in hands-on outreach events, such as Darwin Day. The postdoc will also co-lead a May-term course for undergraduate students on collections-based research. Qualifications

A PhD in biology, ecology and evolution, systematics, or a related field.

Research experience in molecular systematics and plant morphology. Proficiency using bioinformatic tools to infer phylogenetic trees and perform comparative analyses. Excellent verbal and written communication skills. Motivation to engage in botanical outreach and education. Apply online at the link below by 17 August 2025 for full consideration. https://fa-ewlq-saasfaprod1.fa.ocs.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1/job/3791 J.M. Budke, PhD (she/her) Associate Professor & Herbarium Director (TENN) Ecology and Evolutionary Biology University of Tennessee 569 Dabney Hall Knoxville, TN 37996

Office: 431 Hesler Biology Building Office Phone: (865) 974-6204 Lab: 433 Hesler Biology Building Lab Phone:(865) 974-2635 TENN Herbarium Office: 102Temple Hall HerbariumPhone:(865) 974-6212

Budke Laboratory Research:http://jmbudke.github.io/ GLOBAL Bryophyte & Lichen TCN: https://globaltcn.utk.edu/ "Budke, Jessica" <jbudke@utk.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UTexas sanAntonio EvoDevoGenomics

Post-doctoral position - University of Texas San Antonio - Evolutionary and Developmental Genomics

Description:

The Evolutionary & Developmental Genomics (EDGe) lab (https://www.anti-sense.org) at the University of Texas San Antonio combines experimental and computational approaches to study the evolution of genetic conflicts in the germ line, molecular mechanisms underlying sex chromosome drive, and the developmental processes that are compromised as a result of the activities of selfish genetic elements. We foster an environment of collaboration and mentorship, offering opportunities to develop new skills and pursue independent ideas that align with the lab's mission.

Project Focus:

The successful candidate will investigate the consequences of meiotic drive on male gametogenesis and fertility in Drosophila. The project leverages multiple non-model Drosophila species to uncover the molecular and developmental mechanisms underlying gametic dysfunction, and the consequences of sex chromosome meiotic drive, which leads to impaired segregation of sex chromosomes and reduced fertility/infertility.

Recent publications relevant to the proposed project:

1. Vedanayagam J. Small-RNA-mediated suppression of sex chromosome meiotic conflicts during Drosophila male gametogenesis. 2025. Biochemical Society Transcations 53(1): 281-291

2. Vedanayagam J., Herbette M., Mudgett H., Lin C., Gunasinghe H., McDonough- Goldstein C., Dorus S., Loppin B., Meiklejohn C., Dubruille R., Lai E.C. 2023. Essential and recurrent roles for hairpin RNAs in silencing de novo sex chromosome conflict in Drosophila simulans PLoS Biology 21(6): e3002136

3. Vedanayagam J., Lin C., Papareddy R., Nodine M., Flynt A., Wen J., Lai E.C. 2023. Regulatory logic of endogenous RNAi in silencing de novo genomic conflicts PLoS Genetics 19(6):e1010787

4. Vedanayagam J., Lin C., Lai E.C. 2021. Rapid evolutionary dynamics of an expanding family of meiotic drive factors and their hpRNA suppressors Nature Eco. & Evol. 5(12):1613-1623

Responsibilities:

A successful candidate will conduct genetic crosses in Drosophila and perform genomic and transcriptomic analyses to characterize drivers and suppressors of meiotic drive. Key responsibilities include conducting research, contributing to manuscript preparation and dissemination of results at conferences, participating in regular lab meetings and journal clubs, and working independently while mentoring junior researchers. Additionally, excellent written and oral communication skills are a plus!

Required qualifications:

Ph.D. in Evolutionary Biology, Genetics, Genomics, Developmental Biology, or related field. Demonstration of research productivity with first-author and contributing author manuscripts is highly valued. Furthermore, bioinformatics skills are highly preferred (especially R, but also Python or other relevant languages).

Please contact Jeffrey with a cover letter describing your research experience and interests, a CV including publications, and contact information for 2-3 references. The position is open till 8/18/2025 or until a suitable candidate is identified on a rolling basis.

Salary:

This is a grant-funded position, and the salary range is based on the NRSA stipend levels stipulated by the National Institutes of Health, commensurate with experience and qualifications. This is a full-time position with an initial appointment of one year, renewable annually based on performance and funding availability.

Contact:

Jeffrey Vedanayagam Assistant Professor Department of Neuroscience, Developmental And Regenerative Biology Faculty affiliate: School of Data Science University of Texas San Antonio https://www.anti-sense.org Email: jeffrey.vedanayagam@utsa.edu

Jeffrey Vedanayagam <jeffrey.vedanayagam@utsa.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

UWesternAustralia MidwaterSensoryBiol

Hello Evolutionary Biology Colleagues,

Please help us get the word out about a postdoc opportunity at the University of Western Australia dealing with midwater biodiversity and sensory biology.

https://external.jobs.uwa.edu.au/mob/cw/en/job/520501/research-associate-evolutionary-biology Many thanks for spreading the word to your stellar students and colleagues, Karen

Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 osbornk@si.edu http://orcid.org/0000-0002-4226-9257 Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012, Washington, D.C. 20013-7012 USA

Courier Address: Smithsonian Institution, MR 0163, Natural History, West Loading Dock, 10th and Constitution Ave NW, Washington, D.C. 20560

** Due to my schedule, you may get an email outside of your normal working hours. Please do not feel that you need to respond outside of your normal working hours. **

"Osborn, Karen" <OsbornK@si.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

WorkshopsCourses

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online aDNAPopulationGenomics Sep22-26

Dear all,

Only a few seats remain for our upcoming online course “Population Genomics Using Ancient DNA Data” (September 22-26)!

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

In this course, we will explore how ancient DNA (aDNA) is generated and analyzed in population genomics research, with a focus on eukaryotic genomes.

Participants will begin by learning how aDNA differs from modern DNA and how to account for degradation and contamination. The rest of the course will cover key statistical methods used to analyze aDNA, combining theoretical lectures with hands-on exercises based on real research questions.

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

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

“info@physalia-courses.org” <info@physalia-courses.org>

Online BayesianPhylogeneticsBEAST2 Sep18-20

Hi everyone

Instats is excited to offer a 2-day seminar, Bayesian Phylogenetics with BEAST2, running live streaming September 18 - 20 and led by Dr Joëlle Barido-Sottani from the Institute of Biology, ENS-PSL, CNRS. Bayesian phylogenetics has transformed evolutionary research by allowing scientists to incorporate prior knowledge, quantify uncertainty, and analyse complex molecular-evolution models in a coherent probabilistic framework. Over two intensive days, Dr Barido-Sottani will guide participants from the theoretical foundations of Bayesian inference to hands-on proficiency with BEAST2 the modular, plugin-driven platform that uses MCMC to sample across tree space and deliver robust divergence-time and parameter estimates. You’ll learn how to specify informative priors, analyse diverse data types such as DNA sequences and traits, conduct thorough post-analysis diagnostics, and interpret posterior distributions with confidence. Whether you are a PhD student, academic, or research professional already familiar with basic phylogenetics, this seminar will equip you with cutting-edge skills to integrate Bayesian workflows into your own evolutionary studies and produce more reliable, publication-ready results.

https://instats.org/seminar/bayesian-phylogenetics-with-beast2 Sign up today to secure your spot, and feel free to share this opportunity with colleagues and students who might benefit!

Best wishes

Michael Zyphur Professor and Director Institute for Statistical and Data Science https://instats.org mzyphur@instats.org

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

Online CRISPR Oct13-16

Dear colleagues,

registrations are now open for the third edition of the Physalia course: Introduction to CRISPR for Ecology and Evolution Studies (online, 13-16 October) Course website: (https://www.physalia-courses.org/courses-workshops/course53/)

This course offers a practical and theoretical introduction to CRISPR-Cas9 genome editing, with a focus on its application in evolutionary and ecological research. Participants will gain the skills needed to design and implement gene knockout (KO) experiments, with a particular emphasis on non-model organisms.

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

Understand the fundamentals of the CRISPR-Cas9 system

Design and evaluate effective sgRNAs for gene knockouts

Assemble and optimize Cas9/sgRNA mixes

Perform genotyping and mutation screening

Analyze deep sequencing data from KO experiments

Apply CRISPR-based approaches to their own research projects

This course is ideal for researchers, graduate students, and technicians in biology, ecology, and related fields who are interested in integrating CRISPR tools into their work.

For the full list of our courses an workshops, please visit: (https://www.physalia-courses.org/courses-workshops/course53/)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

“info@physalia-courses.org” <info@physalia-courses.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online DemographicInference Nov17-19

[2025 Workshop on Demographic Inference]

Dear all,

We are excited to invite you to our upcoming online workshop on demographic inference. This is a great opportunity to learn how to prepare your sequencing data using ATLAS and to infer demographic history using GADMA. Basic knowledge of UNIX and command-line tools is required.

DATES: November 17-19, 2025 FORMAT: Online FEE: Free of charge COURSE WEBSITE: https://gadmaworkshop.github.io/workshops/2025-11-17-19/ Registration is open until November 2, so please apply soon!

If you have any questions, feel free to email Ekaterina Noskova (ekaterina.e.noskova@gmail.com)

Best regards, Ekaterina Noskova & Daniel Wegmann

Ekaterina Noskova <ekaterina.e.noskova@gmail.com>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online EnvironmentalMetagenomics Oct13-17

Dear all,

registrations are now open for the Physalia online course on Environmental Metagenomics, taking place from 13-17 October (9 am - 1 pm Berlin time).

Course website: (https://www.physalia-courses.org/-

courses-workshops/environmental-metagenomics/)

This hands-on training is designed for researchers interested in exploring microbial communities using state-of-the-art metagenomic approaches. The course will cover both read-based and assembly-based methods, with a focus on metagenome-assembled genomes (MAGs) and the integration of short- and long-read sequencing data (Illumina and Nanopore).

By completing this course, you will: - Understand the basics of metagenomic sequencing and bioinformatic approaches for the analysis of metagenomic data - Be able to plan and execute a metagenomic sequencing project - Have an up-to-date knowledge on the bioinformatic tools and best practices for the analysis of metagenomes - Be able to choose the right tools and approaches to answer your specific research question - Have confidence to learn new methods needed to answer your research question

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

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

info@physalia-courses.org

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online IntrotoNetworks Sep22-Oct1

Dear colleagues,

Registration is now open for the Transmitting Science course: “Introduction to Network Analysis and Modelling”.

Dates and schedule: Online live sessions on September 22nd, 24th, 26th, and 29th & October 1st, 2025; 10:00 to 14:00 (Madrid time zone).

Course webpage: https://www.transmittingscience.com/courses/systems-biology/introduction-to-network-analysis-and-modelling/ Network analysis is increasingly important in phylogenetics, as it allows us to capture evolutionary patterns that cannot be represented by traditional tree models alone.

Programme:

* Introduction to networks: Understand the basics of what networks are and their representation. * Random Graphs and Null Models: Explore fundamental concepts in random graphs and null models to comprehend the structure of real-world networks. * Community Structure and Mixing Patterns: Investigate how networks exhibit interaction structure and analyze mixing patterns within them. * Ranking in Networks: Examine algorithms for ranking nodes within networks to identify their significance. * Introduction to Dynamics on Networks and Dynamics of Networks: An overview of how dynamical processes work on networks and models of network growth.

More upcoming Transmitting Science courses: https://www.transmittingscience.com/courses/#upcoming-courses Best regards,

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses Bluesky @soledeesteban.bsky.social X @SoleDeEsteban Orcid: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or http://transmittingscience.com/additional-terms. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es . Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

Online NanoporeDirectRNAseq Oct27-30

Dear all, registrations are now open for the upcoming online course: An Introduction to Nanopore Direct RNA Sequencing (RNA004) Dates: 27-30 October - 2-7 PM Berlin time

Full program and registration details are available (https://www.physalia-courses.org/courses-workshops/-course59c/)

This 4-day course offers a comprehensive introduction to Nanopore direct RNA sequencing using the latest RNA004 chemistry. Participants will gain both theoretical background and hands-on experience with key topics such as:

Basecalling and data QC

Transcript quantification and isoform analysis

PolyA tail length measurement

RNA modification detection (e.g., m6A)

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 mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

"info@physalia-courses.org" <info@physalia-courses.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online NGSDataAnalysis Oct20-24

Dear all,

We are pleased to announce the Autumn School in Bioinformatics, an online course running from 20-24 October, designed to introduce researchers to the concepts and practical skills needed for analysing Next Generation Sequencing (NGS) data.

Course website: (https://www.physalia-courses.org/-courses-workshops/course68/)

Course Highlights:

Comprehensive Training: From quality assessment to genome assembly & annotation, RNAseq, differential gene expression, and phylogenomics.

Practical Skills: Hands-on sessions using the Linux command line, R/RStudio, Docker/Singularity, and AWS for reproducible workflows.

Beginner-Friendly: We start with foundational Linux skills and guide participants through genomic, transcriptomic, and phylogenomic analyses no prior NGS experience required. Learning Outcomes:

Confidently handle and analyse NGS data

Understand the strengths and limitations of sequencing technologies, using both short- and long-reads

Apply state-of-the-art methods to a variety of -omics datasets For the full list of our upcoming courses, visit: (https://www.physalia-courses.org/courses-workshops/)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

"info@physalia-courses.org" <info@physalia-courses.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online PhylogeneticInferenceWithBeast2 Oct27-Nov7

Dear colleagues,

Transmitting Science is offering the 5-day full course “Bayesian phylogenetic inference with BEAST2”.

Course webpage: Registration and more information: https://www.transmittingscience.com/courses/-evolution/bayesian-phylogenetic-inference-with-beast2/ Online live sessions on October 27th, 29th, and 31st & November 3rd, 5th, and 7th, 2025. 35 hours (21 hours of online live lessons, plus 14 hours of participants working independently with tutored exercises)

Instructors: Dr. Joï¿½lle Barido-Sottani [1] (Ecole Normale Supï¿½rieure de Paris, France) and Dr. Bethany Allen [2] (ETH Zurich, Switzerland)

Course Overview:

Bayesian phylogenetic inference is a powerful tool for reconstructing phylogenies while accounting for complex evolutionary dynamics. It allows prior knowledge to be integrated into the inference, and also provides a detailed picture of the uncertainty present in the dataset. However, the number and complexity of the available models and options can be daunting for users, and can make it difficult to apply inference tools effectively in practice. In this workshop, participants will learn the theoretical concepts underlying the different models involved in Bayesian phylogenetic inference and get hands-on experience using these models in BEAST2. Particular attention will be given to more complex tree models, such as the fossilized birth-death model used to integrate past information into phylogenies, as well as rate-heterogeneous models, which allow for variations in evolutionary dynamics across clades. Finally, the course will give practical information on setting up and troubleshooting analyses in BEAST2.

Do not hesitate to contact me or write to courses@transmittingscience.com if you have any questions.

Best wishes

Sole

Upcoming Transmitting Science courses: www.transmittingscience.com/courses Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/ Bluesky @soledeesteban.bsky.social X @SoleDeEsteban Orcid: https://orcid.org/0000-0002-2049-0890 Links:

[1] https://www.transmittingscience.com/-instructors/joelle-barido-sottani/ [2] https://-/www.transmittingscience.com/instructors/-bethany-allen/ Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

Online PopGenLowCoverageWGS Oct20-23

Dear all,

We are excited to announce that registrations are now open for our upcoming online course (6th edition) “Population Genomic Inference from Low-Coverage Whole-Genome Sequencing Data” taking place from October 20-23.

Course website: (https://www.physalia-courses.org/-courses-workshops/course64/) Course Overview: This course offers a cost-effective approach to survey genome-wide variation at a population scale using low-coverage sequencing. Participants will learn how to navigate the challenges of high genotyping uncertainty through probabilistic frameworks, essential for accurate population genomic inference. Key topics include: Workflows centered around genotype likelihoods for whole-genome and reduced representation studies.

Methods and algorithms in the ANGSD software package and related programs.

Best-practice guidelines for processing and analyzing low-coverage sequencing data.

Target Audience: This course is ideal for researchers with experience in next-generation sequencing (NGS) (e.g., exome, RAD, pooled sequencing) who are interested in low-coverage whole-genome sequencing. It is also suitable for those seeking an introduction to the ANGSD software and its probabilistic framework.

Prerequisites: Participants should have a basic background in population genomics and familiarity with NGS data. Knowledge of UNIX-based command line and R is advantageous. Participants without prior experience in

Unix and R should complete suggested tutorials beforehand, as the course will not cover these environments in detail.

Course Outcomes: By the end of the course, participants will: Understand the use of whole-genome sequencing for population genomics.

Recognize the challenges and statistical frameworks of low-coverage sequencing data.

Be able to build bioinformatic pipelines for various population genomic analyses using ANGSD/ngsTools/Atlas.

Teaching Format: The course includes interactive lectures, small exercises, and longer independent practical sessions each day. Data for exercises will be provided.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/course64/)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

“info@physalia-courses.org” <info@physalia-courses.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online RADseqUsingStacks Oct27-31

Dear all,

registrations are now open for the upcoming Physalia online course: RAD-seq Data Analysis

Dates: 27-31 October Course website: (https://www.physalia-courses.org/courses-workshops/course16/)

This course provides a comprehensive introduction to reduced representation genome sequencing methods (e.g., RAD-seq, ddRAD, 2bRAD, GBS) with a focus on analysing data using Stacks. Participants will learn how to go from raw short-read data to informative genome variants suitable for population genetics, phylogenetics, and genome-wide association studies.

Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group.

For the full list of our courses and workshps, please visit: (https://www.physalia-courses.org/courses-workshops/course16/)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

“info@physalia-courses.org” <info@physalia-courses.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

Online RNAseqAnalysis Jul29-31

The Computational Biology Core at the University of Connecticut is hosting virtual bioinformatics workshops this summer! We still have space available in our RNA-seq Analysis Workshop (virtual but live instruction - July 29-31).

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

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

Learn more & register here: [https://bioinformatics.uconn.edu/cbc-workshops/] WHERE: Virtual (MS Teams) WHEN: 10:00 AM - 2:00 PM EST COST: $400 (UConn affiliates)/$500 (External participants)

Registration is first come, first served.

Questions? E-mail: [cbcsupport@helpspotmail.com]

"Lambert, Karelyn" <zsc25001@uconn.edu>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online SpeciesDistributionModels Sep22-24

Dear colleagues,

Registration is open for our upcoming online course: Species Distribution Modeling with Bayesian Additive Regression Tree (BART) Methods

Dates: 22-24 September

Course website: (https://www.physalia-courses.org/courses-workshops/barts/)

This course will introduce BART methods for species distribution modeling (SDM) and other ecological applications. Participants will learn how BART improves over traditional SDM approaches and gain hands-on experience using the embarcadero and dbarts R packages to select predictors, train models, and project species distributions.

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

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

"info@physalia-courses.org" <info@physalia-courses.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online TranscriptomeBioinformaticTools Oct1-10

Dear colleagues,

Registration is open for the online edition of the course "Bioinformatic tools for transcriptomic data analyses".

Dates: October 1st, 3rd, 6th, 8th, and 10th, 2025.

More information and registrations: https://www.transmittingscience.com/courses/genetics-and-genomics/bioinformatic-tools-for-transcriptomic-data-analyses/ Course Overview:

This is an introductory course aiming at guiding participants through the execution of the most common pipelines used to analyse different types of transcriptomic data generated through RNA sequencing with NGS technologies.

The course focuses on the use of Linux-based software and tools, although no previous experience with Linux is required.

Best wishes,

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses Bluesky @soledeesteban.bsky.social X @SoleDeEsteban Orcid: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or http://transmittingscience.com/additional-terms. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es . Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online TransposableElements Nov3-7

Dear all,

We are pleased to announce the upcoming Physalia online course: Bioinformatic Analysis of Transposable Elements Dates: 3-7 November Course website: (https://www.physalia-courses.org/courses-workshops/course24/)

This course provides a comprehensive overview of transposable element (TE) biology and computational TE analysis. Participants will learn how to discover, annotate, curate, and analyse TEs in genome assemblies, raw read data, and transcriptomes combining both theoretical foundations and hands-on bioinformatics training.

No prior experience in TE analysis is required, but familiarity with the command line is helpful.

More information about our courses and workshops: (https://www.physalia-courses.org/courses-workshops/course24/)

Feel free to share with anyone who might be interested. Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

"info@physalia-courses.org" <info@physalia-courses.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. 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 me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. 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@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.