EvolDir

April 1, 2026

Month in Review

Foreword

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

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Antwerp ConservationGenetics Aug26-28

European Conservation Genetics Meeting on August 26-28, 2026, in Antwerp, Belgium.

Please visit our Website with information on the themes, keynote speakers, preliminary schedule,abstract submission (before April 30), registration/payment link, hotel accommodation and venue. This is an in-person meeting with 5 non-parallel sessions and poster sessions every day. We pay special attention to open (panel) discussions and early career researchers, and offer possibilities for an artistic experience and guided excursions to a nature reserve.

Please, spread the news¡‘

Peter Galbusera Research Coordinator - Antwerp Zoo Centre for Research and Conservation

Peter Galbusera <Peter.Galbusera@kmda.org>

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Bangkok BarcodeOfLife Nov2-6

Dear friends and colleagues, Early bird registration and abstract submission for the 10th International Barcode of Life Conference have opened: http://dnabarcodingconference.com We are inviting colleagues to join us November 2-6, 2026, in Bangkok, Thailand to exchange the latest scientific discoveries and advancements in biodiversity genomics.

We are delighted to welcome delegates to the Siam Kempinski Hotel Bangkok, our venue for the conference. Ideally situated in the heart of Bangkok, the hotel is easily accessible via public transit, with direct connections to the BTS Skytrain at Siam Station and links to Bangkok's airport rail and metro systems.

We are calling for abstract submission across a wide range of topics related to our conference theme Building on Barcodes: Impacting Science & Society (https://dnabarcodingconference.com/abstracts/). The abstract submission deadline is May 29, 2026. Early bird registration ends on August 2, 2026.

As in past conferences there will be a day of pre-conference workshops. Two of those will be held concurrently in the morning, and two more in the afternoon.

https://dnabarcodingconference.com/program/workshops/ Workshops have a limited capacity based on room size, and early registration is encouraged.

We are looking forward to meeting you in Bangkok.

Dirk Steinke

on behalf of the Conference Organizing Committee

Dr. Dirk Steinke (he/him) | Research Scientist Centre for Biodiversity Genomics | University of Guelph CBG Room 109 | 50 Stone Road E | Guelph, Ontario | N1G2W1 519-824-4120 Ext. 53759 | dsteinke@uoguelph.ca | http://biodiversitygenomics.net Dirk Steinke <dsteinke@uoguelph.ca>

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Bath UK InfectionImmunitySymbiosis Apr16-17

The Royal Entomological Society is holding a special interest group meeting on 'Insect Infection, Immunity and Microbionts' in Bath, UK on 16-17 April 2026.

Keynote speakers are: Ann Tate; Vanderbilt University, Tennessee, USA Stuart Reynolds; Emeritus Professor of Biology, University of Bath Abstract submissions for oral and poster presentations are welcome from all research areas across the broad themes of infection, immunity, microbiomes and symbiosis.

For this meeting we are happy to invite contributions from those who consider these topics within non-insect invertebrates, provided the research is relevant to insect systems.

Please follow the link for more details and to submit an abstract: https://www.royensoc.co.uk/event/infection-immunity-microbionts-special-interest-group-sig/ Abstract submission deadline is 23 March 2026.

Ailsa McLean <ailsa.mclean@biology.ox.ac.uk>

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BrockU OntarioEcologyEthologyEvolution Apr30-May2

On behalf of the organizing committee, Brock University is pleased to invite you to attend the 52nd Ontario Ecology, Ethology and Evolution Colloquium from April 30th to May 2nd, 2026. The theme of this year's conference is 'Co-existing within nature' and if you have any questions or comments, please email us at our official email at oe3cofficial@gmail.com. Registration closes March 29 so register now!

For more information: https://www.oe3c.ca/ We are very excited to announce our three plenary speakers: Ecology: Dr. Jesse Pop https://www.wiselab.ca/our-team Ethology: Dr. Mï¿½lanie Guigueno http://www.guiguenolab.ca/ Evolution: Dr. Nancy Chen https://popgenchenlab.github.io/ Location: 1812 Sir Isaac Brock Way, St. Catharines, ON L2S 3A1

When: April 30th to May 2nd, 2026

Registration: The following website can be used for registration to OE3C: registration website < https://brocku.universitytickets.com/w/event.aspx?id=2736 >

Accommodations: Information can be found at our website under the 'Plan your visit' tab. https://www.oe3c.ca/plan-your-visit Please see the attached flyer and more information will be shared soon!

The OE3C 2026 LOC

Kiyoko Gotanda, PhD (she/her)

Assistant Professor Brock University | Department of Biological Sciences | 1812 Sir Isaac Brock Way | St. Catharine's, ON L2S 3A1 | Canada <x-apple-data-detectors://5/1> Traditional lands of the Haudenosaunee and Anishinaabe peoples

Attend the inaugural GRC Conference in Urban Evolution & Ecology < https://www.grc.org/urban-ecology-and-evolution-conference/2027/ >

kgotanda@brocku.ca

http://www.kiyokogotanda.com http://www.pidgephotography.com Kiyoko Gotanda <kgotanda@brocku.ca>

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CambridgeUK VisualisingBiologicalData Apr14-17 DeadlineApr6

Dear Evoldir !

There is still time to register for in-person or online participation at the 16th edition of Visualizing Biological Data. If you cannot make it to Cambridge for April 14-17th, you can watch online, and later engage with speakers and other participants during virtual Masterclass and VIZBI 26 Workshop sessions on 21st and 23rd April.

All workshop participants are able to submit posters for in person or virtual presentation, and publications for VIZBI 2026's Proceedings. See https://vizbi.org/2026 for full details and the link to register. Please also help spread the word by forwarding this email, and displaying the VIZBI 2026 Poster < https://fullstack.vizbi.org/emails/2026/poster/Poster.pdf >.

VIZBI 2026's speaker lineup (https://vizbi.org/2026/People) includes: * Fernanda Viegas & Martin Wattenberg (Google & Harvard, USA): 'Visualization & AI' * Maja Divjak (PeterMac, Australia) 'Scientific storytelling' * Martin Dohrn (Ammonite, UK) 'Ballad of the birds' * Jan Willem Tulp (TULP Interactive, Netherlands) 'Seeing things differently' * Kat Holt (LSHTM, UK) 'Antimicrobial resistance genomics' * Ian Holmes (Berkeley, USA) 'Strings of Life' * Robert Finn (EMBL-EBI, UK) 'Metagenomes' * Marta Szachniuk (PP, Poland) 'RNA structure prediction' * Jernej Ule (KCL, UK) 'RNA regulatory networks' * Maik Wolfram-Schauerte (U. Tï¿½bingen, Germany) 'Integrative transcriptomics & phages' * Syma Khalid (Oxford U., UK) 'Bacterial cell envelopes' * Ivan Viola (KAUST, Saudi Arabia) 'Biomolecular landscapes' * Brady Johnston (UWA, Australia) 'Protein modeling & animation' * Heba Sailem (KCL, UK) 'AI & spatial omics' * Henning Hermjakob (EMBL-EBI, UK) 'Cellular pathways' * Jason Swedlow (CZI BIohub, USA) 'Cellular imaging' * Paola Perin (U. Pavia, Italy) 'Neuroimmunology & physiology' * Thomas Hollt (TU Delft, Netherlands) 'Pixel-level spatial biology' * Teresa Zulueta-Coarasa (EMBL-EBI, UK) 'Bioimage Archive' * Chiara Barbieri (U. Cagliari, Italy) 'Genetics & molecular anthropology' * Timo Lucas (U. Tï¿½bingen, Germany) 'Tracking microbial systems' * Anne Jungblut (Natural History Museum, UK) 'Complex microbial structures'

The University of Dundee is a registered Scottish Charity, No: SC015096

"James Procter (Staff)" <J.Procter@dundee.ac.uk>

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ClevelandOH Evolution Jun20-24

Evolution 2026 is the joint meeting of the American Society of Naturalists, the Society of Systematic Biologists, and the Society for the Study of Evolution. The meeting is one of the premiere international opportunities for sharing research on evolutionary biology.

The conference will be held in 2 parts: A 2 day virtual conference with live online workshops, talks, symposia, and networking events in late May, followed a few weeks later by a 5 day in-person conference in Cleveland, OH, USA at the Huntington Convention Center, June 20-24, 2026. The in-person conference will include plenary addresses from the three societies, concurrent sessions, posters, workshops, mixers, and special events.

Early-bird registration closes April 15.

https://www.evolutionmeetings.org/ Tara A Pelletier, Ph.D.

Associate Professor, Biology 279 Center for the Sciences Box 6931, Radford University Radford, VA 24142 540-831-5146 Website < https://sites.google.com/site/taraapelletier/ >

"Pelletier, Tara" <tpelletier@RADFORD.EDU>

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Columbus Ohio Imageomics Apr14-17

The NSF-funded Imageomics Institute (https://imageomics.org) is hosting the

First Imageomics Conference April 14-17, 2026

at The Ohio State University in Columbus, OH

There will be plenty of room for discussions and insights, including:

- Big Ideas Lab: Mapping the high-level visions and global future of imageomics. - NextGen Day: A faculty-free zone for students and postdocs to connect and lead. - Tools Workshops: Co-design and refine imageomics tools through live, hands-on iteration. - Networking mixers, brainstorming sessions, and collaborative surprises.

Learn more and Register: go.osu.edu/imageomics2026 < http://go.osu.edu/imageomics2026 > (There is no registration fee.)

Conference Overview:

Tuesday, April 14

Pre-Conference Activities:

NextGen Day: Open to all students and postdocs, this faculty-free zone is thoughtfully crafted by NextGens for NextGens. This special day promises an array of engaging activities tailored to the unique needs and aspirations of emerging leaders in their respective fields.

Wednesday, April 15

Conference Day 1 | Big Ideas Lab:

Ignite new research through rapid-fire talks, strategic networking, and future-building labs - a day designed to turn bold ideas into the next era of Imageomics.

Thursday, April 16

Conference Day 2 | Build. Code. Discover.:

Kick off the morning with collaborative breakouts, and rapid-fire tool building and demonstrations before diving into an afternoon of discussion-based technical labs, finishing with a closing celebration to honor the five years of the Imageomics Institute and the community that made it possible.

Friday, April 17

Hands-on Workshop: Part 2: Workshop - Designing for Discovery: Shaping Imageomics Tools for Biologists. https://imageomics.osu.edu/events/2026/04/designing-discovery A follow-up from the tool demonstrations during the Imageomics conference, this half-day workshop will offer a deeper dive with a smaller group of conference participants and will include interactive, hands-on activities. This workshop is dedicated to bridging the gap between advanced computational tools and biological discovery. Within the field of imageomics, researchers have built a powerful suite of open-source tools; now, our mission is to evolve these into usable, community-wide resources. By partnering directly with biologists across all career stages, we aim to pressure-test existing workflows, uncover novel applications, and refine our messaging to ensure these tools are as intuitive as they are innovative.

Travel funding is available for those who require it. Visit the workshop event page (https://imageomics.osu.edu/events/2026/04/designing-discovery) for additional details.

Hilmar Lapp -:- ORCID:0000-0001-9107-0714 < https://orcid.org/0000-0001-9107-0714 > -:- GitHub:hlapp < https://github.com/hlapp >

Hilmar Lapp <hilmar.lapp@gmail.com>

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CornellU CanineFelineGenomics Jun28-Jul1

This summer's ICCFGG conference featuring sessions on canine and feline population genomics and evolution will be held at Cornell University from Jun 28 - Jul 1. The initial abstract deadline is fast approaching; please submit your talk or poster abstracts at the conference website, iccfgg.org, by the April 1st deadline.

The conference will officially kick off the evening of Sunday, June 28th and run through 5:00 PM EST on Wednesday, July 1st.

The conference website lists transportation and lodging options, and a number of discounted hotel rooms in downtown Ithaca are available for conference attendees. Transportation will be provided daily between downtown and the conference venue at the Cornell University College of Veterinary Medicine. Letters of support are available if required for international travel. A limited number of travel grants (up to $750 each) are also available for students or researchers from underrepresented countries.

This year's conference is graciously sponsored by Hill's Pet Nutrition and features numerous scientific sessions, activities and keynote presentations by Andrew Clark (Cornell) and Zhiping Weng (UMass Medical). Learn about the latest advances in canine and feline genomics, and network with researchers, veterinarians and companies working in companion animal health and genetics.

See you in Ithaca!

The International Organizing Committee

Adam Boyko (boyko at cornell dot edu) Claire Wade Eva Furrow Hannes Lohi Jeff Brockman Jeff Kidd Jeffrey Schoenebeck Jennifer Meadows Leigh Anne Clark Maja Arendt

Adam Boyko <arb359@cornell.edu>

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Cornwall UK Evolution Jun29-Jul3

*** Evolution x Ecology 2026 Conference in Cornwall, UK ***

DEADLINE FOR ABSTRACT SUBMISSION: APRIL 1 AT NOON (UK TIME).â€â€

It is still possible to registration for ExE 2026, an evolutionary ecology conference hosted by the University of Exeter's Centre for Ecology and Conservation in beautiful Cornwall.—

Register now at https://evoxeco.uk In addition to cutting-edge research at the interface of evolution and ecology, we have excursions to some of the best places in Cornwall and a fantastic set of pre- and post-conference workshops.—

Any questions, email the organising team at info@evoxeco.uk

We looking forward to welcoming you to Cornwall!

Erik Postma Barbara Tschirren Ben Longdon Alastair Wilson Mark Hanson

evoxeco.uk https://sites.exeter.ac.uk/exe/ "Postma, Erik" <E.Postma@exeter.ac.uk>

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Eawag Zurich OnTriploidyInParasiticWorms Apr14-17

Symposium on Triploidy in Parasitic Worms April 14-17, 2026 Eawag, Dübendorf, 8600, Switzerland

The Symposium on Triploidy in Parasitic Worms is a meeting of researchers from various fields of helminthology. The main idea of the Symposium is to discuss how triploidy (or polyploidy more generally) can affect the ecology and evolution of parasitic worms and, consequently, host-parasite dynamics.

During the symposium, we will have talks on such topics as (but not limited to): Host-Parasite Interaction Drug Resistance Cytogenetics and genomics Evolution of reproductive systems Ecology and Distribution of Triploidy

The preliminary schedule of the Symposium is on the website: https://www.pathogenevolution.ch/-symposium-on-triploidy While most presenters are invited speakers, the Symposium is open to anyone interested in parasitic worms and polyploidy. You are welcome to attend any talk or present results of your own study if you think that your work is connected to any of the topics mentioned before. In any case, don't hesitate to contact me at:

viktor.kovalov@eawag.ch

"Kovalov, Viktor" <Viktor.Kovalov@eawag.ch>

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Firenze Evolution2026 Sep6-10

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

REGISTRATION OPEN

Dear friends and colleagues, Registration is now open for the *SIBE Evoluzione 2026 Congress*, which will take place in *Firenze from 6 to 10 September*. The scientific program will be organized around the following symposia:

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

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

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

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

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

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

Alessio Iannucci Tenure Track Researcher (RTT) Department of Biology University of Florence Via Madonna del Piano 6, I-50019 Sesto Fiorentino (FI), Italy email:alessio.iannucci@unifi.it Tel. +390554574741

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Halifax ZoonosesAMRBioinformatics Jul6-9

As a joint effort across three current CIHR Health Research Training Platforms, registration is now open for a national One Health-focused research meeting at Dalhousie University, July 6-9 that will hopefully be of interest to ICG members!

The meeting will cover evolutionary topics related to emerging zoonoses, antimicrobial resistance, and bioinformatics. We aim to have a strong trainee focus complemented by talks from leading Canadian researchers and training workshops on topics such as research data management and outbreak response. There is plenty of trainee opportunities to present, informative methodologically-focused talks, and an optional hands-on set of biosecurity-focused tours and talks at the agricultural campus.

Registration is only $50 (+$20 for the conference dinner and ag-campus trip) for the full 3.5-day meeting. The program and full details can be found at https://zambi.ca Please register if you are interested in attending or speaking!

Cheers,

Fin

Dr. Finlay Maguire Assistant Professor Computer Science and Community Health & Epidemiology Dalhousie University

Lab Website: maguire-lab.github.io

Finlay Maguire <Finlay.Maguire@dal.ca>

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KewGardens UK PlantsFungi Jun29-Jul1 TravelBursaries

Last call: Travel bursaries for the State of the World’s Plants and Fungi Symposium

Apply by 16 March

View in browser

Dear friends and colleagues of Kew,

Hurry - the deadline for travel bursary applications for the international

State of the World's Plants and Fungi Symposium is approaching quickly. Read on to find out how to apply, and how to submit a poster abstract.

State of the World's Plants and Fungi Symposium

>From 29 June to 1 July 2026, join international experts at Kew and online to explore the digitisation of herbarium and fungarium collections, including its applications and implications. Don't miss your chance to be part of the conversation to shape the future of biodiversity research.

Travel bursaries

We are offering three bursaries to support in-person attendance at the symposium for delegates from low-income countries. Each bursary covers the symposium registration fee, attendance at the symposium dinner and up to 3,000 towards travel and accommodation costs. Visit the symposium webpage for details about eligibility requirements and how to apply.

Deadline for applications: 16 March 2026.

Apply for a bursary

Apply for a bursary

Poster abstracts and prizes

In-person attendees are invited to submit an abstract for a poster presentation accompanied by a one-minute flash talk. Prizes will be awarded for the best student and early career researcher posters.

Deadline for abstracts:24 April 2026.

Submit an abstract

Submit an abstract

For more information, visit the symposium web page.

We look forward to welcoming you to the symposium.

Best wishes,

The State of the World's Plants and Fungi Steering Committee

kew.org/sotwpf-symposium

Kew Science <email@enews.kew.org>

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LongIsland AmericanSocietyNaturalists Proposals Apr30

The American Society of Naturalists

Proposals for Symposia at the ASN stand-alone meeting in Long Island 2027

Due April 30, 2026

The American Society of Naturalists will be holding an East Coast meeting in 2027 (announcement < https://www.amnat.org/announcements/ASN-mtg-2027.html > here) in Glen Cove, New York, to hold our stand-alone conference - Long Island 2027 - on 8-12 January 2027!

Have an idea for a special symposium? We want to hear it!

The ASN Symposium Committee invites you to submit proposals for a special symposium. Proposed symposium topics should support the Society's goal to advance the conceptual unification of the biological sciences and to further knowledge in evolution, ecology, behavior, and organismal biology. Topics could center around important emerging issues in evolution, ecology, or behavior or focus on a pivotal historical paper, tracing its impact and exploring current cutting-edge research inspired by this work. A budget of up to $5,000 is available to defray travel, registration, and lodging costs for speakers.

Proposals should include (1) a title; (2) a description of the symposium topic (up to one page); (3) a list of six speakers, including institutional affiliations, who have agreed to participate in the symposium; (4) a justification for the symposium, explaining why the topic and speakers are appropriate for an ASN symposium (up to one page).

Please submit proposals by email (cas383@miami.edu) no later than midnight Eastern Time on April 30, 2026. Send your proposal as a single pdf attachment, under subject heading "ASN Long Island 2027 Symposium Proposal".

In line with the ASN's commitment to diversity, we encourage including speakers from groups who have been historically excluded from STEM. Therefore, proposals that include a diverse list of speakers from a range of backgrounds, institutions, career stages, geography, gender, race, etc. are especially encouraged. The Society's selection committee will evaluate proposals based on their potential to attracting substantial audience and stimulate discussion, the significance and timeliness of the topic, and on the topic's differing substantively from recent symposia hosted by the Society. Applicants will be notified of the decision before the end of May 2026.

Christopher Searcy ASN Symposium Committee Chair Department of Biology University of Miami cas383@miami.edu

cas383@miami.edu

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LongIsland Proposals ASN Standalone 2027

The American Society of Naturalists

Proposals for Symposia at the ASN stand-alone meeting in Long Island 2027

Due April 30, 2026

The American Society of Naturalists will be holding an East Coast meeting in 2027 (https://www.amnat.org/announcements/ASN-mtg-2027.html) in Glen Cove, New York (our biennial stand-alone conference - Long Island 2027) on 8-12 January 2027!

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Christopher Searcy ASN Symposium Committee Chair Department of Biology University of Miami cas383@miami.edu

"Fuller, Becky Claire" <rcfuller@illinois.edu>

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LundU HermaphroditicOrganisms Apr22-23 DeadlineMar31

The SHOW registration deadline is approaching fast!

SHOW (Simultaneously Hermaphrodite Organisms Workshop) is a forum for researchers studying hermaphroditic species to share their findings and plan long-term collaborations. Running since 2011, the workshop initially focused on simultaneous hermaphrodites (organisms producing male and female gametes simultaneously) but now covers hermaphrodite evolution more broadly. The event spans two days and emphasizes diverse presentations from different research groups, fostering a wide range of ideas across various systems and disciplines. Its relaxed environment encourages early-career researchers to present in topics included population genetics, gene expression, sexual conflict, mating systems, gamete evolution, and experimental evolution.

Our website is now open for registration! https://colin-olito.github.io/SHOW2026.github.io/ SHOW 2026 will be held in Lund, Sweden, on April 22nd-23rd. We can offer free registration for up to 50 participants.

Keynote speakers: Beatriz Vicoso (https://ist.ac.at/en/research/vicoso-group/) Sophie Karrenberg (https://www.uu.se/en/department/ecology-and-genetics/research/plant-ecology-and-evolution/karrenberg-lab)

Welcome to Lund in April!

On behalf of the SHOW organizing committee.

Dr. Jessica K. Abbott Professor of Evolutionary Genetics Department of Biology Division of Biodiversity and Evolution Lund University Kontaktvï¿½gen 10 223 62 Lund, Sweden Phone: 046 222 9304 Website: https://tinyurl.com/jessicakabbott "It is those who know little, and not those who know much, who so positively assert that this or that problem will never be solved by science." - Charles Darwin, Descent of Man

Jessica Abbott <jessica.abbott@biol.lu.se>

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Memphis Pangenomics May11-15

Memphis.PangenomicsCourseConferenceBiohackathon.May11-15

MemPanG26 Memphis Pangenomics 2026 Epicenter HQ, Memphis, TN, USA | May 11-15, 2026

https://pangenome.github.io/MemPanG26/ A 5-day event combining a hands-on practical course, a one-day conference, and a biohackathon, focused on computational pangenomics building and analyzing pangenome graphs from whole-genome assemblies and applying them to comparative genomics, variation analysis, sequence alignment, and phenotype association.

Practical Course / Workshop (Mon-Tue, May 11-12) Participants will learn to build pangenome graphs using tools such as PGGB, ODGI, and VG, and apply them to complex research questions involving multiple genomes. Topics include pangenome graph construction, sequence partitioning, implicit pangenomics, pangenome-based genotyping, and local ancestry inference. Lunch provided. Prerequisite: solid knowledge of Linux/shell; familiarity with genomics formats (FASTA, VCF, BED) is a plus.

Conference (Wed, May 13) Free & Open to the Public In-person and virtual attendance. Speakers will cover methods, genome assembly, data visualization, AI, and collaborative pangenome projects across diverse species contexts. Open call for speakers submission deadline April 15, 2026.

Biohackathon (Thu-Fri, May 14-15) Collaborative software development on pangenomic tools. Bring your own projects!

Instructors: Erik Garrison (UTHSC), Andrea Guarracino (TGen), Franco Marsico (UTHSC)

Organizers: Erik Garrison, Andrea Guarracino, Flavia Villani, Pjotr Prins, Enza Colonna, Tamara Brock

Registration deadline: April 10, 2026 Cost: $250 (academic, financial support available) / $500 (industry)

Contact: aguarracino@tgen.org, vcolonna@uthsc.edu

Vinc(Enza) Colonna | enza.colonna@gmail.com | +39 339 7485 437 https://colonnalab.github.io/laboratory_WebPage/ enza colonna <enza.colonna@gmail.com>

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MersinU Turkey EEBST EvolBiol Jul6-10

We would like to announce the Ecology and Evolutionary Biology Symposium in Turkey (EEBST), which will take place this year on 06-10 July 2026 at the Mersin University,Mersin.

EEBST2026 will be the twelfth in a series of international symposia organized annually by the Ecology and Evolutionary Biology Society of Turkey. We invite you to share your latest research and be a part of this exciting event. Please note the following important details for your submission:

Deadline: Please ensure all abstracts are submitted by April 15th.

Word Limit: Abstracts must not exceed 300 words.

Submission Link: You can access the abstract submission system directly through our website: https://eebst.ekoevo.org/ If you have any questions or need further assistance, please feel free to email us at eebst@ekoevo.org.tr.

We would be grateful if you help us to disseminate the news in your networks. We look forward to having you all in Mersin this July. EEBST 2026 Organizing Committee

Sibel Kucukyildirim,PhD Hacettepe University Department of Biology Beytepe ï¿½ankaya Ankara 06800 TURKEY

sibel kucukyildirim <sibelkucukyildirim@gmail.com>

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Mertola NaturalSelection AbstLastCall Apr17-19

MERTOLA EVOLUTION CONFERENCES- 2026 EDITION: NATURAL SELECTION IN THE WILD 17 - 19th of April 2026, Mertola, Portugal

!!!!! Abstract submission is closing on the 6th of March!!!!! Dear Colleagues,

It is a pleasure to announce that the registration for the second edition of Mertola Evolution Conferences (MECs), which will occur in the Spring at the beautiful historical town of Mertola, Southern Portugal, is now open. Do not miss this opportunity and submit your abstract asap!

The MECs are annual meetings on Evolutionary Biology (each year a specific topic) for researchers and students to present cutting-edge studies on the field, as well as a forum for informal discussion, fostering new ideas and collaborations among researchers all over the world. Mertola Conferences are promoted by EBM - Biological Station of Mertola in collaboration with other national and international institutions.

Mertola is located in Southeast Alentejo region of Portugal, near the Spanish border, crossed by the Guadiana River and in the center of the Natural Park of Guadiana Valley. The antiquity of Mertola is attested by the many archaeological remains that prove the continuous human occupation of this territory. Despite being and biodiversity hotspot of Mediterranean ecosystems, the first traces of human presence dating back to the Neolithic period, five thousand years ago, with different civilizations, like Iberians, Phoenicians, Greeks and Carthaginians. More information at https://www.visitmertola.pt/mertola-vila-museu/ The MEC 2026 edition, entitled "Natural Selection in the Wild". It counts with prominent speakers in the field: Rosemary Gillespie (University of California, Berkeley, USA), Jeremy Searle (Cornell University, USA), Matthew P. Hare (Cornell University, USA), Silvia Matesanz Garcia (Universidad Rey Juan Carlos, Spain) Jose Melo-Ferreira (University of Porto)

The conference programme will be announced next week and includes a Bird Watching Tour in the last day of the conference around Mertola, where an enormous variety of species can be observed.

Important information Venue and date: Cineteatro de Mertola, April 17th to 19th 2026 Abstract submission deadline: 6th of March 2026 Registration deadline: 13 of March 2026

Registration and abstract submission: Among the submitted abstracts, only 8 will be selected for a short oral presentation. For registration and abstract submission, please fill this form: https://forms.gle/gGWuWpgWs4Ak2fDj7 Participation is free of charge for BIODIV Students (M BGE & PhD) & CIBIO's TwinLabs (If applicable, payment will be made to Associacao BIOPOLIS - VAT No. 516033727). Fees: 60 euros (other students and Biopolis non-students) | 120 euros (other participants).

The organizing committee, Jeremy Searle Miguel Carneiro Rui Faria Paulo Celio Alves

Rui Faria, PhD

1. Researcher and SEAGEN Group Leader CIBIO, Centro de Investigaï¿½ï¿½o em Biodiversidade e Recursos Genï¿½ticos, InBIO Laboratï¿½rio Associado BIOPOLIS Program in Genomics, Biodiversity and Land Planning Campus de Vairï¿½o Rua Padre Armando Quintas, nï¿½ 7 4485-661, Vairï¿½o, Portugal

2. Invited Assistant Professor, Department of Biology Faculty of Sciences at the University of Porto, Rua Campo Alegre s/n 4169-007, Porto, Portugal

Webpages: Littorina Research Community < https://littorina.at.biopolis.pt/ > https://rmigueldefaria.wixsite.com/farialab-1 https://sites.google.com/biopolis.pt/littorina/winklewatch Rui Faria <ruifaria@cibio.up.pt>

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Mertola NaturalSelection lastcall Apr17-19

MERTOLA EVOLUTION CONFERENCES- 2026 EDITION: NATURAL SELECTION IN THE WILD 17 - 19th of April 2026, Mertola, Portugal

Dear Colleagues,

The deadline for abstract submission and registration for the second edition of Mertola Evolution Conferences (MECs) was postponed.

New dates: Abstract submission deadline: 16th of March 2026 Registration deadline: 20 of March 2026

Use the form below to register!

The MECs are annual meetings on Evolutionary Biology (each year a specific topic) for researchers and students to present cutting-edge studies on the field, as well as a forum for informal discussion, fostering new ideas and collaborations among researchers all over the world. Mertola Conferences are promoted by EBM - Biological Station of Mertola in collaboration with other national and international institutions.

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Registration and abstract submission: Among the submitted abstracts, only 8 will be selected for a short oral presentation. For registration and abstract submission, please fill this form: https://forms.gle/gGWuWpgWs4Ak2fDj7 Participation is free of charge for BIODIV Students (M BGE & PhD) & CIBIO's TwinLabs (If applicable, payment will be made to Associacao BIOPOLIS - VAT No. 516033727). Fees: 60 euros (other students and Biopolis non-students) | 120 euros (other participants).

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Mertola NaturalSelection LastCall Apr17-19

MERTOLA EVOLUTION CONFERENCES- 2026 EDITION: NATURAL SELECTION IN THE WILD 17 - 19th of April 2026, Mertola, Portugal

Dear Colleagues,

The general programme of the 2026 edition of the Mertola Conferences in Evolution is now online: https://www.cibio.up.pt/en/events/mertola-evolution-conferences-2026-edition-natural-selection-in-the-wild/ There are still some places available. Thus if you join us this Spring in Mertola, use the form below to register until the end of March.

The MECs are annual meetings on Evolutionary Biology (each year a specific topic) for researchers and students to present cutting-edge studies on the field, as well as a forum for informal discussion, fostering new ideas and collaborations among researchers all over the world. Mertola Conferences are promoted by EBM - Biological Station of Mertola in collaboration with other national and international institutions. Mertola is located in Southeast Alentejo region of Portugal, near the Spanish border, crossed by the Guadiana River and in the center of the Natural Park of Guadiana Valley. The antiquity of Mertola is attested by the many archaeological remains that prove the continuous human occupation of this territory. Despite being and biodiversity hotspot of Mediterranean ecosystems, the first traces of human presence dating back to the Neolithic period, five thousand years ago, with different civilizations, like Iberians, Phoenicians, Greeks and Carthaginians. More information at https://www.visitmertola.pt/-mertola-vila-museu/ The MEC 2026 edition, entitled "Natural Selection in the Wild". It counts with prominent speakers in the field: Rosemary Gillespie (University of California, Berkeley, USA), Jeremy Searle (Cornell University, USA), Matthew P. Hare (Cornell University, USA), Silvia Matesanz Garcia (Universidad Rey Juan Carlos, Spain) Jose Melo-Ferreira (University of Porto) The conference programme will be announced next week and includes a Bird Watching Tour in the last day of the conference around Mertola, where an enormous variety of species can be observed. For registration and abstract submission, please fill this form: https://-forms.gle/gGWuWpgWs4Ak2fDj7 Participation is free of charge for BIODIV Students (M BGE & PhD) & CIBIO's TwinLabs (If applicable, payment will be made to Associacao BIOPOLIS - VAT No. 516033727). Fees: 60 euros (other students and Biopolis non-students) | 120 euros (other participants). The organizing committee, Jeremy Searle Miguel Carneiro Rui Faria Paulo Celio Alves

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MPI Ploen TracingEvolThroughCellLineages Oct12-14

We are pleased to announce the symposium "Tracing Evolution through Cell Lineages", which will take place 12-14 October 2026 at the Max Planck Institute for Evolutionary Biology in Plön, Germany.

This workshop aims to bring together researchers at the interface of evolutionary, developmental, and stem cell biology to explore how evolutionary change is mediated through cell lineages. While phenotypic evolution is often studied at the level of whole organisms, this symposium focuses on the cellular processes cell states, lineage architecture, fate decisions, and dynamics that ultimately generate morphological and functional diversity. Particular emphasis will be placed on how changes in lineage topology, timing, and spatial deployment contribute to the emergence of novel cell types and to phenotypic diversification across and within taxa.

The workshop will begin with a kick-off session on the evening of Monday, October 12, followed by two full thematic days. The second day will focus on how cellular processes underpin phenotypic change, while the third day will emphasize the evolution and diversification of cell types and lineages. The program will include invited speakers, contributed talks, a poster session, structured discussions, and ample time for informal exchange.

Invited speakers include: Gunther Wagner Athanasia Tzika Leslie Babonis Alexa Sadier Henrik Kaessmann Detlev Arendt Patrick Tschopp Andrea Streit Arnau Sebé-Pedrós

We welcome contributions from researchers working within this framework. Participants may present their work as a poster or be considered for a short talk. Register here: https://workshops.evolbio.mpg.de/event/145/-overview With kind regards, the organizing committee: Gianmarco Cavalli, Nathalie Feiner, Linda Kappes, Markéta Kaucka, Robin Pranter

Robin Pranter <pranter@evolbio.mpg.de>

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Online ESEB InternalConflictsSTN Mar17

Dear colleagues,

We would like to invite you to the next online seminar for the “Internal Conflicts and Organismal Adaptation” Special Topic Network (STN) funded by the European Society for Evolutionary Biology, which will take place on March 17, 16:00 UTC. Our speakers for this seminar are:

Grace Lee (UC Irvine): Epigenetic silencing of genomic parasites: unintended consequences for genome evolution.

Manisha Munasinghe (University of Minnesota): The silver lining of recessive lethals.

We expect the meeting to take approximately 1.5 hours.

Meeting details: Date: March 17, 2026. Time: 16:00 UTC <https://www.timeanddate.com/worldclock/fixedtime.html?msg=STN+seminar+19&iso 260317T16&p1=40&ah=1&am0> . Meeting link: https://georgetown.zoom.us/j/94519554978 If you would like to get on our mailing list and take part in our upcoming events, please visit our website (https://internalconflictsstn.wordpress.com/) for more information.

Sincerely,

The Internal Conflicts and Organismal Adaptation STN

Martijn Schenkel, Manus Patten, Arvid Sgren, Nina Wedell, and Thomas Hitchcock

ESEB-funded Special Topic Network “Internal Conflicts and Organismal Adaptation” https://internalconflictsstn.wordpress.com/ https://eseb.org/prizes-funding/special-topic-networks/ Internal Conflicts STN <internalconflictsstn@gmail.com>

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Online ESEB STN Speciation Apr7

Dear colleagues,

The next session of the online seminars organised by the ESEB-funded STN network ≪ Integration of Speciation Research ≫ ([https://speciation-network.pages.ist.ac.at/]) will take place Tuesday 7th of April at 9am CET.

This session falls within the theme “Early Career Researchers in Speciation”, with this theme’s new format featuring two talks (1 hour total):

1. Charlotte Wright (Postdoc @ Wellcome Sanger Institute, UK) “The Evolution of Chromosome Rearrangements across Butterflies and Moths. 2. Alexander Mackintosh (Postdoc @ U. Uppsala, Sweden): ”Evidence for Chromosomal Speciation in Brenthis Butterflies.“

followed by a 30 min Q&A with Sally Potter (Macquarie U., Australia) about her career path.

To attend, please use the following link: https://gu-se.zoom.us/j/63912851182 Talks (but not the Q&A) will be recorded and made available here: https://www.youtube.com/channel/UClEkDdE_5sDw70SQq78DIAA, where you can also find previous seminar recordings.

The IOS network aims to promote both scientific and community integration across speciation research. A main objective is to foster diversity and inclusion across the field. We alternate time slots every month to maximise the geographic diversity of attendees. The seminar series and subsequent discussions are open to everyone, from students to established researchers and non-scientists. Please share this email with anyone who may be interested, especially those in countries that are typically underrepresented in scientific discourse. However, please do not post the zoom link on social media.

The seminar programme is announced by email, on Bluesky (@speciation-network) and Twitter (@Speciation_net), here on EvolDir, and on the IOS network website. To automatically receive the programme and other news from the IOS network, sign up to the mailing list via the IOS website.

We look forward to seeing you there!

The STN IOS organising committee:

Jonna Kulmuni (chair), Sean Stankowski, Carole Smadja, Sonal Singhal (co-chairs), Chris Cooney, Liz Scordato, Joana Meier, Richard Merrill, Konrad Lohse, Nick Barton, Roger Butlin, Jonah Walker, Parvathy Suendranadh, Hilde Schneemann and Rowan Schley

Hilde Schneemann <Hilde.Schneemann@ist.ac.at>

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Online ESEB STN Speciation Mar3

Dear colleagues,

The online seminars organised by the ESEB-funded STN network ≪ Integration of Speciation Research ≫ ([https://speciation-network.pages.ist.ac.at/]) is about to restart, with the first session taking place Tuesday 3rd of March at 5pm CET.

This session falls within the theme “Early Career Researchers in Speciation”, with a new format featuring two talks (1 hour total):

1. José Cerca (Group Leader @ Swedish Museum of Natural History) “The identity Crisis of Speciation Genomics” 2. Andrea Estandia (Postdoc @ U. Oxford, UK): “Evolutionary Consequences of Island Colonisation in the Silvereye.”

followed by a 30 min Q&A with Mark Ravinet (U. Oslo, Norway) about his career path.

We are grateful to José Cerca for stepping in at short notice as our previously announced speaker Nare Ngoepe sadly had to cancel.

To attend, please use the following link: https://gu-se.zoom.us/j/68669501529 Talks (but not the Q&A) will be recorded and made available here: https://www.youtube.com/channel/UClEkDdE_5sDw70SQq78DIAA, where you can also find previous seminar recordings.

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Online EVOLTREE-AdaptiveVariation-R Nielsen Apr8

Dear all,

EVOLTREE is pleased to announce a new event in the network’s series of online seminars.

For Spring 2026, we have will have the honour of hearing from UC Berkeley’s Prof Rasmus Nielsen, a leading evolutionary biologist who has pioneered methods revealing how adaptation takes place at the genomic level. Please make a date in your diaries and join us for what promises to be a fascinating talk!

8th April 1600 CEST, Prof Rasmus Nielsen: “Mapping adaptive genetic variation in non-model species”

Prof. Rasmus Nielsen is an evolutionary biologist and geneticist who studies human evolution, population genetics, and statistical genomics. He is best known for developing computational methods to detect natural selection in genomes and for his discoveries on human adaptation to high-altitude environments and ancient interbreeding with Neanderthals and Denisovans. Prof Nielsen’s research integrates evolutionary theory, bioinformatics, and molecular biology to uncover the genetic basis of adaptation and diversity across species. He is

Professor of Integrative Biology and Statistics at UC Berkeley and a member of the Center for Theoretical Evolutionary Genomics. Prof Nielsen has— published more than 350 peer reviewed publications including many in Nature, Science, and Cell, and is a member of the US National Academy of Sciences and the Danish Royal Academy of Sciences.

Links: https://vcresearch.berkeley.edu/faculty/rasmus-nielsen ***LINK FOR REGISTRATION: https://www.evoltree.eu/evoltree-online-webinar-8-april-2026*** More info is available from the EVOLTREE website: https://www.evoltree.eu/webinars/webinar/evoltree-online-webinars-spring-2026 Santiago C. Gonzalez-Martinez,

INRAE, France

EVOLTREE Coordinator

“Santiago C. González-Martínez” <santiago.gonzalez-martinez@inrae.fr>

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PennsylvaniaStateU MicrobiomeEvol May13-14

We are hosting our biennial One Health Microbiome Symposium on May 13-14, 2026 at Penn State University (University Park, PA). Registration is currently open, and abstract submissions are open until March 13.

“The One Health Microbiome Center at Penn State University invites researchers to the 2026 One Health Microbiome Symposium, May 13-14, 2026. This two-day meeting will bring together evolutionary biologists, microbiologists, ecologists, and computational scientists interested in microbiome dynamics across human, agricultural, and environmental systems. We especially welcome work exploring host-microbe coevolution, microbial community assembly, evolutionary genomics, transmission and adaptation, and the evolutionary consequences of microbiome change in a One Health framework.

Keynote speakers include Joy Bergelson, Arturo Casadevall, and Martin Weidmann. The program will also feature trainee talks, poster sessions, workshops, and opportunities for cross-disciplinary discussion. Learn more and register here: https://www.huck.psu.edu/institutes-and-centers/microbiome-center/2026-one-health-microbiome-symposium Grace Deitzler, PhD (she/her)

Research Project Manager | One Health Microbiome Center

Office: W207 Millennium Sciences Complex

Huck Institutes of the Life Sciences

Pennsylvania State University

”Deitzler, Grace“ <gfd5230@psu.edu>

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

Reading UK BESMacroEvol Jul15-17

We are delighted to announce that registration is now open for BES Macro 2026!

The annual meeting of the British Ecological Society's Macroecology and Macroevolution Special Interest Group is this year hosted by the University of Reading, UK, and running from 15-17 July. This year we will also be running a pre-conference ECR workshop on publishing, reviewing, and editing in ecological journals.

Anyone who is interested in generalisable ecological and/or evolutionary patterns over broad spatial and/or temporal and/or taxonomic scales is welcome to attend! Tickets are available for both in-person and online attendance.

Go to https://www.eventbrite.co.uk/e/bes-macro-2026-tickets-1983441181968 for registration and more information.

Key dates

* Main conference dates: 15 July 2026 2 PM - 17 July 2026 5 PM. * Pre-conference workshop: 15 July 2026, 10 AM - 1:30 PM. * Location: Agriculture Building, University of Reading (Whiteknights Campus), Reading, UK * Registration deadline for presenters: Friday 17 April 2026, 17:00 BST (for all presenters, including student plenary applications) * Final in-person registration deadline: Friday 15 May 2026, 17:00 BST. * Online registration deadline: Friday 3 July 2026, 17:00 BST.

Plenary speakers

* Dr Laura Antāo, Assistant Professor of Ecology and Evolutionary Biology, University of Turku * Prof. Deepa

Senapathi, Professor of Applied Ecology and Head of Department of Sustainable Land Management, University of Reading * Prof. Chris Venditti, Professor of Evolutionary Biology, University of Reading * Student plenary (applications now open!)

The University of Aberdeen is a charity registered in Scotland, No SC013683. Tha Oilthigh Obar Dheathain na charthannas clàraichte ann an Alba, Ã. SC013683.

“Sheard, Catherine” <catherine.sheard@abdn.ac.uk>

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SMBE Copenhagen EarlyBirdRegistrationMar31

Dear colleagues,

A quick reminder that the early bird registration deadline for the Society for Molecular Biology and Evolution’s 2026 conference (SMBE 2026) is March 31.

We encourage you to register soon and take advantage of the discount available during this period here www.smbe2026.org/registration/ SMBE 2026 will take place in Copenhagen between June 28th and July 2nd, 2026, and we are excited to share a programme that brings together leading voices in molecular evolution. Highlights include:

* Plenary lectures by internationally recognised experts (Emma Telling, Mehmet Somel, Moises Exposito-Alonso and Nandita Garud) * A diverse set of symposia covering the breadth of molecular and evolutionary biology * Workshops, poster sessions, and community networking events * A strong focus on emerging methods, ancient DNA, conservation and population genomics, evolutionary genomics, pathogen evolution, and more

Explore the full preliminary programme and registration details on our website: www.smbe2026.org/programme/ We look forward to welcoming you to Copenhagen for an inspiring meeting - and we recommend registering before March 31 to secure the reduced early–bird rate.

Best regards, SMBE 2026 Organizing Committee

Tom Gilbert <tgilbert@sund.ku.dk>

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

TahoeCity California PolygenicAdaptationInAChangingWorld Oct4-7

The American Genetic Association is happy to announce our 2026 Symposium: “Polygenic Adaptation in a Changing World” hosted by AGA President Michael Nachman.

“We now have good examples of the genetic basis of adaptation for many simple traits. However, most evolutionary change involves complex traits, and our understanding of their evolution remains rudimentary. This symposium will promote a broad, synthetic discussion of adaptive evolution for complex traits, bringing together theoreticians and empiricists working on diverse organisms”

Keynote Speaker

Rasmus Nielsen, U California, Berkeley

Invited Speakers

Rachael Bay, UC Davis

Graham Coop, UC Davis

Jeff Good, University of Montana

Thomas Juenger, University of Texas

Joanna Kelley, UC Santa Cruz

John Kelly, University of Kansas

Sarah Kocher, UC Berkeley

Julia Kreiner, University of Chicago

Katie Lotterhos, Northeastern University

Bret Payseur, University of Wisconsin

Dmitri Petrov, Stanford University

Paul Schmidt, University of Pennsylvania

Molly Schumer, Stanford University

Guy Sella, Columbia University

Jenny Tung, Max Planck Institute Leipzig

Trisha Wittkopp, University of Michigan

Samuel Yeaman, University of Calgary

Jianzhi Zhang, University of Michigan

AGA Symposia are small, friendly meetings that provide excellent opportunities for relaxed interaction with speakers and attendees. All attendees *must* be AGA members - join us now!

https://www.theaga.org/members The event runs from mid-day October 4th to the evening of October 6th. Checkout is on the 7th. All events take place at Granlibakken Lodge in Tahoe City, California. Bookings are made through Granlibakken, click the link for details -

https://www.theaga.org/agatwentytwentysix Your reservation through Granlibakken includes all room, board, conference fees, and registration fees ($400 individual/$200 student) to the event.

Please contact < theaga@theaga.org > with questions.

Carlos Driscoll, DPhil Managing Editor, Journal of Heredity < https://academic.oup.com/jhered > American Genetic Association < http://www.theaga.org/- > Follow AGA on Bluesky Social < https://-/bsky.app/profile/theaga.bsky.social > and X < https://twitter.com/theAGA_org > and on our blog!: http://blog.theaga.org/ Managing Editor <theaga@theaga.org>

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USheffield EvolEcoGenetics Apr15-17

#EGG2026: 70th Anniversary of Ecological Genetics 15-17 April University of Sheffield & Online

https://www.britishecologicalsociety.org/content/-egg2026-70th-anniversary-of-ecological-genetics/ Registration opens until 30 Mar (in-person) and 10 Apr (online) here: https://egg2026.eventbrite.com As the longest running Special Interest Group and annual meeting since 1956, Ecological Genetics Group (EGG) is entering an unparalleled milestone our 70th anniversary. We have been dedicated to building a forum for ecologists and practitioners on the nexus of ecology, evolution, and genetics. The field has evolved so much in the past decades, with new methods and tools opening up revolutionising ways to answer fundamental and applied problems.

We are pleased to invite all to join us in Sheffield, to celebrate this special moment, to reflect on the history, and to discuss the cutting-edge developments that will move the field forward. Alongside the exciting program of talks and posters, we will also host roundtables and horizon scans that will lead to opinion pieces for publication.

The first day will be a joint thematic session on environment DNA, co-hosted with UK DNA Working Group (UKDNA), which will serve as a bilateral platform for academics and practitioners conservationists, consultants, and policy makers to identify how ecological genetics can be translated to applications of environmental DNA.

EGG2026 will be a hybrid event. Talks will be livestreamed and recorded for online delegates, so that time zone or distance do not need to be a barrier.

We look forward to welcoming you at this special moment.

Genetics <genetics@britishecologicalsociety.org>

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Aberdeen Scotland PlantTraitMacroevolution

THE PROJECT

A fully-funded PhD studentship (tuition waiver, stipend, and research & training budget) is available at the University of Aberdeen, with Dr Catherine Sheard as lead supervisor. The project, 'Trait-based drivers of the ornamental plant trade', combines macroevolutionary methods, global databases of plant traits, and cultural evolution techniques to understand the forces shaping temporal, spatial, and taxonomic variation in the household plant trade. The Royal Botanic Garden Edinburgh is a 'CASE partner', facilitating further opportunities for collaboration and skill development.

ELIGIBILITY

UK 'Home' students (e.g., 'settled' UK citizens or permanent residents, refugees, and other eligible categories) only.

DEADLINE

Apply by April 22.

START DATE

September 2026.

WANT TO LEARN MORE?

Please see https://www.findaphd.com/phds/-project/quartiles-dla-case-trait-based-drivers-of-the-ornamental-plant-trade/?p191547 for more information about the project and for instructions on how to apply.

Best wishes,

Catherine

Dr Catherine Sheard (she/her) Interdisciplinary Fellow School of Biological Sciences University of Aberdeen catherine.sheard@abdn.ac.uk

The University of Aberdeen is a charity registered in Scotland, No SC013683. Tha Oilthigh Obar Dheathain na charthannas clï¿½raichte ann an Alba, ï¿½ir. SC013683.

“Sheard, Catherine” <catherine.sheard@abdn.ac.uk>

BC-CAS Czechia ButterflyGenomicsHighElevations

Graduate position: BC-CAS_Czechia.ButterflyGenomicsHighElevations

PhD Position: Genomics of butterflies at high elevations

(Please, feel free to distribute to all potential candidates)

Closing date: May 8, 2026

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

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

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

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

Required qualifications:

Masters degree in biology or related fields (awarded before start).

Good communication skills in English.

Independence and documented research productivity.

Funding and Environment:

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

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

How to apply:

Send your application in English to pavel.matos@entu.cas.cz, consisting of one single PDF containing the following:

Cover letter, outlining your motivation, how your background and skills fit the project, and your potential plans within the research focus of this position (max. 2 pages).

CV, including contact details of at least two referees familiar with your work.

The deadline for applications is May 8, 2026. The top ranked candidates will be selected for an interview in English. The start date is expected in autumn 2026 (Czechia).

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

Dr. Pavel Matos-Maravi

Biology Centre, Czech Academy of Sciences Branisovska 31, 37005, Ceske Budejovice, Czechia Email: pavel.matos@entu.cas.cz Web: https://pavelmatos.wordpress.com/ Matos Maravi Pavel Fortunato <pavel.matos@entu.cas.cz>

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Brno CzechRepl EvolParasitology

Doctoral position in Ecological and Evolutionary Biology

TOPIC: The role of parasites and microbiota in the success of invasive freshwater fishes

Doctoral position for 4 years (starting September 2026) is available at the Department of Botany and Zoology, Faculty of Science, Masaryk University, located in Brno, Czech Republic. All applications submitted before 3 April 2026 will be fully considered. Selected candidates will be interviewed online.

The study will be done in Ecological and Evolutionary Biology doctoral program.

The doctoral project aims (1) to investigate the effects of invasive fish species on parasite and microbial communities of native fish species at the level of different host tissues, (2) to reveal interactions between parasites (including both ecto- and endoparasites) and microbiota in invasive and naturalized/native host species, and (3) to assess interactions between external microbiota diversity, host vulnerability to a single parasite infection and host overwintering under experimental conditions. Two fish systems will be used in this project (1) invasive gibel carp Carrasiusgibelio and naturalized economically important common carp Cyprinus carpio (Cypriniformes, Cyprinidae), (2) invasive pumpkinseed Lepomis gibbosus and native European perch Perca fluviatilis and (Eupercaria). Field and experimental approaches will be used for realization. Microbiota (bacterial communities) will be analyzed using DNA metabarcoding.

Selected candidate will work in the international Aquatic Parasitology group. One of the scientific topics of this group is the invasion biology of aquatic and semi-aquatic vertebrates, including the issue of co-introduction of non-native parasites and the transfer of pathogens to native species. The research also includes the study of hybrid zones (hybrid systems of fish and amphibians in southern Europe). In connection with the newly acquired project, the topics of invasion biology and microbial ecology are interconnected, in particular the study of the potential transfer of microorganisms in connection with biological invasions and their success.

QUALIFICATIONS Master study in Biology or related discipline. We expect applications from candidates with a background in host-parasite ecology, evolution or fish parasitology.

SCHOLARSHIP 25,000 CZK corresponding to 1,030 EUR per month is a scholarship provided by Masaryk University (this amount is sufficient for life in the Czech Republic) plus additional 15% in form of the working contract will be covered by the project funding. All research expenses will be covered from the project of the supervisor.

APPLICATION PROCEDURE Feel free to consult through informal enquires by email to prof. Andrea Veteníková imková, e-mail: simkova@sci.muni.cz (supervisor of the doctoral thesis).

For formal applications, please submit a CV with explanations of your previous work and motivation to apply for this position in your Cover Letter (1-2 pages). You include the contacts for your former supervisors or coworkers.

Submit your application until 3 April 2026. Shortlisted candidates will be interviewed online in April.

Andrea Veteníková imková <simkova@sci.muni.cz>

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CzechRepublic RapidEvolutionInCommunities

PhD - Rapid Evolution in Communities We invite prospective candidates for a four-year PhD Studentship funded by ERC grant of Jan Hrcek to explore exciting questions on the interface of population genetics and community ecology.

It is increasingly clear that evolution can be rapid, with important traits changing within a few generations. But we are only beginning to understand the consequences of this eco-evolutionary process for dynamics of host - parasite interactions and stability of entire communities. We ask how rapid evolution impacts maintenance of diversity in communities and maintenance of genetic variation in populations - processes which have been mostly studied separately.

To address these questions, our collaborative project uses a novel experimental community model system of wild Drosophila species and their parasitoids from tropical Australia.

We are able to perform multigenerational laboratory microcosm experiments and track eco-evolutionary dynamics in fine detail. The candidate will use a combination of approaches: experimental community evolution, population genomics, and eco-evolutionary modelling. The specific PhD projects will result from a discussion between the candidate and the supervisor.

The successful applicant will join the Laboratory of Experimental Ecology [http://lab.hrcek.net] at the Biology Centre, Czech Academy of Sciences, Ceske Budejovice, Czech Republic, under the supervision of Dr Jan Hrcek. The laboratory is a multinational team of postdocs, PhD students and technicians. The applicant will thus have the opportunity to work extensively with other team members. The laboratory obtained prestigious high-level funding (ERC Consolidator grant) and therefore can provide substantial resources and support for exceptional research. The laboratory is part of a dynamic international centre for research in species interactions.

Together with the PhD student we will choose a co-supervisor from current international collaborators or start new collaborations. The position will include a research stay abroad.

The deadline for applications is 7th May 2026 with interviews short after. The position can start from Sept 2026 onwards.

Recently, guaranteed income for PhD students has become a law in the Czech Republic and the student will thus receive a salary which comfortably covers living expenses in the Czech Republic.

The working language is English and applicants from all countries are eligible. A MSc degree is required to enter PhD in Czech Republic. Following experience is an advantage:

§Research experience with laboratory experiments

§Experience with population genetics or molecular ecology

§Experience in eco-evolutionary dynamics or population genetic modelling

To apply please send one document comprising a motivation letter, CV, and contact details for two references to Jan Hrcek [janhrcek@gmail.com].

Jan Hrcek <janhrcek@gmail.com>

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EPFL Lausanne BacterialCommunicationEvolution

Graduate position: EPFL_Lausanne.BacterialCommunicationEvolution

PhD Position: Evolution of Bacterial Communication Systems

Systems and Synthetic Evolutionary Biology Lab Institute of Bioengineering, EPFL Lausanne, Switzerland

PROJECT DESCRIPTION

Bacteria have evolved diverse chemical communication systems to coordinate collective behaviours such as biofilm formation, pathogenicity, and interspecies interactions. Yet the molecular mechanisms by which these systems diversify remain poorly understood.

This project will investigate the evolution and functional diversification of bacterial communication systems, with a focus on how quorum sensing proteins evolve new functions. The work will combine experimental and computational approaches, including high-throughput characterization of protein variants, phylogenetic methods, and evolutionary simulations.

REQUIREMENTS

* Master's degree (by start date) in Evolutionary Biology, Microbiology, Molecular Biology, Biochemistry, Bioinformatics, Quantitative Biology, or a related field * Genuine curiosity about the molecular mechanisms underlying evolutionary change * Motivation to work at the interface of experimental and computational biology * Very good English communication skills

Experience in evolutionary biology, phylogenetics, molecular microbiology, protein biochemistry, bioinformatics, or programming (Python, R) is desirable.

WE OFFER

* A fully funded PhD position with competitive Swiss salary * Access to outstanding research infrastructure at EPFL * A highly interactive and collaborative research environment

START DATE: between September 2026 and January 2027.

HOW TO APPLY

Applications must be submitted through one of the following EPFL doctoral programs (deadline April 15, 2026): * EDMS (Molecular Life Sciences) * EDBB (Biotechnology and Bioengineering) * EDCB (Computational and Quantitative Biology)

Interested candidates are strongly encouraged to contact Caua Westmann directly before or while applying at caua.antuneswestmann@epfl.ch. Please include a CV, a brief statement of research interests and motivation (max. one page), and names of two references.

Caua Westmann <caua.antuneswestmann@epfl.ch>

Cauï¿½ Antunes Westmann <caua.antuneswestmann@epfl.ch>

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EPFL Lausanne EvolutionCentriole

PhD Position: Uncovering evolutionary history and interactive of centriolar proteins

CO-SUPERVISION

Laboratory of Computational Biology and Theoretical Biophysics, Prof. Bitbol

Laboratory of Cell and Developmental Biology, Prof. Gï¿½nczy

PROJECT DESCRIPTION

Centrioles are ancient eukaryotic organelles critical for cell division, motility and signaling. In this joint project between the groups of Prof. Bitbol and Prof. Gï¿½nczy, the evolutionary history of centriolar proteins will be uncovered using novel structure-aware phylogeny inference algorithms. Moreover, protein and proteome language models will be developed and deployed to infer the interactome of centriolar proteins, and investigate its evolution. Furthermore, building blocks of the centriole will be sought outside eukaryotes, thereby potentially uncovering the evolutionary origin of this critical organelle.

REQUIREMENTS

- Master's degree in computational biology, evolutionary biology, or related field (by start date)

- Interest in understanding mechanisms of organelle evolution and molecular phylogenetics

- Strong programming skills

- Good English communication skills

WE OFFER

- A fully funded PhD position with competitive Swiss salary

- A collaborative research environment

START DATE

- June 2026 (or thereafter, upon mutual arrangement)

APPLICATIONS

Submit your application through the Computational and Quantitative Biology (EDCB) EPFL doctoral program -deadline April 15, 2026 (https://www.epfl.ch/-education/phd/edcb-computational-and-quantitative-biology/edcb-how-to-apply/)

Further information can be obtained from Anne-Florence Bitbol (anne-florence.bitbol@epfl.ch) or Pierre Gï¿½nczy (pierre.gonczy@epfl.ch)

Pierre Gï¿½nczy <pierre.gonczy@epfl.ch>

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Frankfurt BeetleSociality

Graduate position:

PhD Position (w/m/d, 65 %, EG 13 TV-L, 3 years)

Transcriptional Regulation in Beetle Sociality

Senckenberg Biodiversity and Climate Research Institute, Frankfurt, Germany. Collaboration with Bayreuth University, Freiburg University, LMU MÃÂ¼nchen and Coventry University.

PROJECT DESCRIPTION

Subsociality is widely considered a prerequisite for the evolution of eusociality, as it introduces key behaviours, such as parental care and prolonged parent-offspring interactions, that can be co-opted and elaborated upon to form more complex social systems. Recently, we have been investigating the genomic basis of subsociality in 20 species of two distantly related beetle families, the weevils (Curculionidae) and carrion beetles (Staphylinidae: Silphinae), with varying degrees of sociality. Our comparative genomics analyses revealed convergent gene losses and a relaxation of selection with the onset of offspring attendance. Gene expression analyses reveal that the switch from the non-caring phase to pre-hatching care behaviour results in the strongest change in gene expression across species. Interestingly, both the genomic and transcriptomic analyses identifed gene regulatory mechanisms as being most strongly associated with social behaviour. We now plan to identify gene regulatory mechanisms involved in the differences and changes in gene expression associated with parental care and thus the onset of sociality.

The accompanying project in MÃÂ¼nchen and Coventry will conduct a genome-wide screen for patterns associated with sociality using state-of-the-art machine learning approaches, and develop stochastic models to infer the importance of regulatory mechanisms. This project will thus shed light on the evolution of mechanisms involved in the transition from solitary to social life in insects.

We are looking for a highly motivated PhD candidate with interest in molecular evolution, genomics, epigenetics, and behavior to identify key regulators and epigenetic modifications shaping the evolution of social behavior using a multi-omics approach.

YOUR TASKS

* Conduct experimental work to collect samples from eight beetle species across three parental-care phases from carrion and ambrosia beetles. * Perform essential laboratory work (e.g. RNA extraction, library preparation * Carry out bioinformatic analyses to integrate gene-expression data with epigenetic regulatory states. * Publish results in internationally peer-reviewed journals, and present those at international conferences. * Closely collaborate with the modelling counterpart

YOUR PROFILE

* Master's degree (by start date) in Biology, Evolutionary Biology, Molecular Biology, Bioinformatics or related field * Strong interest in behavior, evolution, and genomics * Prior experience with NGS data, R, another programming language is a plus * Experience with formulating scientific questions, planning and executing a research project * Very good English communication skills; curiosity, independence, and interest to collaboratively work in an interdisciplinary team

DESIRABLE SKILLS

* Experience in conducting experiments * Experience in dissection of specific tissues * Experience in molecular laboratory procedures, including RNA extraction, preparation of Enzyme-seq and CUT&Tag libraries * Experience in the bioinformatic analyses of transcriptome, methylation and/or histone modifi-cation data

WE OFFER

* Access to an international network of scientists, policymakers, and research organizations * Integration in an interdisciplinary consortium studying the "GEvol: Genomic Basis of Evolu-tionary Innovations — (GEvol)"

with additional training opportunities and collaborations across Germany. * A dynamic working environment in Frankfurt, a diverse and vibrant city offering a high quality of life.

TO APPLY

Please upload your application as a single PDF file including letter of motivation with a short description of your previous and current research foci, a CV, certificates of academic achievements, list of publications as well as letter(s) of recommendation, if available) (as a single PDF file) on our website (https://www.senckenberg.de/de/stellenanzeigen/) by March 29, 2026. Job Announcement Ref. #11-26011

Expected starting date: as early as possible.

If you have any specific questions about the position, please contact Dr. Barbara Feldmeyer at barbara.feldmeyer@senckenberg.de https://www.senckenberg.de/en/research/institutes-overview/sbikf-institut/sbikf-ag-molecular-ecology/

Dr. Barbara Feldmeyer

Molecular Ecology Group Senckenberg Biodiversity and Climate Research Centre (SBiK-F) Georg-Voigt-Str. 14-16 D-60325 Frankfurt am Main Germany

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Frankfurt OdorantEvol

Graduate position:

PhD Position (w/m/d, 65 %, EG 13 TV-L, 3 years)

Transcriptional Regulation of Odorant Perception

Senckenberg Biodiversity and Climate Research Institute, Frankfurt, Germany. Collaboration with Freiburg University, Mainz University, TUM MÃÂ¼nchen, WÃÂ¼rzburg University.

PROJECT DESCRIPTION

Understanding the evolution of complex communication systems requires investigating both signal production and signal perception. In insects, cuticular hydrocarbons (CHCs) are central to chemical communication, yet the genomic mechanisms underlying the ability to perceive particular CHC compound blends remain largely unknown. Odorant receptor (OR) gene expression levels change when their corresponding encoded receptor proteins bind to specific odorants. The aim of this project is to determine the epigenetic mechanisms in regulating OR gene expression, and whether this regulation is consistent across our hymenopteran study species. This multi-omics approach will yield key insights into the genomic basis of the evolution of complex chemical communication systems, revealing how sender and receiver traits have evolved in concert.

The project is in close collaboration with the research groups of PD Dr. Florian Menzel (Johannes Gutenberg University Mainz), PD Dr. Jan BÃÂ¼llesbach (Technical University of Munich), and Prof. Dr. Thomas Schmitt (University of WÃÂ¼rzburg) and involves close cooperation with a second PhD student in the project who will lead the chemical ecology and comparative genomics analyses located in the groups of Prof. Dr. Oliver Niehuis and PD Dr. Volker Nehring (University of Freiburg).

We are recruiting a highly motivated PhD candidate with interest in molecular evolution, genomics, epigenetics, and chemical ecology to identify epigenetic mechanisms regulating odorant receptor expression, one of the key traits in chemical communication systems.

YOUR TASKS

* Conduct experimental work to collect samples from eight beetle species across three parental-care phases from carrion and ambrosia beetles. * Perform essential laboratory work (e.g. RNA extraction, library preparation * Carry out bioinformatic analyses to integrate gene-expression data with epigenetic regulatory states. * Publish results in internationally peer-reviewed journals, and present those at international conferences. * Closely collaborate with the modelling counterpart

YOUR PROFILE

* Master's degree (by start date) in Biology, Evolutionary Biology, Molecular Biology, Bioinformatics or related field * Strong interest in behavior, evolution, and genomics * Prior experience with NGS data, R, another programming language is a plus * Experience with formulating scientific questions, planning and executing a research project * Very good English communication skills; curiosity, independence, and interest to collaboratively work in an interdisciplinary team

DESIRABLE SKILLS

* Experience in conducting experiments * Experience in dissection of specific tissues * Experience in molec-

ular laboratory procedures, including RNA extraction, preparation of Enzyme-seq and CUT&Tag libraries * Experience in the bioinformatic analyses of transcriptome, methylation and/or histone modifi-cation data

WE OFFER

* Access to an international network of scientists, policymakers, and research organizations * Integration in an interdisciplinary consortium studying the “GEvol: Genomic Basis of Evolu-tionary Innovations — (GEvol)” with additional training opportunities and collaborations across Germany. * A dynamic working environment in Frankfurt, a diverse and vibrant city offering a high quality of life.

TO APPLY

Please upload your application as a single PDF file including letter of motivation with a short description of your previous and current research foci, a CV, certificates of academic achievements, list of publications as well as letter(s) of recommendation, if available) (as a single PDF file) on our website (https://www.senckenberg.de/de/stellenanzeigen/) by April 6, 2026. Job Announcement Ref. #11-26010

Expected starting date: as early as possible.

If you have any specific questions about the position, please contact Dr. Barbara Feldmeyer at barbara.feldmeyer@senckenberg.de https://www.senckenberg.de/en/research/institutes-overview/sbikf-institut/sbikf-ag-molecular-ecology/ Dr. Barbara Feldmeyer

Molecular Ecology Group Senckenberg Biodiversity and Climate Research Centre (SBiK-F) Georg-Voigt-Str. 14-16 D-60325 Frankfurt am Main Germany

Phone: +49 69 7542 1839 Email:barbara.feldmeyer@senckenberg.de

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Gothenburg ComputationalBiology

Doctoral student in Computational Genomics Chalmers University of Technology, Gothenburg, Sweden

We are looking for a PhD student to join an exciting project at the intersection of genomics and data science. This project focuses on studying genetic variations in noncoding regions of the human genome by leveraging evolutionary information and developing models that predict the effects of variants. We tackle this challenge via two main directions: (1) developing efficient pangenomic data structures and evolutionary models, and (2) designing deep learning architectures trained on genomic data.

Requirements: Proficient in a programming language and demonstrated experience in one of the following areas, with a willingness to learn one another: (1) genome sequences and omics data, (2) deep learning, and (3) compressed data structures for strings. 4) Mathematical modeling of DNA or protein evolution.

Apply here: https://www.chalmers.se/en/about-chalmers/work-with-us/vacancies/?rmpage=job&rmjob=14653 All the best, Sina Majidian Computational Genomics Research Lab Chalmers University of Technology https://CGRlab.github.io/ Sina Majidian <sina.majidian@gmail.com>

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NCStateU eDNA AquaticSpecies

PhD Graduate Research Assistantship: eDNA Monitoring and Co-Occurrence Patterns of Imperiled Species & Invasive Predators in North Carolina Rivers

Description: The federally listed Carolina Madtom & Neuse River Waterdog have declined across their historical ranges in the Tar??Neuse river basins of North Carolina. The invasion of non-native Flathead Catfish is one of the primary factors hypothesized to impact these imperiled species. This project will develop joint sampling & monitoring approaches using environmental DNA (eDNA) & occupancy modeling to detect & predict occurrences of these three priority species across the Tar??Neuse river systems, with the ultimate aims of 1) clarifying species distributions, 2) testing species-environmental relationships, 3) evaluating co-occurrence patterns, & 4) integrating eDNA monitoring into agency frameworks.

The PhD student will work directly with Dr. Corey Dunn (USGS NC Cooperative Fish & Wildlife Research Unit, NC State University), Dr. Nadya Mamoozadeh

(NC State University, Molecular Ecology Lab) & management biologists while learning in-demand skills transferable to broader applications in conservation such as lab development & field application of eDNA surveillance methods, occupancy modeling, habitat assessment, & imperiled species management.

Qualifications: Completed bachelor??s degree (master??s degree preferred) in biology, natural resources, or closely related field before start date. Prior experience with molecular applications, quantitative methods, & aquatic conservation. Candidates should have interests in both lab & field research, species distribution modeling, R programming, & science communication.

Salary & benefits: Graduate Assistantship >$30,000 per year (Research x 3.5yr, Teaching x 0.5yr) + health insurance, tuition waiver, computer, professional travel, federal safety training.

Start date: Anticipated start date of July 2026 (preferred).

Apply: Apply here (https://forms.gle/5dmdTxDAQi5aRNou8) by uploading a single, merged PDF: 1. brief cover letter describing experiential background, career goals, & project interest 2. resume/CV with GPA 3. unofficial university transcripts 4. email & phone numbers for three professional references (we will ask before contacting references) 5. optional (but encouraged) writing example from research or coursework

Applications will start being reviewed March 20; position closes April 5, 2026. Email inquiries about this position are welcome (corey_dunn@ncsu.edu; nrmamooz@ncsu.edu).

Helpful links: Lab webpages: https://bit.ly/riverine_fishes; http://www.mamoozlab.com/ Department of Applied Ecology at NC State: https://cals.ncsu.edu/applied-ecology Nadya Mamoozadeh, PhD Assistant Professor Dept. of Applied Ecology http://www.mamoozlab.com/ Nadya Mamoozadeh <nrmamooz@ncsu.edu>

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UCollegeLondon EvolutionaryBiol

For To best prepare for a PhD in an evolutionary topic, choose to complete a year long Masters by Research (MRes) project in The Centre of Life's Origins and Evolution at University College London.

We are at the forefront of research to the resolve the mysteries of the origin of life on earth and understand the process that govern organismal evolution across the tree of life. Research labs offer projects to students using an array of approaches, from statistical and theoretical methods, through data science, modelling and deep learning to high-throughput experimental and genomics techniques. From the deep sea to the crater lakes of Tanzania, field work is also commonly used to understand how biodiversity evolves in the Anthropocene, together with lab-focused projects.

You can choose an evolutionary topic in the most relevant research group, and spend the year developing advanced research skills. The course structure closely matches that of a first year PhD and helps you develop the generic and specialised skills to launch your research career. More details can be found here https://www.ucl.ac.uk/biosciences/mres-biosciences/evolution-and-origins-life-stream With the evolutionary programme being part of the umbrella MRes Biosciences the overview of the course structure can be found here https://www.ucl.ac.uk/biosciences/mres-biosciences Details of how to apply are found here https://www.ucl.ac.uk/prospective-students/graduate/taught-degrees/biosciences-mres And please make clear in your cover letter that you are interested in the Evolution and Origins of Life stream

Questions on the programme can be directed to either Dr. Ferdinand Marlétaz Email f.marletaz@ucl.ac.uk or Professor David Murrell d.murrell@ucl.ac.uk

Professor David Murrell Centre for Biodiversity and Environmental Research, Department of Genetics, Evolution and Environment, University College London, Medawar Building Gower Street London WC1E 6BT United Kingdom

Programme Lead for MRes Biosciences https://www.ucl.ac.uk/biosciences/study/masters/mres-biosciences Personal research website https://profiles.ucl.ac.uk/604-david-murrell Telephone: 020 31087696

Email: d.murrell@ucl.ac.uk

David Murrell <d.murrell@ucl.ac.uk>

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UFribourg TheoreticalEvolutionaryBiol

Graduate position: UFribourg.TheoreticalEvolutionaryBiology

PhD position in Theoretical Evolutionary Biology: “The evolution of monoecy in flowering plants”

A 4-year PhD position is available to start September 1st, 2026 in the Department of Biology at the University of Fribourg (Switzerland) as part of an SNSF-funded Ambizione research project led by Dr. Thomas Lesaffre (https://thomas-lesaffre.github.io/).

Short scientific description:

The way flowering plants distribute their reproductive resources between their male and female function is diverse. Most species are cosexual, meaning that individuals produce both pollen and ovules, but vary widely in how much they allocate to each function. Others have evolved polymorphic sexual systems where individuals specialise to varying degrees into their male or female function, so that essentially any combination of cosexual and unisexual male and female individuals may coexist in a single population. This great diversity of ways in which male and female function are distributed amongst individuals has attracted much attention from evolutionary biologists. As a result, the mechanisms driving its evolution are now thought to be fairly well-understood. However, plant sexual strategies do not only vary between individuals, but also within individuals, as sexual reproduction in flowering plants occurs through the production of many flowers that may each contain different amounts of pollen and ovules. This is most striking in the case of monoecy, where male and female function are carried by different flowers on the same individual. Monoecy is the second most frequent sexual system in Angiosperms after hermaphroditism (where flowers are bisexual), but the mechanisms driving evolutionary transitions to and from this system remain poorly understood. This is in part because theoretical models on sexual system evolution have focused on explaining variation at the individual level, leaving within-individual patterns of allocation largely unaccounted for. In this project, the PhD student will work together with Dr. Lesaffre to develop new theory exploring the evolutionary mechanisms underlying the diversity of within-plant patterns of allocation.

Consider applying if you: * Hold (or will soon obtain) a Master’s degree in biology, mathematics or physics. * Are interested in evolutionary ecology, especially that of plants and flowers. * Have a keen interest for mathematical modelling and conceptual thinking. * Enjoy problem solving and coding.

The position is open to applicants worldwide. We welcome applications from individuals of all backgrounds and encourage candidates from underrepresented groups to apply.

Applications should be addressed to Dr. Lesaffre (thomas.lesaffre@unil.ch) before the end of the day on April 24th, 2026. Your application should include the following elements: * A personal motivation letter (one or two pages). * Your CV with the contact details of two references. * Your Master’s thesis if available, or a short description of it in the form of an abstract. * Your academic transcripts.

More practical information:

The PhD position is funded for four years from September 1st, 2026. During that time period, the student will be registered at the doctoral school and will benefit from two fixed-term work contracts: an initial one-year contract followed by a three-year one. The gross annual salary is around 53’000 CHF per year (exact amount may be vary according to SNSF and institutional guidelines). Funding is available for conference, course and workshop attendance. Because Dr. Lesaffre does not currently hold a tenured position, the PhD student will be co-supervised by Prof. Thomas Flatt, who will be their official supervisor for the duration of their studies. Fribourg is vibrant medieval university town with a large student population situated close to the beautiful Alps and well-connected by train. It is a bilingual French/Swiss German part of Switzerland, with a French-speaking majority. Though research will be conducted in English and knowledge of local languages is not expected, learning a few words of French might prove useful in everyday life.

Contact for further information: For informal enquiries, please contact Dr. Lesaffre directly at thomas.lesaffre@unil.ch

Thomas LESAFFRE <thomas.lesaffre@unil.ch>

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UGalway Ireland MacroevolutionBiogeography

Graduate Position: U.Galway_PhDmacroevolutionBiogeography

We are seeking a highly motivated candidate to pursue a PhD in our Biodiversity and Macroevolution Lab at the University of Galway. The idea is that, aligning the candidate?s interests and our expertise, we will together prepare a competitive application for a postgraduate scholarship from The Irish Research Council (currently named Research Ireland).

***About the group In the recently established Biodiversity and Macroevolution group (https://herrera-alsina.tilda.ws/) we deal with questions at large temporal and spatial scales. We mostly focus on the following themes: 1) Change in species distributions over time, 2) Evolutionary/ecological responses to change, 3) Ecological constraints to species diversification, 4) Biogeographic patterns, and 5) Trait evolution. A key element of the group is that we develop tools (i.e., R packages) using both likelihood methods and individual-based simulations to answer our questions. We then apply such methods to different taxa, ranging from archaea to vertebrates and plants. We also operate in the opposite direction: inspiration for projects comes from observing patterns in nature so that sometimes a research question is what calls for developing a new model. Our extensive international network enables the members of our lab to work together with other groups all over the world. The strategic placement of our group in the School of Mathematical and Statistical Sciences allows opportunity to collaborate with highly-trained people in maths and machine learning to develop state of the art models of evolutionary diversification.

***Our view on PhD supervision I believe that me, as supervisor, should monitor three key aspects of a PhD student. First, the general wellbeing of the student. This includes encouraging them to have a healthy work-life balance. Second, the PhD student should learn. It is fundamental to use the best mentoring strategy to make sure the student develops the appropriate analytical and practical skills. Third, the PhD student should also produce tangible outputs. A PhD student should be guided to produce scientific papers, patents, or software that reflect their research and enable them to be competitive in the academic world.

***About the University The University of Galway is now ranked in the top 2% of universities worldwide and the top 100 universities in Europe. Ranked Ireland's #1 university for sustainable development in the Times Higher Education World Rankings (THE). Galway is one of those small cities which offers a wide range of cultural and sporting activities with a high standard of quality of life.

**About you You are an enthusiastic person with a background in environmental or natural sciences, biology, or computer science. Your interests in science align with the themes of the group (there is always room for doing something different of course). You are happy to have independence when doing research but are also happy seeking guidance when needed. You are passionate about research and motivated to share your results with others. You are also experienced or willing to learn programming in R, Python and/or C++. According to the rules of the funding body, you also need to be national of a European Union member state (including the Republic of Ireland) OR Iceland, Norway, Liechtenstein, Switzerland, or the United Kingdom or Ukraine.

***What now? Together with the preferred candidate, we will put together a strong and competitive application for Research Ireland in the September 2026 call. Once the funding is successful, the candidate will start sometime in 2027.

Please email me (leonel.herrera-alsina@universityofgalway.ie) the following documents: 1) One-page cover letter outlining research interests, and research experience, 2) One-page motivation letter, and 3) academic CV.

Leonel H. Alsina

Assistant professor/Lecturer in Bioinformatics, School of Mathematical and Statistical Sciences University of Galway https://herrera-alsina.tilda.ws/ "Herrera-Alsina, Leonel" <leonel.herrera-alsina@universityofgalway.ie>

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UGuelph CaribouMetagenomics

Msc Opportunity - Metagenomics and Metabarcoding for Caribou and Moose diets, at University of Guelph (Ontario, Canada) ?¿‘ Department of Integrative Biology Co-supervised by: Edeline Gagnon & Quinn Webber

Full ad available here: https://drive.google.com/file/d/1CpCkaSRESdb0zpeHC_96wbpJ5zMqveBJ/view?usp=drive_link We are seeking a highly motivated graduate student (MSc or PhD) to join a collaborative research project focused on developing and applying genomic tools to understand dietary partitioning between caribou and moose. Due to funding constraints, we are only accepting Canadian applicants at the moment to the position.

This project offers an exciting opportunity to help shape the future direction of our research program in collaboration with students from both the Gagnon and Webber labs, as well as academic and non-academic partners.

Application Instructions: Please consult the ad and assemble the requested elements into a single application as a single PDF to:

Dr. Edeline Gagnon (edeline.gagnon@uoguelph.ca) Dr. Quinn Webber (qwebber@uoguelph.ca)

Thank you for your interest. We look forward to hearing from you!

edeline.gagnon@gmail.com

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

ULille IntegrativeEvolutionaryBiology

PhD position in integrative evolutionary biology (100% for 3 years)

Influence of life-history strategies and ecology on population differentiation, speciation and macroevolutionary dynamics in mollusks from Lake Tanganyika

Lille University, CNRS, UMR 8198 Evolution, Ecology, Paleontology (UMR 8198; https://eep.univ-lille.fr/en/presentation-english/), Lille, France under supervision of Dr. Bert Van Bocxlaer (DR, CNRS), Prof. Dr. Hugo Gante (Associate Professor KU Leuven, Royal Museum for Central Africa, Belgium); Dr. Anne Duputié (MCF, Univ. Lille). Contact: bert.van-bocxlaer|at|univ-lille.fr, hugo.gante|at|kuleuven.be, anne.duputie|at|univ-lille.fr

Start date and duration: October 2026 for 3 years

Vacancy description: We are pleased to announce a fully funded PhD fellowship for a highly motivated, enthusiastic and independent person with a keen interest in integrative phylogenetics and population genetics studies of both extant and extinct biodiversity. We will focus on comparative analyses of environmental, phenotypic and molecular data (for extant taxa only) to understand how differentiation occurs among populations and how such differentiation contributes to lineage divergence. Strong knowledge and competences in computational evolutionary biology are expected. Advanced knowledge in bioinformatics, morphometrics and/or ecological data analysis are plus-points.

Project description: A central aim of modern evolutionary biology is to understand how new species arise and how they cope with environmental changes. At the microevolutionary scale, research has focused on the mechanisms driving trait evolution and progressive reproductive isolation up to speciation in living taxa. At the macroevolutionary scale, paleontologists have accrued data on how species diversity waxed and waned over time, while phylogenetic approaches have been developed to infer rates of trait evolution, speciation and extinction. To what extent and how the mechanisms that generate intraspecific variation and population differentiation contribute to macroevolution remain central questions, however. In the project divEARS, we will address these questions via integrative studies of three mollusk families from the East African Rift Systems (EARS) at both microevolutionary and macroevolutionary scales. We will generate data on ecology, life-history traits, reproductive strategies, phenotypes and single-copy orthologous genes to document intraspecific variation, dynamics of population differentiation up to speciation, as well as phylogenetic rates of diversification and phenotypic evolution, leveraging new advances in phylogenetics.

In this PhD project, we will study how differences in life-history strategies and ecology influence intraspecific variation, population differentiation, and ultimately dynamics of speciation in six clades of endemic mollusks from Lake Tanganyika. We will use phylogenetics to identify ~15-20 species pairs for subsequent comparative population genomic analyses. This approach will enable us to assess variation in genetic diversity and phenotypic disparity within populations, among populations and among species in the context of differences in life-history and ecology, providing insight into how intrinsic drivers of population differentiation contribute to the dynamics of speciation. If time permits, we will apply phylogenetic approaches on continent-wide representatives of the mollusk families that containing the six previously mentioned clades to examine how extrinsic (habitat heterogeneity, environmental stability) and intrinsic differences (life-history strategies and ecology) contribute to variation in macroevolutionary patterns as well as rates of diversification and trait change throughout the

EARS.

Methodologically, we will use a recently developed next-generation sequencing pipeline (Ortiz-Sepulveda et al. 2023) to obtain data on ~1500 genes to develop backbone phylogenomic and population genomic datasets. Morphological disparity will be documented with trait measurements and geometric morphometrics, whereas ecological data will be derived from metadata collected at sampling localities.

Setting and requirements: The PhD fellowship is funded by Lille University and data acquisition by ANR PRC project divEARS (2026-2030). This PhD project will be developed at UMR 8198 Evo-Eco-Paleo of the CNRS and Lille University in the context of an international collaborative network, notably with the Department of Biology of the KU Leuven. Master students that are graduating in the academic year 2025-2026 are invited to apply. More information on studying at Lille University can be found on the Lille University webpage: https://www.univ-lille.fr/home/international-student/ . Profile:

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

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Umontreal MolecularPrimatology

The Multiomic Anthropology and Primatology Laboratory for Evolution (MAPLE) at the Universitï¿½ de Montrï¿½al, led by Dr. Joseph Orkin (bioanth.ca), invites applications for a funded PhD position in molecular primatology. The lab integrates genomics, proteomics, and microbiome research to study the evolution, adaptation, and conservation of wild primates.

Application deadline March 25, 2026, for a start date in Fall 2026. Apply here:https://forms.gle/fYcQwgGVGn6Gm3gNA Project Description

The PhD student will investigate ecological and anthropogenic influences on the molecular ecology and evolution of white-faced capuchin monkeys across Central America. The project integrates genomic, proteomic, microbiome, and ecological datasets to understand how environmental pressures shape primate diversity and adaptation in wild populations. It builds on an expanding multiomic dataset from multiple capuchin populations and offers opportunities for laboratory, computational, and field-based research.

The student will receive training in population genomics, proteomics, and computational analysis of multiomic data and will develop independent research questions within the broader project. Opportunities will also be available to participate in field research at an established primate field site in Costa Rica.

Applicant Profile

The successful applicant will have a degree in biological anthropology, biology, bioinformatics, or a related field and experience working with genetic and/or proteomic data. Candidates with either a masterï¿½s degree or a strong undergraduate degree with research experience are encouraged to apply.

Excellent written and spoken English is required (minimum C1 level). French language ability is preferred but not required at the time of application.

Both Canadian and international candidates are encouraged to apply.

Environment and Language

The Universitï¿½ de Montrï¿½al is one of Canadaï¿½s leading research universities and is located in Montrï¿½al, a vibrant and affordable city with a strong international research community. Although the Universitï¿½ de Montrï¿½al is a French-language university, knowledge of French is not required at the time of application but is advantageous. Language training is available, and many international students develop proficiency during their PhD.

Multi-year funding is available through research assistantships and fellowships. Students will also be encouraged and supported in applying for external scholarships (e.g., NSERC, SSHRC, FRQ, Vanier, etc.).

Joseph Orkin joseph.orkin@umontreal.ca

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

UMontreal MultiomicsFermentedFoods

The Multiomic Anthropology and Primatology Laboratory for Evolution (MAPLE) at the Universitï¿½ de Montrï¿½al (bioanth.ca), led by Dr. Joseph Orkin, invites applications for a funded PhD position in the multiomic anthropology of food. The lab integrates genomics, proteomics, and microbiome research to study the evolution, adaptation, and diet of humans and other primates. Ongoing research in the lab focusses on traditionally fermented foods and smoked salmon.

Application deadline March 25, 2026, for a start date in Fall 2026. Apply here: https://forms.gle/-HHv4zcigNiQ4mSi87 Project Description

This PhD project is situated at the intersection of anthropology, food science, and multiomic research on traditional food preservation. It investigates how traditional food preservation practices such as fermentation, salting, and smoking shape the molecular, microbial, and biochemical properties of foods in culturally specific ways. The student will combine molecular approaches-including microbiome analysis, proteomics, and lipidomics-with anthropological perspectives on food traditions to examine how cultural knowledge and practice influence processes of food transformation, preservation, and meaning.

The student will receive training in molecular laboratory techniques, bioinformatics, statistics, and ethnographic research.

Applicant Profile

The successful applicant will have a degree in biological anthropology, biology, food science, or a related field, and some experience working with microbiome, proteomics, lipidomics, metabolomics, or related molecular data. Candidates with either a masterï¿½s degree or a strong undergraduate degree with research experience are encouraged to apply.

Excellent written and spoken English is required (minimum C1 level). French language ability is preferred but not required at the time of application.

Both Canadian and international candidates are encouraged to apply.

Environment and Language

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Joseph Orkin joseph.orkin@umontreal.ca

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UMuenster EvoReproCavefishMHC

PhD Position

MHC in cavefish and human reproduction

Group of Dr. R. PeuÃÂ, Institute for Intgrative Cell Biology and Physiology at the University of Muenster, Germany (https://www.uni-muenster.de/Biologie.IMZ/en/-rohner/people/peuss.html)

Research Assistant (m/f/d) (salary grade E 13 TV-L, 65 %)

Your tasks:

The position is embedded in the DFG-funded Collaborative Research Centre 1748 'Principles of Reproduction'. The CRC 1748 involves scientists of the University, University Hospital, and Max Planck Institute MÃÂ¼nster as well as of the RWTH Aachen. Our central objective is to elucidate the genetic, molecular, and cellular mechanisms governing the formation and function of the testis, production and function of sperm, fertilisation, as well as early embryonic development - in both health and disease. To this end, we combine interdisciplinary research in molecular, structural, and cell biology as well as in physiology, biophysics, epi /genetics, (bio)informatics, and multimodal data analysis.

The PeuÃÂ group focuses on topics within the field of evolutionary immunology, including the interaction of immunity and reproductive biology. This joint project together with Prof. Joachim Kurtz at the Institute for Evolution and Biodiversity will address the role of the Major Histocompatibility Complex (MHC, or HLA in human) for fertilisation and male infertility. We combine the strengths of two fish species, the Mexican cavefish (Astyanax mexicanus) and the three-spined stickleback, exploiting their natural MHC variability together with analyses of human genomic datasets to identify HLA variants associated with infertility.

Your task is the genetic analysis of MHC in different A. mexicanus ecotypes (surface fish and cavefish) and creating hybrids using in-vitro fertilisation to conduct experiments on the role of MHC for spermatogenesis, sperm function and gamete interaction using techniques ranging from standard sperm fitness test, single-cell

RNA sequencing and metabolic measures using the Seahorse system. You will further be involved in the analysis of human whole exome sequencing (WES) data of infertility cases and controls. This position is tied to working towards a doctorate.

Our expectations:

* Applicants must have (the equivalent of) a master's degree in biology, preferentially with a focus on evolution, molecular biology, reproductive biology or a related field. * A background, and ideally some experience, in any of the following areas will be useful: molecular laboratory skills, spermatogenesis and/or practical fish work. * Applicants should have excellent communication skills and be able to work both independently and as part of a multidisciplinary team. * The working language of the Institute and the lab is English, therefore good proficiency in spoken and written English is a requirement; a willingness to learn German is desirable.

Advantages for you:

* Working in the highly collaborative environment of the CRC 'Principles of Reproduction' with access to state-of-the-art technology and datasets. * Benefiting from collaboration with another PhD student carrying out related work in the three-spined stickleback and with our external collaborator, Prof. Tobias Lenz (University of Hamburg), who is an expert on both fish and human MHC. * A unique opportunity to combine basic research in evolutionary ecology with applied research on human reproduction. * Appreciation, commitment, openness and respect - values which are important to us. * Our broad range of diverse work-time models offers great flexibility - also when working from home. * If you have family members or young children in your care, our Family Service Office offers concrete support to help you balance your private and professional responsibilities. * As an educational institution, we are deeply committed to offering occupational training and continuing education opportunities tailored to your individual needs. * From A - Z, Aikido to Zumba, our sport and health programmes ensure a healthy work-life balance. * As a university employee, you are entitled to numerous benefits afforded to public servants, e.g. an attractive company pension scheme (VBL), an annual end-of-year bonus and a position that is shielded from economic fluctuations.

The University of MÃÂ¼nster strongly supports equal opportunity and diversity. We welcome all applicants regardless of sex, nationality, ethnic or social background, religion or worldview, disability, age, sexual orientation or gender identity. We are committed to creating family-friendly working conditions. We actively encourage applications

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Jobs

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AbuDhabi UAE BarcodingBiodiversity

Staff Scientist in Molecular Ecology, OIKOS Genomics, UAE Location: Abu Dhabi, United Arab Emirates Organisation: OIKOS Genomics

We are seeking a Staff Scientist in Molecular Ecology to drive the development and application of molecular tools for biodiversity assessment and monitoring. This role emphasizes research and development (R&D) in molecular ecology, including DNA metabarcoding and environmental DNA (eDNA), across diverse habitats, from arid landscapes to wetlands and marine environments. The position focuses on development and refining of laboratory and analytical pipelines that directly support conservation programmes.

OIKOS Genomics is a member of EKTHAR who leads regional and international initiatives in wildlife conservation and biodiversity genomics, with ongoing initiatives in Morocco, the United Arab Emirates, Uzbekistan, and Kazakhstan, and an expanding footprint across new regions. The position will be hosted by OIKOS Genomics and will lead R&D initiatives that advance species detection, biodiversity metrics and molecular ecology applications, ensuring that new tools and workflows translate into tangible conservation outcomes.

The role is inherently collaborative, linking Conservation Genomics with other parts of the organisation (i.e. conservation medicine, conservation breeding, field ecology, and applied research), as well as a dynamic global network of partners to ensure that molecular tools and data are effectively integrated into ongoing conservation efforts. Research and development in this position will focus on existing conservation initiatives as well as a newly launched programme to measure biodiversity. The Staff Scientist will play a critical role in ensuring the success of new programmes aimed at measuring biodiversity at scale on both land and sea.

Working closely with laboratory staff and bioinformaticians, the scientist will identify opportunities to refine workflows, enhance data quality, and improve operational efficiency; while providing informed feedback to senior leadership on research progress and technical needs, ensuring that program-level decisions are grounded in practical laboratory realities and responsive to emerging challenges.

This role is ideal for a molecular ecologist seeking to pivot from academia to a career with direct conservation impact, while continuing to engage and collaborate with a global network of academic researchers.

Key Responsibilities - Lead R&D projects in metabarcoding and eDNA for biodiversity assessment and ecological monitoring. - Develop and refine laboratory and bioinformatics pipelines to support species detection, community analyses, biodiversity monitoring, and ecological baselines using molecular ecological approaches. - Contribute to the creation and curation of reference barcoding libraries and databases. - Work across divisions to integrate molecular tools into broader conservation and management programmes. - Identify and address technical or operational gaps within lab workflows to ensure consistency, reliability, and reproducibility. - Support capacity building and contribute to technical documentation, training, and protocol development.

Required Qualifications - PhD in Molecular Ecology, or related field; with 2-4 years of postdoctoral experience. - Demonstrated experience in one or more of the following: o DNA barcoding, metabarcoding, and eDNA applications. o Development and optimisation of molecular workflows and contamination control. o Experience with both short read and Oxford Nanopore sequencing technologies. - Strong understanding of how molecular data can inform conservation practice. - Excellent teamwork, communication, and project management skills. - Fluency in English, both spoken and written; expertise in additional languages is a significant advantage.

Application - Interested candidates are invited to send at join-us@reneco.org: o A detailed CV o A cover letter describing relevant experience and motivation o Contact information for two referees - Applications will be accepted until the position is filled.

This is a full-time position based in Abu Dhabi, United Arab Emirates, reporting to the Head of Conservation Genomics.

For informal enquiries please email Loïc LESOBRE: llesobre@oikosgenomics.org

LESOBRE Loïc <llesobre@reneco.org>

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

ColumbiaU Three SummerResAssistant

Tick Summer Research Assistant Seeking Tick Research Field Assistants for Summer 2026! The Eco-Epidemiology Lab at Columbia University has multiple paid positions for highly motivated Research Interns to assist with field research and outreach activities for the 2026 summer field season. This work will contribute to our long term project studying the eco-epidemiology of vector-borne diseases throughout New York City and Long Island, and creating a tick urban surveillance system (TUSS) intended to inform public health programs.

Through this work, the successful candidate will gain experience working in the field conducting tick collection and identification, general field-research techniques, and science engagement with the public.

What you will do (one or more of): * Conduct field collections of ticks in a variety of NYC and Long Island greenspaces * Conduct data collection * Manage field notes and datasheets * Prep field materials (i.e. fill tubes, organize equipment) * Work as a part of a field crew of 3-4 people * Engage with the park-going public and answer questions about our work

What you will bring: * A passion for ecology, epidemiology, and/or the natural sciences * A positive attitude and ability to work in a dynamic team environment * The ability to work outside in various conditions * Valid driver's license and willingness to drive to field sites within NYC and on Long Island * Previous field experience is preferred but not required

This is a full-time, temporary and seasonal position for Summer 2026 (May to August). Daily hours may be irregular (due to long travel distances and traffic conditions) and may include weekend work, but weeks will not exceed 35 hours per week. Overnight stays near field sites on Long Island may also be required. Hotel or Airbnb accommodation will be provided.

This will be a fieldwork-intensive position. Applicants should be capable of working outdoors in challenging environmental conditions (e.g. rain, heat, overgrowth, steep slopes, fog, vector-infested habitat, etc.).

Compensation: $22.50/hour.

To apply, please email our lab manager Adara (aa5294@columbia.edu) with your CV and a brief message outlining your interest in working with our lab and why you would be a strong fit for the position.

—

Avian Summer Research Assistant Seeking Avian Research Field Assistants for Summer 2026! The Eco-Epidemiology Lab at Columbia University has multiple paid positions for highly motivated Research Interns to assist with field research and outreach activities for the 2026 summer field season. This work will contribute to our long term project studying the eco-epidemiology of vector-borne diseases throughout New York City and Long Island, and inform public health programs.

Through this work, the successful candidate will gain experience working in the field conducting avian sampling (including mist-netting, IDing, banding, processing, and blood collection), general field research techniques, and science engagement with the public.

What you will do (one or more of): * Participate in avian point counts * Conduct avian banding surveys using mist nets * Collect and process avian biological samples * Collect and process bird-attached ticks * Conduct field collections of ticks * Conduct ecological assessments of larger public spaces such as parks and preserves * Coordinate data collection and management with a field crew of 3-4 people Required qualifications: * Previous experience handling, extracting birds from mist nets, and banding birds is required * Available early mornings and weekends, flexible schedule (due to the unpredictable nature of fieldwork) * The ability to work outside in various weather conditions * The ability to work in a standing position for long periods of time

Preferred qualifications: * Local (NYC) bird identification experience highly preferred * Previous experience processing and collecting avian blood samples highly preferred * A passion for ecology, epidemiology, and/or the natural sciences * A positive attitude and ability to work in a dynamic team environment * Valid driver's license and willingness to drive to field sites within NYC and on Long Island is required * Access to a personal vehicle is desirable (but not required)

This is a full-time, temporary and seasonal position for Summer 2026 (May to August). Daily hours may be irregular (due to long travel distances and traffic conditions) and may include weekend work, but weeks will not exceed 35 hours per week. Overnight stays near field sites on Long Island may also be required. Hotel or Airbnb accommodation will be provided.

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Compensation: $22.50/hour To apply, please email our lab manager Adara (aa5294@columbia.edu) with

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FloridaIntlU TropicalEvolution

Florida International University < https://fiu.edu > is a Top 50, preeminent public research university with 55,000 students from all 50 states and more than 140 countries, as well as an alumni network of more than 340,000. Located in the global city of Miami, the university offers more than 200degree programs at the undergraduate, graduate and professional levels, including medicine and law. FIU faculty are leaders in their fields and include National Academy members, Fulbright Scholars and MacArthur Genius Fellows. A Carnegie R1 institution, FIU drives impactful research in environmental resilience, health and technology and innovation. Home to the Wall of Wind and Institute of Environment, FIU stands at the forefront of discovery and innovation. With a focus on student success, economic mobility and community engagement, FIU is redefining what it means to be a public research university.

Walter and Rosalie Goldberg Distinguished Professorship in Tropical Ecology

Position Description and Qualifications FIU is seeking applicants for the Walter and Rosalie Goldberg Distinguished Professorship in Tropical Ecology. The successful candidate will have a record of academic distinction working on the sustainability, resilience, conservation, or anthropogenic disruption of terrestrial, freshwater or marine tropical systems. Candidates for this tenured/tenure track position must have attained the rank of Associate or Full Professor by the time of applying. The Distinguished Professor is expected to have a national or international public profile and to engage in broad and highly visible public science communication and/or engagement activities in addition to their research, teaching and service duties. The successful candidate will join a large and productive faculty of scientists whose work focuses on tropical ecology supported by FIU's Institute of Environment, < https://environment.fiu.edu/ > and numerous research programs and facilities including the International Center for Tropical Botany, < https://environment.fiu.edu/ictb/ > Aquarius Reef Base < https://environment.fiu.edu/aquarius/about/ >, the National Science Foundation-funded Florida Coastal Everglades Long-Term Ecological Research program < https://fcelter.fiu.edu/index.html >, Coastal Conservation and Restoration Laboratory < https://environment.fiu.edu/facilities-research-groups/coastal-conservation-and-restoration-laboratory/ >, Water -OMICS facility, and the Robotics and Autonomous Systems Laboratory for Coastal Conservation and Restoration.

FIU is close to many subtropical ecosystems, including lakes, rivers, hardwood hammocks, pine forests, wetlands, mangrove forests, seagrass meadows, coral reefs and the coastal ocean. Faculty are also conducting research in tropical ecosystems worldwide. The Goldberg professor's departmental tenure home in the College of Arts, Sciences and Education will be determined by the qualifications and research profile of the applicant.

Application Details Qualified candidates are encouraged to apply to Job Opening ID *536963* at careers.fiu.edu < https://hr.fiu.edu/careers/ > and attach a (1) cover letter, (2) curriculum vitae, (3) statement of research, (4) statement of teaching and mentoring philosophy, and (5) statement outlining their public science communication achievements and strategic plan for their future research and public outreach at FIU. Candidates will be requested to provide names and contact information for at least three (3) references who will be contacted as determined by the search committee. Applications will be accepted until the position is filled. Please direct inquiries about this search to the chair of the search committee, Dr. James Fourqurean (jim.fourqurean@fiu.edu).

Review Date Review of candidates will begin April 12, 2026 and continue until the position is filled. The expected start date is August 13, 2026.

*Applicants are encouraged to review Florida International Universityâ euro s immigration and visa requirements, if applicable, prior to applying: * < https://hr.fiu.edu/employees-affiliates/working-at-fiu/immigration-process >

*FIU is a State University System of Florida member, Equal Opportunity, Equal Access, and Affirmative Action Employer for individuals with disabilities and veterans. All qualified applicants will receive consideration for employment decisions, programs, and events without regard

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Senckenberg Wilhelmshaven MarineBenthicSpatialModelling

Dear all,

please find this new job opportunity at Senckenberg Wilhelmshaven, Germany:

Researcher (m/f/d) for Marine Benthic Ecology and Spatial Modelling (CONMAR-Habitat)

(full time / part-time options available)

Location: Wilhelmshaven Employment scope: Full-time (40 hours per week) / part-time options available Type of contract: The contract shall ideally start in June 2026 and is limited for the project duration until 30. November 2027.

Remuneration: Collective agreement of the state Hesse, TV-H E 13

Senckenberg - Leibniz Institution for Biodiversity and Earth System Research (SGN), headquartered in Frankfurt am Main, is seeking to fill the following position at its institute Senckenberg am Meer in Wihelmshaven, starting as of June 2026:

Senckenberg is one of the world's leading research institutions in the field of Biodiversity and Earth System Research, with eight research institutes and three natural history museums across Germany and scientists from over 40 nations. Our headquarter is located in the thriving commercial metropolis of Frankfurt in the heart of Germany, which also hosts one of our most famous facilities, the Senckenberg Natural History Museum. Named for its location bordering the North Sea, our northernmost institute "Senckenberg am Meer" in Wilhelmshaven cooperates with major marine research institutions and universities. The area around Wilhelmshaven is well-known for its unspoilt nature and general recreational value.

For the project CONMAR-Habitat "Spatio-temporal variability of benthic communities and environmental parameters in munition sink areas and reference sites in the North and Baltic Sea", embedded in the "Deutsche Allianz Meeresforschung (DAM)" joint research project "CONcepts for conventional MArine Munition Remediation in the German North and Baltic Sea (CONMAR)" applications are welcome.

Your tasks

- Active participation in several research cruises per year (approx. two weeks each) in the North and Baltic Sea - Taxonomic identification and quantitative analysis of marine benthic infauna and epifauna communities - Multivariate statistical analysis of community and environmental datasets - Spatial analysis and georeferencing of ecological data using GIS - Development and implementation of species distribution models - Preparation of project reports and publication of results in peer-reviewed scientific journals - Contribution to interdisciplinary collaboration within the CONMAR consortium

Your profile

- PhD in Benthic Ecology, or in Marine Biology, or a related natural science discipline - or a Master degree with demonstrated expertise in points 1-4 of the tasks - Experience in Taxonomy of North Sea Infauna and Epifauna - Strong background in multivariate statistical analyses (e.g. R or comparable software) - Proven experience in GIS-based spatial analyses - Experience in species distribution modelling - Track record of peer-reviewed scientific publications - Experience in ship-based sampling campaigns - Ability to work independently as well as collaboratively in interdisciplinary research teams - Excellent command of written and spoken English

We offer

- access to an international network of scientists, policymakers and research organizations

- an attractive job within the inspired and dynamic working environment of an internationally recognized research institution

- flexible working hours - mobile working options - employee ID card with free admission to Senckenberg museums - annual special payment - collectively agreed vacation entitlement - company pension plan

Senckenberg is committed to diversity. We benefit from the different expertise, perspectives and personalities of our staff and welcome every application from qualified candidates, irrespective of age, gender, ethnic or cultural origin, religion and ideology, sexual orientation and identity or disability. Applicants with a severe disability will be given special consideration in case of equal suitability. Senckenberg actively supports the compatibility of work and family and places great emphasis on an equal and inclusive work culture.

How to apply? Please upload your application (letter of motivation with a short description of your previous and current research foci, a CV, certificates of academic achievements, list of publications as well as letter(s) of recommendation, if available) as a single PDF on our website by 16. April 2026.

https://senckenberg.career.softgarden.de/jobs/63579654/Researcher-m-f-d-for-Marine-Benthic-Ecology-and-Spatial-Modelling-CONMAR-Habitat- Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt a.M. E-Mail: recruiting@senckenberg.de

If you have any specific questions about this role, please contact

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StCloudStateU Minnesota EvolutionaryBiology

St. Cloud State University

Department of Biology and Chemistry

Assistant/Associate Professor of Biology

Apply here: https://minnstate.wd1.myworkdayjobs.com/en-US/Minnesota_State_Careers/job/Assistant-Associate-Professor-of-Biology—State-University-Faculty_JR0000004290 Institution: St. Cloud State University

City: St. Cloud, MN

Salary Range: $64,963.00 - $188,620.00

Classification: Tenure-track

Job Description: St. Cloud State's Department of Biology and Chemistry invites applications for a tenure track Assistant/Associate Professor position in Biology. The position will be part of a faculty team and graduate teaching assistants educating over 500 undergraduates in courses each year. St. Cloud State University faculty and staff collaborate to offer relevant and rigorous academic programs in a supportive environment that emphasizes active and applied learning, community engagement, sustainability and global and cultural understanding. There is access to state-of-the-art teaching and research facilities including a vivarium, imaging center, integrated research building and technology-enhanced human anatomy suite. The faculty contract includes professional development funding.

The successful candidate will have scholarly research and expertise to teach courses in a biomedical sciences curriculum. They will team-teach Human Anatomy & Physiology (BIOL 202/204) lecture and participate with staff and graduate teaching assistants in coordinating laboratory sections. Additional teaching assignments will be based upon applicant expertise and existing course needs in biomedical sciences.

The successful candidate will demonstrate the ability to:

- Teach effectively
- Conduct scholarly research
- Continue preparation and study in discipline
- Contribute to student growth and development
- Provide service to the university and community.

The ideal candidate will share St. Cloud State's commitment to our mission and values, especially our commitment to educating our diverse student population. They should be willing to participate in teaching using alternative delivery methods such as online and hybrid. They will regularly engage in ongoing professional development and innovation opportunities focused on pedagogical growth offered within the University. Employment for this position is covered by the collective bargaining agreement for the Inter Faculty Organization which can be found at: https://www.ifo.org/ Minimum Qualifications

- Ph.D. in Biology or related discipline at time of application
- At least one year's teaching experience in postsecondary Human Anatomy & Physiology (both lecture and laboratory)
- Experience working with human cadaver-based instruction
- Evidence of ability to contribute to Biomedical Sciences program curriculum and advising
- Ability to develop a research program within disciplinary focus involving undergraduate and master's level students
- Evidence of demonstrated ability to teach and work with people from diverse background

Preferred Qualification

- Post doctoral research in Biology or related field
- Evidence of grants and peer reviewed publications

- Experience teaching Human Anatomy & Physiology for health professions students

- Experience teaching upper division/graduate level courses in biomedical sciences

- Experience mentoring students including underrepresented groups in STEM fields

Other Requirements

Please note that successful applicants must be eligible to work in the United States on or before the effective date of appointment. Eligibility includes being a U.S. citizen or national, a lawful permanent resident, or a foreign national authorized to work in the U.S. without the need for employer sponsorship. Employees must maintain work authorization without sponsorship for the duration of their appointment.

Required Documents to Apply (Upload with Application)

- Resume/CV

- Cover Letter

- Unofficial Transcripts (Official transcripts will be required at time of employment)

Additional information about the department and St. Cloud State University can be found at https://www.stcloudstate.edu/biology/ and http://www.stcloudstate.edu About

The successful candidate will share St. Cloud State's commitment to our mission, and in particular, the value we place in diversity, equity, and inclusion (DEI) as outlined in SCSU's It's Time strategic framework. Notably, we uphold the advancement of diversity, equity, and inclusion and engage in intentional actions to address systemic inequities throughout the university and surrounding environment. DEI values, practices, and strategies are embedded into the fabric of our

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UCollegeLondon ComputationalGenomics HealthDisease

We have an open position for a Professor / Associate Professor of Computational Genomics in Health and Disease at University College London. The post is based in the Department of Genetics, Evolution and Environment, and the UCL Genetics Institute, and is funded by the UCL Health Strategy.

Deadline 25th March.

Link: https://www.ucl.ac.uk/work-at-ucl/search-ucl-jobs/details?nPostingId=17496&nPostingTargetId=42200&id=Q1KFK026203F3VBQBLO8M8M07&LG=UK&languageSelect=UK&mask=ext The role: We seek to appoint an outstanding academic as a Professor or Associate Professor of Computational Genomics in Health and Disease. The post will be based within the Genetics, Evolution and Environment (GEE) department. The postholder will lead a world-class research programme at the interface of human genomics, computational biology and evolutionary population genetics to understand the molecular and evolutionary processes that generate diversity that influences health and disease. The candidate will combine experimental and computational approaches in the study of fundamental biological questions. Research areas of particular interest include: 1) The origin and evolution of germline mutations in humans; 2) The genetic bases of disease or health-related phenotypes and their differences among populations; 3) The dynamics of population and evolutionary processes on the fate of genetic variants that shape health and disease. We particularly welcome interdisciplinary approaches that are rooted in theory. Fundamental and evolutionary approaches (which are strong in our department) are very welcome, as long as they further our understanding of human health or disease. The post includes start-up funds and is an exciting opportunity to join an excellent and dynamic scientific community in the heart of London.

Who we are: The Division of Biosciences of UCL is a foremost centre for research and teaching in the biological sciences. We have an outstanding international reputation and a community of over 500 staff and more than 300 PhD students engaged in cutting edge research and collaboration. Within Biosciences, the Research

Department of Genetics, Evolution and Environment (GEE) provides a stimulating and diverse research and training environment of international standing in exciting areas of computational biology, human genetics, evolutionary and population genomics, development, aging, microbiology, ecology and biodiversity. The UCL Genetics Institute (UGI) is an internationally leading centre for genomics within GEE. UGI focuses on the development and application of computational tools for large genomic datasets to address important questions in biology ranging from the genetic determinants of human disease, the origin and evolution of modern humans, the processes mediating environmental adaptations, the improvement of crop varieties or antibiotic resistance. Collectively we aim to help address major current challenges such as population health disparities, food security or the biodiversity crisis through the study of genomes. We are located in the heart of London.

GEE: https://www.ucl.ac.uk/life-sciences/gee UGI: https://www.ucl.ac.uk/life-sciences/ugi Aida Andres <a.andres@ucl.ac.uk>

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UHawaii EvolutionaryMarineBiology

Description

Title: Assistant / Associate Professor (Marine Biologist) Position Numbers: 0082434 Hiring Unit: College of Natural Sciences - School of Life Sciences Location: Manoa Date Posted: February 25, 2026 Closing Date: Application review begins March 19, 2026 Salary Information: Commensurate with qualifications and experience Monthly Type: 9 Month Tenure Track: Tenure Full/Part Time: Full time Temp/Perm: Permanent Funding: General Funds

Position Description The School of Life Sciences (SoLS) at the University of Hawai'i at Manoa seeks a candidate for an Assistant (F3) or Associate Professor (F4) of Marine Biology position who uses integrative approaches to investigate the underlying mechanisms of responses of marine organisms, populations, or communities to environmental change. Research should connect organismal biology and ecology, and may integrate multiple biological, spatial, and/or temporal scales. Research that will focus on Hawaiian species is of particular interest. The successful candidate can have research experience in any area of marine biology, including but not limited to physiological, ecological, and/or evolutionary approaches. This is a permanent, tenure-track, full-time, 9-month facutly appointment to begin August 1, 2026, subject to position clearance, availability of funds and satisfactory performance.

The University of Hawai'i at Manoa (UHM) is a Carnegie Research 1 University with strong emphases on research and undergraduate and graduate education. Our campus welcomes all students but given our responsibilities to the community in which we operate, as part of our strategic mission, we strive to become a Native Hawaiian Place of Learning, a place that is committed to integrating Native Hawaiian language, culture and/or values into its academic and campus environment. Our vision is to be locally and globally recognized as a premier student-centered and community-serving university (https://manoa.hawaii.edu/strategicplan/). The School of Life Sciences hosts the largest academic program on the University of Hawai'i's flagship campus, serving over 1,500 undergraduate majors and 150 graduate students for degrees in biology, botany, marine biology, microbiology, molecular cell biology, and zoology. Research interests of the 40 faculty members span all biological scales, with many focusing on ecology, evolution, and conservation biology. The School of Life Sciences is committed to serving our community and state and to excellence in research and teaching. (https://manoa.hawaii.edu/lifesciences/).

Assistant Professor Duties and Responsibilities - Develop and sustain an innovative, externally funded research program - Mentor and advise graduate and undergraduate students in the School of Life Sciences - Provide high-quality teaching in support of the Marine Biology B.S. and B.A. degree programs - Develop and teach graduate courses in their area of expertise that directly contribute to one or more of the graduate degrees offered by the School of Life Sciences - Serve on departmental, college, and university committees as appropriate - Render service to the professional and local/regional community that is relevant to the individual's academic specialty

Associate Professor Duties and Responsibilities - In addition to the duties and responsibilities associated with the Assistant Professor rank, the role encompasses leadership at the University and national levels.

Assistant Professor Minimum Qualifications

- A Ph.D or equivalent terminal degree from a college or university of recognized standing in a field relevant to the position. - Research experience in marine biology or a related field - Excellence and creativity in research, as demonstrated by publications in peer-reviewed journals - Ability to teach and mentor students of various backgrounds in core classes in the Marine Biology major, such as algal diversity, invertebrate biology, fish biology, marine microbiology, marine ecology and evolution, or an advanced capstone course, among others - Commitment to supporting the key principles of the School of Life Sciences, which include personal and professional integrity, and the pursuit of excellence in instruction and research - Professionalism in meeting and conferring with others.

Associate Professor Minimum Qualifications In addition to those of Assistant Professor, Associate Professor minimum qualifications include: - Four years in the rank of Assistant Professor - Documented participation in the scholarly and academic affairs of their Department, University, or professional organization - Clear recognition among peers at the local and/or regional levels

Assistant Professor Desirable Qualifications - Postdoctoral research experience

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UMayotte France EvolutionLagoons

Dear colleagues,

The University of Mayotte (France) invites applications for a Lecturer position (Maï¿½tre de confï¿½rences, CNU sections 67/68) in Ecology of lagoon ecosystems.

The successful candidate will develop research on population and community ecology of lagoon ecosystems (coral reefs, seagrass beds, mangroves), with a particular focus on understanding the effects of anthropogenic pressures on biodiversity and ecosystem functioning. Approaches may include functional ecology, biodiversity assessment, population dynamics, ecological modelling, bioindication, participatory science, or environmental monitoring.

The position is affiliated with the MARBEC research unit (UMR 9190, Montpellier/Sï¿½te) and offers strong opportunities for collaboration within a rapidly developing research environment focused on marine socio-ecosystems in the Western Indian Ocean. The position benefits from access to field and laboratory facilities (scientific diving, molecular biology, remote sensing, experimental platforms) and from close interactions with local stakeholders (e.g. Mayotte Marine Natural Park).

Teaching duties will be carried out in the Life Sciences licence, including ecology, biodiversity, and quantitative methods. The candidate is expected to be involved in teaching, student supervision, and academic life, within a young and dynamic department.

Mayotte hosts one of the largest enclosed lagoon systems in the world, providing exceptional opportunities for research on tropical marine ecosystems under strong anthropogenic pressure.

Applicants must hold (or obtain) a national qualification for Lecturer positions (CNU sections 67 or 68). Applications must be submitted through the official national platform Odyssï¿½e: https://odyssee.enseignementsup-recherche.gouv.fr/ Deadline for application: April 3, 2026

Contacts: chiraz.trabelsi@univ-mayotte.fr patricia.cucchi@umontpellier.fr

Best regards,

CORSE Emmanuel Maitre de confï¿½rences Universitï¿½ de Mayotte Dï¿½partement Sciences & Technologies

Contact: 0633349243

Emmanuel CORSE <emmanuel.corse@univ-mayotte.fr>

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UNacionalAutonomaDeMexico SystematicsAraneae

Faculty Position. Systematics of Araneae (Arachnida) Institute of Biology. Universidad Nacional Autonoma de Mexico

https://www.ib.unam.mx/ibunam/-Convocatoria_Inv_Araneae_28Feb26.pdf The Universidad Nacional Autonoma de Mexico (UNAM, www.unam.mx) is the preeminent public higher-education center in Mexico and is among the highest-ranking Spanish-speaking and Latin American universities. UNAMs Institute of Biology is a research center on the Universitys main campus in Mexico City.

Its mission is to discover, describe and systematically document biota, conducting scientific research about the evolutionary processes that originate and maintain it; its composition, distribution and interactions, and its sustainable use. The Institute of Biology houses the National Biological Collections of Mexico, including ten zoological collections, and the National Herbarium. Its Faculty include over 160 scientists and academic technicians who conduct research, teach and supervise undergraduate and graduate students, and participate in outreach activities, all to contribute to the understanding and conservation of biological diversity and to improve scientific advancement and the well-being of society.

To fulfill its mission, the Institute of Biology seeks qualified applicants for one tenure-track position as a full-time Research Scientist (Investigador/a Asociado/a C de Tiempo Completo) in the field of systematics of Araneae, in the Department of Zoology.

Candidates profile: We seek a scientist to conduct research in systematic biology of Order Araneae (Class Arachnida) (e.g., species discovery and description, classification, phylogenetic relationships), applying innovative theoretical concepts and methodological tools for phylogenetic reconstruction with genomic data, or for comparative phylogenetics, to investigate evolutionary processes above the species level (e.g., morphological diversity and evolution, species richness, diversification, distribution), combining field work and use and development of biological collections.

Requirements: - Doctorate or Ph.D. degree in zoology, arachnology, systematics or evolution. - Preferably with postdoctoral experience. - Knowledge and professional experience of at least three years in research in phylogenetic systematics and evolution of a group of Order Araneae. - Experience using biological collections. - Experience in field work. - Ability to teach and supervise undergraduate and graduate students from UNAMs School of Science and Graduate Programs, as well as to participate in outreach and institutional activities. - Develop their own line of independent research, including procurement of funds for research, and interaction and collaboration with other research groups. - Non-native speakers must be fluent in the Spanish language. - Because this position is available through the Subprograma de Incorporacion de Jovenes Academicos de Carrera (SIJA) UNAM aimed at incorporating early-career faculty, female applicants should be 39 years old or younger, and male applicants should be 37 years old or younger on the day of hire approved by the Consejo Tecnico de la Investigacion Cientifica (CTIC, Technical Council for Scientific Research).

Application and supporting documents: To apply, please send the following documents to sacademica@ib.unam.mx, with copy (Cc:) to secacad_vl@ib.unam.mx 1. Curriculum vitae (CV), including academic degrees, publication history and experience in systematics of Araneae. 2. Description of research conducted during at least the past 3 years (maximum 2 pages). 3. Research plan to be developed in one year, in the context of a longer research proposal, on the systematics and evolution a group of Araneae, preferably with a focus on groups distributed in Mexico (maximum 10 pages). 4. Cover letter addressed to the Director, Prof. Susana Magallon, stating the motives and interest in developing an academic career at the Institute of Biology, UNAM (maximum 2 pages). 5. Proof of age (birth certificate or passport). 6. Shortlisted candidates should provide 3 letters of academic recommendation.

Applications, accompanied by supporting documents, will be received from March 2nd, 2026 until the close of this call, on April 27th, 2026 at 18:00 h (Mexico City time). Shortlisted candidates will be contacted to request recommendation letters, a seminar and a personal interview.

Contact: For any questions regarding this announcement, please contact the Office of Academic Affairs of the Institute of Biology at sacademica@ib.unam.mx and/or secacad_vl@ib.unam.mx.

s.magallon@ib.unam.mx

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UPadova Italy Two BioinformaticsAnthropology Mar17

We are opening two research positions in bioinformatics and physical anthropology linked to the research project posted below. The applicant must be within 6 years of their MSc graduation. Holding a PhD is desirable but not required.

If you are interested AND you have relevant experience, please send your cv or motivation letter to luca.pagani@unipd.it and adeline.morez@unipd.it by the 17th March 2026.

Start date: anytime after 15th of April 2026. Duration: 24 months. Salary range: 1800-2500 EUR after all taxes (depending on experience and seniority) Work place:

Molecular Anthropology lab, Department of Biology, University of Padova PI: Prof. Luca Pagani

Position 1: A bioinformatic position to implement an aDNA and metagenomics bioinformatic pipeline.

Position 2: A physical anthropology/palaeopathology position focused on the study of the mostly unexamined Anthropology collection of the Department of Biology (hosted at the Museum of Nature and Humankind of the University of Padova). The collection hosts around 1000 Italian human remains ranging fromthe Neolithic to the Middle Ages.

Some background about the project: The Po Valley, a critical corridor connecting Europe to the Mediterranean Basin, has played a pivotal role in human migration and cultural exchange since the earliest settlement of Europe (~45 kya). Despite its importance, ancient DNA from this region remains understudied, leaving significant gaps in our understanding of how past migrations shaped genetic diversity, cultural transformations, and health-related traits across Europe. Our FIS3 POP-CORE project, funded by the Italian Ministry of University and Research, aims to generate high-resolution genomic data from Italian human remains spanning the Neolithic to the present day, leveraging the extensive Anthropology Collection of the University of Padova.

Our team: The successful candidates will join the dynamic Molecular Anthropology Lab, comprising one professor, one associate professor, two postdocs and two PhD and several Master students. The project will be conducted in close collaboration with Dr Nicola Carrara (Museum of Nature and Humankind, University of Padova) and the broader Anthropopgen research network (www.anthropopgen.it).

Luca Pagani <luca.pagani@unipd.it>

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UTuebingen ExperimentalBiodiversityResearch

The Faculty of Science at the University of Tübingen invites applications for a tenured

W3-Professorship of Experimental Biodiversity Research

starting October 1, 2027

The position corresponds to a full professorship in the German academic system. It will be created in the framework of the Cluster of Excellence 3121 "TERRA: Terrestrial Geo-Biosphere Interactions in a Changing World", together with three tenure-track professorships at the University of Tübingen and a W3-professorship at the University of Hohenheim. TERRA will develop an integrated understanding of how geo-biosphere interactions in terrestrial systems induce and respond to environmental changes. A team of more than 25 research groups will use evidence from both the geological past and the present to improve projections of future global-change impacts and assess the effectiveness of mitigation and adaptation strategies.

We are looking for an enthusiastic and creative colleague who is a recognized expert in biodiversity research in terrestrial systems. We are particularly interested in colleagues working with animals, and addressing one or more of the following topics: responses of soil biodiversity to environmental changes, plant-soil fauna interactions, below-ground food webs, or biodiversity effects on biogeochemical cycles or other geo-biosphere interactions. While experiments should be at the core of the candidate's research, additional molecular and/or theoretical approaches are a plus.

The candidate is expected to link his/her research to existing strengths within the Cluster of Excellence and its participating institutions. In this context, we are particularly keen to identify candidates who can link bio- and geosciences and/or bridge across temporal or spatial scales.

The professorship will be associated with the Institute of Evolution and Ecology in the Department of Biology. It will contribute to basic and advanced teaching in ecology and biodiversity.

Required qualifications include a PhD or equivalent degree as well as postdoctoral qualifications and teaching experience equivalent to the requirements of a full professorship. An outstanding, internationally visible research profile is expected. The candidates should have a documented track record in acquiring external research funding, and in collaborative research.

The University of Tübingen is committed to equity and diversity and actively promotes equal opportunities. Female academics, in particular, are explicitly invited to apply, as are applicants from outside Germany. Applications from equally qualified candidates with disabilities will be given preference.

General information on professorships, hiring processes, and the German academic system can be found here: https://uni-tuebingen.de/en/213700 . Questions regarding the Cluster of Excellence can be directed to the spokespersons of TERRA (terra-admin@uni-tuebingen.de).

Please submit your application documents via the online application portal of the University of Tübingen at https://berufungen.uni-tuebingen.de— by April 26, 2026. Questions about the call for applications and questions about the online application portal can be directed to the Dean of the Faculty of Science, Prof. Dr. Thilo Stehle, University of Tübingen, Germany (career@mnf.uni-tuebingen.de).

See also https://uni-tuebingen.de/en/university/-careers/newsfullview-job-advertisements/article/w3-professorship-of-experimental-biodiversity-research/ Prof. Dr. Oliver Bossdorf University of Tübingen Plant Evolutionary Ecology oliver.bossdorf@uni-tuebingen.de

GROUP: www.uni-tuebingen.de/plantevoeco HERBARIUM: www.uni-tuebingen.de/herbarium PUBLICATIONS: https://scholar.google.com/-citations?user=hAPepaEAAAAJ "Boßdorf, Oliver" <oliver.bossdorf@uni-tuebingen.de>

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Wisconsin FreshwaterMussel SummerResTech

Summer Freshwater Mussel Research Technician (multiple openings)

Dates: May 1st - Sept. 15th(flexible start and end dates)

Salary: $17/hour

Location: Rhinelander, Wisconsin

Description:Conduct aquatic surveys (snorkeling/ swimming) for native freshwater mussels in the Great Lakes region as part of a collaborative research project with the UGA and USDA Forest Service. Applicants must be available for overnight travel over multiple days (lodging, food stipend, and transportation provided).

Apply by: March 18, 2026

Questions? Dr. Shay Keretz (Shay.Keretz@usda.gov) or Dr. Rachel Toczydlowski (Rachel.Toczydlowski@usda.gov)

To Apply: https://www.ugajobsearch.com/postings/-470841 Dr. John Wares University of Georgia Odum School of Ecology, Graduate Program Director Department of Genetics www.wareslab.net John P Wares <jpwares@uga.edu>

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BestStudentPaper AnimalBehaviorSociety

2026 Warder Clyde Allee Competition

The 2026 Warder Clyde Allee Competition for Best Student Paper will be held during the annual meeting of the Animal Behavior Society, which will take place July 14-18 in Cincinnati, Ohio.

The Allee Competition is a great opportunity for graduate students (and new postdocs) to present their research to a large and supportive audience.

Participation includes submission of an extended written abstract and an oral presentation at the annual meeting.

Applications, including the extended abstract, are due by the meeting's abstract submission deadline, March 23, 2026.

More information, including eligibility requirements and application instructions, can be found at:

https://www.animalbehaviorsociety.org/web/awards-allee.php Greg Grether <ggrether@g.ucla.edu>

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CallForNominations HarrySmithPrize

Nominations open for the 2026 Harry Smith Prize, recognizing early-career research published in Molecular Ecology

The editorial board of the journal Molecular Ecology is seeking nominations for the Harry Smith Prize, which recognizes the best paper published in Molecular Ecology or Molecular Ecology Resources in the previous calendar year (2025) by graduate students or early career scholars with no more than five years of postdoctoral or fellowship experience. The prize comes with a cash award of US$1000 and an announcement in the journal and in the Molecular Ecologist. The winner of this annual prize is selected by a committee of former prize winners, chaired by Angel Rivera-Colon.

The prize is named after Professor Harry Smith FRS, who founded Molecular Ecology and served as both Chief and Managing Editor during the journal's critical early years. He continued as the journal's Managing Editor until 2008, and he went out of his way to encourage early career scholars. In addition to his editorial work, Harry was one of the world's foremost researchers in photomorphogenesis, where he determined how plants respond to shading, leading to concepts such as "neighbour detection" and "shade avoidance," which are fundamental to understanding plant responses to crowding and competition. More broadly his research provided an early example of how molecular data could inform ecology, and in 2008 he was awarded the Molecular Ecology Prize that recognized both his scientific and editorial contributions to the field.

Please send a PDF of the paper you are nominating, with a short supporting statement (no more than 250 words; longer submissions will not be accepted) directly to molecol.social@gmail.com by Friday 24 April 2026. The subject line should include "2026 Harry Smith Prize". Self-nominations are encouraged.

"Rieseberg, Loren" <loren.rieseberg@botany.ubc.ca>

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

CallForNominations MolecularEcologyPrize

We are soliciting nominations for the annual Molecular Ecology Prize.

The field of molecular ecology is young and inherently interdisciplinary. As a consequence, research in molecular ecology is not currently represented by a single scientific society, so there is no body that actively promotes the discipline or recognizes its pioneers. The editorial board of the journal Molecular Ecology therefore created the Molecular Ecology Prize in order to fill this void, and recognize significant contributions to this area of research. The prize selection committee is independent of the journal and its editorial board.

The prize will go to an outstanding scientist who has made significant contributions to molecular ecology. These contributions would mostly be scientific, but should also include other kinds of contributions that were crucial to the development of the field. The previous winners are: Godfrey Hewitt, John Avise, Pierre Taberlet, Harry Smith, Terry Burke, Josephine Pemberton, Deborah Charlesworth, Craig Moritz, Laurent Excoffier, Johanna Schmitt, Fred Allendorf, Louis Bernatchez, Nancy Moran, Robin Waples, Scott Edwards, Victoria Sork, Fuwen Wei, Kerstin Johannesson, Uma Ramakrishnan, Mike Whitlock, and Rosemary Gillespie.

Please send your nomination with a short supporting statement (no more than 250 words; longer submissions will not be accepted) and the candidate's CV directly to Clarisse Palma da Silva (cpalma@unicamp.br) by Friday, April 24, 2026. Organized campaigns to submit multiple nominations for the same person are not necessary and can be counterproductive. Also, note that nominations from previous years do not roll over. Thus, previous nominations should be resubmitted with an updated supporting statement and CV.

With thanks on behalf of the Molecular Ecology Prize Selection Committee

"Rieseberg, Loren" <loren.rieseberg@botany.ubc.ca>

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

CETAF E-SCoRe Award

Dear all,

The Consortium of European Taxonomic Facilities (CETAF) < https://cetaf.org/ > initiative, the 7th edition of the *E-SCoRe Award* (Excellence in Scientific Collections-based Research) celebrates the new generation of scientists working with natural history collections to document and understand life on Earth. This annual initiative recognizes innovative research based on natural history collections that addresses global challenges like integrative taxonomy and biodiversity sustainability.

The *CETAF E-SCoRe Award 2026* will be *exclusively dedicated to **early-career researchers **(no **PhD students**). *The deadline has been extended to *1 May 2026*.

The award includes a prize (euro 1,000 cash) and a research trip grant (euro 1,500)

If you or someone in your network works with natural history collections, don't miss this opportunity!

More information and application details: https://cetaf.org/template-activities/cetaf-initiatives/escore/
*Prof. Gila Kahila Bar-Gal, *C.W.F.S. Director of National Natural History Collections

Head of Laboratory of Molecular Evolution, *Koret School of Veterinary Medicine* The Hebrew University of Jerusalem T +972.54.8820273 | W +972. 8.9489888 | F +972.8.9467940 gila.kahila@mail.huji.ac.il

Gila Kahila <gila.kahila@mail.huji.ac.il>

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Education InstitutPasteur

Pasteur Education Connect

Welcome to the Institut Pasteur Education Newsletter! Each month, we'll bring you the latest updates on online and in-person courses, PhD opportunities, trainings, and education news. Stay informed and discover new learning opportunities in life sciences and health.

###**Online learning courses**

Our online courses are in the MOOC format (Massive Open Online Course), offering free and open access to quality education for everyone, anytime, anywhere.

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Clinical Trials in Infectious and Tropical Diseases

Learn how to design and manage ethical clinical trials, including in low-resource settings, and gain practical insights from real-world examples. A valuable resource for those seeking to deepen their expertise in international clinical research.

Enroll now (https://r.ipb.pasteur.fr/mk/cl/f/sh/SMK1E8tHeG13EXcjI4mzn3GsJqkz/TBVgP541eikB)

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You can obtain the Institut Pasteur's Digital Diploma in Infectious Diseases (DNM2IP), if you pass the final exam of 5 Institut Pasteur MOOCs.

More information (https://r.ipb.pasteur.fr/mk/cl/f/sh/SMK1E8tHeGEm8pGdeP5xyhsMGRvV/KDSVrxGGvZt2)

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With **45 courses covering fields from infectious diseases to public health**, it's your chance to boost your expertise and make a global impact.

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Advances in Stem Cell Biology

>From June 22 to July 3, 2026

Registration deadline:—

April 5, 2026

Learn more (https://r.ipb.pasteur.fr/mk/cl/f/sh/SMK1E8tHeGLday5apZFS4XB6EkVl/MAGlV4RI1Odj)

Cryo-ET: Image Processing for—

Electron Microscopy/

Tomography

>From June 8 to June 12, 2026

Registration deadline:—

April 6, 2026

Learn more (https://r.ipb.pasteur.fr/mk/cl/f/sh/SMK1E8tHeGSV36uY0jOwAMTqD361/DogWrdkMqDj)

Cryo-EM: Cryo Electronic Microscopy

>From June 15 to June 26, 2026

Registration deadline:—

April 30, 2026

Learn more (https://r.ipb.pasteur.fr/mk/cl/f/sh/SMK1E8tHeGZMVFjVBtYQGBmaBLgH/wdVZqxnxXOY6)

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Watch testimonials here (https://r.ipb.pasteur.fr/mk/cl/f/sh/SMK1E8tHeGn5PXNPYDrORqO47wqn/UtrVk79CCd-z)

News

** *Matilda: the clip that gives voice back to women in science

Women in science, move forward without limits!*—

On**—International Women's Day,** we are proud to share the new music video by**—Yaëlle Wormser, PhD student of the Université Paris Cité** in microbiology at the Institut Pasteur,**—aka Lady Pipette**.—

In this powerful track, in French available with English subtitles, she highlights **the Matilda Effect**, the persistent invisibilization

— / —

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

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ESEB ECR AchievementAward DeadlineJul01

ESEB Under-represented ECR Achievement Award

Two annual awards of €2,000 will highlight the achievements of under-represented early-career researchers (ECRs) who have faced difficult circumstances while conducting their work. Applicable difficult circumstances may be but are not limited to disabilities, social/cultural/political persecution, refugee status, single parenting or other caring responsibilities that have created unequal opportunities. This year's winners will also be invited to speak at the ESEB Hub Congress in 2027.

DEADLINE: 1 July 2026

Please find all further details about the application and previous winners at https://eseb.org/prizes-funding/-equal-opportunities-initiative/eseb-under-represented-ecr-achievement-award/ – European Society for Evolutionary Biology (ESEB) Email: office@eseb.org Website: https://eseb.org –

ESEB Office <office@eseb.org>

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ESEB EqualOpportunitiesInitiativeFund DeadlineJun1

ESEB EO Initiative Fund - Annual Call for Applications

Next deadline: Monday, June 1st, 2026

The ESEB Equal Opportunities Committee invites proposals for activities that increase awareness of inequalities and improve representation and equal opportunities within evolutionary biology. This call supports initiatives directly related to the field, including activities that benefit researchers, students, or communities engaged with evolutionary biology. Proposals must clearly demonstrate how the activity will improve knowledge, awareness, representation, or equal opportunities within ESEB or the broader evolutionary biology community.

Further information and details on the application procedure are available at the ESEB Equal Opportunities Initiative Fund website: https://eseb.org/-prizes-funding/equal-opportunities-initiative/equal-opportunities-initiative-fund/ European Society for Evolutionary Biology Website: eseb.org ESEB Office - office@eseb.org

ESEB Office <office@eseb.org>

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EvolutionCommunication Survey

Dear colleagues,

Science communication skills are essential for students to respond to complex societal challenges. Undergraduates are uniquely poised to reach both science and non-science audiences, but there has been little progress towards helping students to develop as effective science communicators.

Researchers in a multi-institutional, interdisciplinary collaboration are working to identify and build science communication learning objectives for use in undergraduate biology courses. If you are a biology instructor who has taught a science communication course, or integrated a science communication activity into your biology course, we would like to invite you to complete a brief survey about your course. We are particularly interested in courses that have been taught within the last two years. The survey should take ~15 minutes of your time, and instructors who agree to participate will be entered into a drawing to win one of five $50 prepaid cards.

If you are interested in participating as an instructor in this study, you can access the survey here: https://jmu.co1.qualtrics.com/jfe/form/-SV_eEUpn9w7YOBXURo This study was reviewed by the IRB (protocol FY26-298) and determined to be Exempt. Thank you for your support, and please feel free to reach out if you have any questions!

Best wishes,

Rosario Marroquï¿½n-Flores,Ph.D. (she/her)

Assistant Professor Department of Biology James Madison University

“Maupin, Callie - maupincr” <maupincr@dukes.jmu.edu>

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InsectsJournal EvolPlantDefenseAgainstInsects

Dear Evoldir community,

I hope this email finds you well. Prof. Juan NÃÂºÃÂ±ez-FarfÃÂn and I have the pleasure of serving as Guest Editors for the Special Issue "Evolutionary and Ecological Mechanisms of Plant Defense Against Insects" in the open-access journal Insects. For those working on research about insects and their interactions with plants, we would like to extend a cordial invitation for you to contribute either an original research article or a comprehensive review to this Special Issue.

Further details about the Special Issue can be found below in this link: https://www.mdpi.com/journal/insects/special_issues/OF7LQRA5K9 The submission deadline is 31 October 2026, but accepted papers will be published online on an ongoing basis as soon as they are accepted. Please ensure that your submission is not under consideration elsewhere.

The article processing charge (APC) is CHF 2,600. If you are interested, please email zena.yu@mdpi.com (Zena Yu). Zena will address any inquiries you may have regarding submission and can also assist with any potential discount arrangements.

We sincerely hope you will consider this invitation, and we look forward to the possibility of your contribution.

Best regards,

Dr. Xosé LÃÂ³pez-Goldar and Prof. Juan NÃÂºÃÂ±ez-FarfÃÂn.

Dr. Xosé LÃÂ³pez Goldar (@XGoldar < https://urldefense.com/v3/__https://twitter.com/XGoldar__;!!HXCxUKc!0XDjtF8Abz_PZ2QQJRlxTMDEQT8PjOqN59UxA7fADKs3sbWczuFv9eDxvavQwqguJhPDvLki70htQDa >) Assistant Professor in Evolutionary Ecology 125 S. Fell Avenue, Science Laboratory Building (SLB < https://maps.illinoisstate.edu/locations/science-laboratory/ >) School of Biological Sciences < https://biology.illinoisstate.edu/ > Illinois State University Normal, IL 61761 Email: xlopezg@ilstu.edu Website: https://goldarlab.weebly.com/

LinneSys ProjectFunding DeadlineMar27

Dear all,

This year's edition of the LinneSys is open.

You can apply for up to 1,500GBP for systematics and/or taxonomy projects.

The only requirement is that you are a member of The Systematics Association < https://systass.org/membership/ > or the Linnean Society of London < https://www.linnean.org/our-fellows >.

Applications close 23:59 GMT+1 Friday, March 27th

More details: https://systass.org/linnesys/ On behalf of the Systematics Association Council, Ana Serra Silva Communications Officer for the Systematics Association

Communications SystAss <communications@systass.org>

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LinneSys Scheme DeadlineMar27

Dear all,

Reminder that this year's edition of the LinneSys is open.

You can apply for up to 1,500GBP for systematics and/or taxonomy projects.

The only requirement is that you are a member of The Systematics Association < https://systass.org/membership/ > or the Linnean Society of London < https://www.linnean.org/our-fellows >.

Applications close 23:59 GMT+1 Friday, March 27th

More details: https://systass.org/linnesys/ On behalf of the Systematics Association Council, Ana Serra Silva Communications Officer for the Systematics Association

Communications SystAss <communications@systass.org>

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OmennPrize BestArticleOnEvolutionMediccine

What is the best 2025 article you have read...or written!...in the area of evolution, medicine and public health? Share your nomination now. It only takes a minute and the winner gets the $5000 prize and a trip to the Annual Meeting of International Society for Evolution, Medicine, and Public Health to present a talk. The deadline is March 15, 2026. Details at https://isemph.org/Omenn-Prize A direct link to the nomination form is below. https://airtable.com/appBV61kAMPLS9JU6/pagV3oO6FX9hian6y/form The Omenn Prize is awarded by the International Society for Evolution, Medicine, and Public Health https://isemph.org for the best article published in the previous calendar year on a topic related to evolution in the context of medicine and public health. The first author is invited, expenses paid, to present a plenary talk at the Society's annual meeting. This year's meeting will be July 28-31 in Kiel Germany. Abstracts for the meeting are still welcome.

The winning article is announced in May and the prize is awarded to the first author of the article at the ISEMPH annual meeting. The prize includes travel, lodging, and an invitation to present at talk at the ISEMPH annual meeting. All peer-reviewed articles that use evolutionary principles to advance understanding of a disease or disease process are eligible. The prize committee will give priority to articles with implications for human health, but many basic science or theoretical articles have such implications. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome.

The prize is made possible by a generous donation by Gilbert Omenn, M.D., PhD. Director of the Center for Computational Medicine and Bioinformatics at the University of Michigan where he is a Professor of Internal Medicine, Human Genetics, and Public Health. Dr. Omenn served as Executive Vice President for Medical Affairs as Chief Executive Officer of the University of Michigan Health System from 1997-2002. He is a past president of the American Association for the Advancement of Science and a member of the Institute of Medicine of the National Academy of Sciences.

nesse@umich.edu

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Survey GenAIInEvolutionResearch

Dear colleagues,

We are conducting a brief voluntary survey of the research community to examine how researchers use and perceive Generative AI (GenAI) tools in research practice and request your participation.

The survey takes < 7 minutes to complete and has been approved by the Clemson University Institutional Review board (IRB2026-0127). Results from this study will provide a clearer picture of current practices and attitudes within our community and will be published and shared in aggregate form. Responses are completely anonymous. Researchers in ecology, evolutionary biology, or allied fields that are at least 18 years of age (any career stage) are eligible.

Survey link: https://clemson.ca1.qualtrics.com/jfe/form/SV_0AIiyOikmB1l8G2 Your perspective is valuable regardless of whether you frequently use GenAI tools or have never used them. We would also greatly appreciate it if you could share this widely. If you have any questions, I would be happy to answer them.

Thank you for your consideration!

Casey

– Casey Youngflesh Assistant Professor Department of Biological Sciences Clemson University Clemson, SC 29634 USA He / Him / His www.YoungfleshLab.com Casey Youngflesh <cyoungf@clemson.edu>

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Australia ConservationBiol

Of plastics and plastic responses: the transgenerational nature of microplastic toxicity

We have a postdoc position to work on our recently funded Australian Research Council Discovery Project that will seek to understand the transgenerational implications of microplastic toxicity. This 2-year position will suit an ECR that has a background in behavioural or evolutionary or wildlife ecology and who is passionate about conservation issues that impact Australian fauna. We are encouraging people with demonstrated field and mammal handling experience to apply. Previous experience in microplastic analysis would be ideal. We will be considering applicants that have a proven ability to publish research papers (relative to opportunity); papers that demonstrate strong analytical skills appropriate for independent scientific research.

Interested people should reach out to Renï¿½e (renee.firman@uwa.edu.au) and send through both their CV and a letter stating their interest and relevant experience.

There is also scope for us to support a PhD student, and so we are also asking that any prospective students that are passionate about studying the impacts of microplastics on wildlife (the PhD opportunities have the breadth to be taxonomically broad) to get in touch.

Renee Firman <renee.firman@uwa.edu.au>

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CentralMichiganU Competition Speciation

The Dijkstra lab at Central Michigan University is seeking one or more postdoctoral researchers. Research in the lab focuses on how social competition shapes evolutionary divergence in body coloration and stress resilience in highly social cichlid fishes. We combine behavioral experiments, physiological assays, and genetic/neurobiological approaches.

Postdocs and students in the lab may work on a range of topics related to our NSF-funded research on social learning, aggression biases, and speciation or our NIH-funded work on social history and bioenergetic adaptation in the brain. The project will be shaped in part by the candidate's expertise.

Ideal candidates will have a strong interest in evolutionary biology, behavioral ecology, and integrative organismal biology. Experience with behavioral experiments as well as molecular or neurobiological techniques is desirable. Strong analytical and writing skills are essential.

Application details: https://sites.google.com/site/-peterdijkstrausnl/home Review of applications will begin March 20 and continue until the position is filled. Interested candidates are welcome to email Dr. Peter Dijkstra at dijks1p@cmich.edu.

Peter D Dijkstra

Professor | Department of Biology Neuroscience Program | Institute for Great Lakes Research Central Michigan University 4105 Biosciences Building Mount Pleasant, MI 48859

P: 989-774-2918 | F: 989-774-3462 Lab website: https://sites.google.com/site/peterdijkstrausnl/home Webex room: https://cmich.webex.com/meet/dijks1p "Dijkstra, Peter Douwe" <dijks1p@cmich.edu>

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Dartmouth EvolutionaryBehaviorGenetics

The Behrman Lab (behrman-lab.org) in the Department of Biological Sciences at Dartmouth College invites applications for a postdoctoral researcher with expertise in molecular genetics or neuroscience.

Our research investigates the mechanisms underlying adaptation to environmental variation. We integrate evolutionary genetics, functional genomics, physiology, and organismal biology to understand how genetic and neural variation translate into phenotypic and behavioral differences in natural populations. We are particularly interested in connecting molecular and neural mechanisms to whole-organism function and evolutionary processes.

We seek a highly motivated scientist with strong molecular and/or neurobiological expertise who is excited about addressing evolutionary and physiological questions that span levels of biological organization. The successful candidate will develop an independent research program aligned with the lab's integrative framework while contributing to ongoing collaborative projects.

This position is full-time, non-remote, in-residence at Dartmouth in Hanover, NH, with start date as early as June 1, 2026. The appointment will be for one year with opportunity to renew annually.

Intellectual community: The Behrman Lab is housed in the Department of Biological Sciences and is actively engaged in three interdepartmental programs that connect across the College, the Geisel School of Medicine, and the Thayer School of Engineering: Cell and Molecular Biology, Integrative Neuroscience at Dartmouth and Ecology, Evolution, Environment and Society. Affiliation with these programs provides a vibrant intellectual community, with access to interdisciplinary collaborations, seminar series, reading groups, and annual retreats. Dartmouth also offers extensive shared research infrastructure, including the Molecular Tools and Molecular Interactions Imaging Core, Genomics Core, and the Imaging Facility, providing broad support for molecular, genetic, and imaging-based research.

Postdoc specific resources:

Postdoctoral scholars at Dartmouth benefit from institutional support through the Guarini School of Graduate and Advanced Studies. In addition to campus-wide professional development opportunities including grant writing through GrantGPS and pedagogy through Dartmouth Center for the Advancement of Learning -postdocs have access to programing tailored specifically to their career stage. Postdocs are also supported by the Dartmouth Postdoc Society, which fosters community building, peer mentoring, and professional networking across disciplines.

Dartmouth is committed to academic excellence and encourages the open exchange of ideas within a culture of mutual respect. Dartmouth welcomes people with different backgrounds, life experiences, and perspectives and believes that diversity in all its forms enhances academic excellence.

Application: https://apply.interfolio.com/182614 Questions should be directed to Emily Behrman (Emily@Dartmouth.edu)

Emily L. Behrman (she/her) Assistant Professor Department of Biological Sciences Dartmouth College Hanover, NH 03755 email: Emily@Dartmouth.edu lab website: https://behrman-lab.org/ "Emily L. Behrman" <Emily.L.Behrman@dartmouth.edu>

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FAU UBT Germany EarthSystemsEvolution

Dear colleagues,

We are seeking six postdocs for up to five years each to support research and training in Earth system science in Germany. Two of these projects will focus on aspects of evolution:

- Quantifying climate-driven extinction risk in plants across time and space (Project 2, based at UBT)
- Integrating life and Earth system data through Bayesian phylogenetics (Project 5, based at FAU)

More information about individual subprojects is available here: https://fau-earth-system-science.github.io/-index.html The positions are supported through an initiative that aims to establish a new international Masters of Science in Earth System Dynamics and Evolution. The program will provide training in Earth system science and science diplomacy, with an emphasis on inter- and transdisciplinary research. The project is funded by the Elite Network of Bavaria and is a collaboration between Friedrich-Alexander University of Erlangen-Nuremberg (FAU), where the program is based, and the University of Bayreuth (UBT).

Postdocs in the cohort will undertake independent projects in Earth system science and/or science diplomacy in collaboration with a project leader, while also working together on joint teaching initiatives related to the overarching research theme. Postdocs will be mentored and encouraged to pursue their own research ideas. Applicants are expected to apply for research grants, and should show willingness to conduct independent research and pursue a habilitation. A habilitation is an additional degree that can be obtained in Germany, which recognises excellence in research and teaching - it requires engaging in a range of tasks that are relevant to a career in academic research (e.g., publishing, grant writing, teaching, curriculum development, student supervision).

Application guidelines

Application deadline: 09.04.26.

For your application, please send a single PDF to es-master@fau.de. The subject of the email should refer to the individual project/position you are applying to.

For postdocs, the PDF should comprise:

- Cover letter (indicating which project/position you are applying for, and stating your background and motivation for the project) (max. 1 page)
- CV, including a list of relevant publications (max. 3 pages)
- A short research and teaching concept (max. 2 pages)
- University degree certificates
- Contact details for two potential references

For further information about Project 2 (Climate-driven plant extinctions) contact Prof. Dr. Lisa Hï¿½lsmann and Prof. Dr. Manuel Steinbauer, Bayreuth Centre for Ecology and Environmental Research, UBT, e-mail: lisa.huelsmann@uni-bayreuth.de and manuel.steinbauer@uni-bayreuth.de.

For further information about Project 5 (Phylogenetics and Earth system change) contact Prof. Dr. Rachel Warnock, FAU, e-mail: rachel.warnock@fau.de.

For general enquiries contact es-master@fau.de.

"Warnock, Rachel" <rachel.warnock@fau.de>

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

I2BC France GeneticConflict

Postdoc opportunity : Characterized the role of an heterochromatin protein during Drosophila spermatogenesis.

The EVOGEN team (https://www.i2bc.paris-saclay.fr/-equipe-intragenomic-conflict-and-evolution/) is seeking a highly motivated postdoctoral researcher to participate in a project aimed at elucidating the role of an heterochromatin protein during Drosophila spermatogenesis.

Project

Spermatogenesis is a complex biological process essential for species survival. One intriguing phenomenon that disrupts this process is sex-ratio (SR) meiotic drive, which alters normal inheritance patterns to bias offspring sex ratios. This mechanism, found in various organisms, manipulates sex chromosome segregation during meiosis, yet its molecular basis remains largely unknown. We study an X-linked (XSR) meiotic drive system, known as the Paris sex-ratio (SR) system, in D. simulans. In males carrying the XSR chromosome, we observe non-disjunction of the sister chromatids of the Y chromosome during meiosis II, resulting in defective spermatids that fail to produce functional sperm. Consequently, XSR carrying males produce strongly female-biased progeny (>90%). The drive is associated with a dysfunctional allele of HP1D2. HP1D2 exhibits three notable features: (1) It belongs to the Heterochromatin Protein 1 (HP1) family, involved in heterochromatin regulation; (2) it originated from a duplication of the autosomal HP1D/Rhino gene; (3) HP1D2 is expressed in spermatogonia and binds the Y chromosome. The goal of this project is to characterize the function of HP1D2 during spermatogenesis and understand its contribution to the Paris SR meiotic drive.

Activity

The project comprises three major objectives:

1. Characterize the binding sites of HP1D2 on the Y chromosome. The postdoc will develop a CUT&Tag approach in Drosophila testes.

2. Identify HP1D2 protein partners. In collaboration with Peter Andersen (Aarhus University, Denmark), the postdoc will establish a TurboID proximity-labeling strategy in Drosophila testes.

3. Characterize the phenotypic impact of an HP1D2 knockout. The postdoc will design and generate a HP1D2 knockout line using transgenesis and assess its effects on spermatogenesis.

Candidate profile

- PhD in biology (genetics, genomics, evolutionary biology, or related fields).

- Strong interest in molecular biology, evolutionary genetics, and genome regulation.

- A solid background in biochemistry (e.g., protein-protein interactions) is a strong asset. Experience with Drosophila, bioinformatics, or confocal microscopy is advantageous but not required.

- Ability to work both independently and collaboratively.

- Initiative and capacity to lead a research project.

Work environment:

The Institut de Biologie Intégrative de la Cellule (I2BC) is a joint research unit (CNRS, CEA, and Université Paris-Saclay) located on the CNRS campus of Gif-sur-Yvette. The institute is made up of around sixty research teams divided into five departments, as well as 17 high-level technological platforms. The project will be conducted within the "Intragenomic Conflict and Evolution - EVOGEN" team in the "Genome Biology" department, led by Cécile Courret, recently established at the I2BC institute. This 2-year postdoctoral position is funded through an ATIP- Avenir grant. The project includes collaboration with Peter Andersen (Aarhus University, Denmark), and the postdoc will have opportunities to visit his team.

Compensation and benefits

Salary: €3081-€4653 gross per month (depending on experience)

Annual leave + RTT: 44 days

Starting date: Before the end of 2026. Applications will be considered on a rolling basis until the position is filled.

Want to apply?

Please submit your CV and a motivation letter, detailing your previous research experience and professional goals, and contact information for 2 referees, on this platform:

https://emploi.cnrs.fr/Offres/CDD/UMR9198-CECCOU-001/Default.aspx For more information contact cecile.courret@i2bc.paris-saclay.fr

"cecile.courret@i2bc.paris-saclay.fr"
<cecile.courret@i2bc.paris-saclay.fr>

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IVPP CAS China AncientDNA

Postdoctoral research fellow in the field of ancient DNA

Institute of Vertebrate Paleontology and Paleoanthropology (IVPP) Chinese Academy of Sciences (CAS), Beijing, China

Multiple postdoctoral positions are available in the team of Prof. Qiaomei Fu at the Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences (IVPP-CAS).

About the team Prof. Qiaomei Fu is a paleogeneticist who has been specifically exploring human origins and evolution using ancient DNA and proteins. Over a decade of research, Prof. Fu has contributed significant insights into the history and biology of humans in Eurasia and has made innovative methodological advances in related fields. The Fu Lab team is a well-known, world-class molecular paleontology team with expertise in ancient DNA, ancient microbial genomics, and paleoproteomics. We apply these advanced approaches to explore key questions at the interface of paleontology and evolutionary biology, including population history, adaptation, and speciation. You may find recent work of the team via Google Scholar: https://scholar.google.com/citations?user=mzKctXoAAAAJ&hl=en About the position We are looking for researchers interested in leveraging ancient DNA data to understand the process of evolution in humans and other species. We are particularly interested in two types of candidates: method developers and/or data analysts.

1.Candidates for method development will implement high-performance computing algorithms to develop new models and methods for understanding natural selection in human populations over time and space, using large-scale time-transect ancient DNA data. Candidates should be proficient in scientific computing and interested in applying computational and statistical approaches to evolutionary genetics and genomics; experience in statistical inference is an advantage.

2.Candidates for data analyst positions will be bioinformaticians or evolutionary biologists with strong computational skills and an interest in investigating large-scale ancient DNA or ancient microbial genomics data to perform comparative or population genomic analyses.

Requirement Candidates must hold a PhD (or be in the final stages of their doctoral studies, expecting to obtain the degree within the coming months) in evolutionary biology, population genomics, molecular paleontology, computer science, statistics, or a related field. Applicants are expected to have excellent written and verbal communication skills, as well as a demonstrated record of research productivity (e.g., at least one peer-reviewed publication).

How to Apply For formal applications, interested applicants should contact Prof. Qiaomei Fu (fuqiaomei@ivpp.ac.cn) directly. Please compile the following documents into a single PDF file:

1.A cover letter outlining your interest in the position and how your expertise aligns with the requirements. 2.A complete curriculum vitae (CV). 3.Contact information for three professional references. 4.At least one representative publication.

Review of applications will begin immediately and continue until all positions are filled.

Start date, salary, and benefits The start date will be 1 September 2026 or as soon as possible thereafter. Salary will be commensurate with experience and will follow the relevant regulations for postdoctoral positions at the Chinese Academy of Sciences. The initial appointment term is limited to two years and can be renewed for another two years, subject to continued funding and satisfactory performance. This is a paid, full-time, benefits-eligible position. Although it is not a condition of the position, you are encouraged to seek a fellowship award or your own research funding to help cover your salary and research expenses, as this would be helpful for your career and the lab.

If you have any questions about these positions, please feel free to contact Dr. Yue-Chen Liu (liuyuechen@ivpp.ac.cn) for further inquirie

liuyuechen@ivpp.ac.cn

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JohnInnesCentre UK SymbiosisDevelopment

A three-year postdoctoral position is available to join the newly appointed group of Dr Hassan Salem at the John Innes Centre in the Department of Molecular Microbiology (www.mutualisms.net). Working as part of a team led by Dr Hassan Salem, and in collaboration across the Department of Molecular Microbiology, and the research groups of Dr. Aileen Berasategui (The Sainsbury Laboratory) and Dr. Tatsuya Nobori (The Sainsbury Laboratory) you will investigate the developmental basis of symbiosis in beetles.

This role will include:

* Designing and conducting symbiont- and host-focused transcriptomic and genomic analyses, including tissue- and cell-type-specific approaches targeting symbiotic organs.

* Applying functional genetic tools to manipulate symbiont or host pathways (e.g., RNAi, heterologous expression).

* Reconstructing and testing symbiont-encoded metabolic pathways, linking gene content and expression to host physiology and performance.

* Using confocal microscopy, fluorescence in situ hybridization (FISH), and immunostaining to localize symbionts, host tissues, and gene expression patterns.

* Integrating evolutionary, ecological, and functional data to understand how symbiosis shapes host diet breadth, adaptation, and diversification.

* Disseminating results through high-impact publications, conference presentations, and mentoring of students.

The ideal Candidate: You will have a PhD (or equivalent) in evolutionary genomics, molecular biology, microbiology, entomology, chemical ecology, or a related discipline.

The successful candidate will have:

* Experience with RNA-seq, comparative genomics, or pathway-level analyses, ideally in host-microbe systems.

* Experience with or strong interest in functional genetic manipulation of insects (e.g., RNAi, CRISPR).

* Familiarity with confocal microscopy, FISH, and/or interest in spatial gene expression methods.

* Strong computational skills for biological data analysis (preferably R and/or Python).

* Demonstrated ability to develop independent, hypothesis-driven research at the interface of evolution and mechanism.

* You will also have excellent communication skills, experience mentoring students or visitors, and the ability to work both independently and collaboratively in an interdisciplinary research environment.

Additional information: For further information and details of how to apply can be found here < https://jobs.jic.ac.uk/Details.asp?vacancyID=3D21045 > or contact the Human Resources team on 01603 450814 or nbi.recruitment@nbi.ac.uk quoting reference 1006057.

This role meets the criteria for a visa application, and we encourage all qualified candidates to apply. Where the successful applicant requires a visa, we will fund the costs for their visa and the Immigration Health Surcharge. Please contact the Human Resources Team if you have any questions regarding your application or visa options.

We are an equal opportunities employer, actively supporting inclusivity and diversity. As a Disability Confident organisation, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy. We are proud to hold a prestigious Gold Athena SWAN award in recognition of our inclusive culture, commitment and good practices towards advancing of gender equality. We offer an exciting, stimulating, diverse research environment and actively promote a family friendly workplace. The Institute is also a member of Stonewall's Diversity Champions programme.

The John Innes Centre is a registered charity (No. 223852) grant-aided by the Biotechnology and Biological Sciences Research Council.

About the Salem Group: The Salem Group studies the evolution, function, and adaptive consequences of herbivore-microbe symbioses. Our research focuses on how extracellular bacterial symbionts upgrade host digestive physiology, enable dietary specialization, thereby facilitating herbivory.

By integrating comparative and population genomics, symbiont transcriptomics, functional genetics, microscopy, and biochemical assays, we investigate how streamlined symbiont genomes maintain host-beneficial functions, how symbiont gene expression dynamically matches host nutritional demands, and how digestive symbioses originate and persist over deep evolutionary time. Our work aims to uncover general principles governing the emergence, maintenance, and evolutionary impact of obligate mutualisms.

We seek a postdoctoral researcher to lead mechanistic and multi-omics studies of obligate symbiosis, building directly on our recent work.

For more information, please contact Hassan Salem (Hassan.Salem[at] jic.ac.uk)

Hassan Salem, Ph.D.

Group Leader

John Innes Centre

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

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MichiganStateU DevelopmentalPhenotypicPlasticity

The lab of Fredric Janzen (http://www.kbs.msu.edu/research/labs/janzen/) is recruiting 1-2 Postdoctoral Research Associates to join us at the W. K. Kellogg Biological Station (KBS), Michigan State University (http://www.kbs.msu.edu). The Janzen Lab leverages long-term population monitoring and expertise in theoretical modeling, quantitative genetics, and experimentation to understand the evolution ecology of a classic polyphenism temperature-dependent sex determination (TSD) that occurs in many reptiles. In so doing, we also gain insight into phenotypic plasticity relevant to responses of imperiled taxa to anthropogenic habitat/climate change. We seek 1-2 omics-savvy biologists to work on collaborative projects exploring TSD as a model for developmental phenotypic plasticity.

The successful candidate(s) will work collaboratively with the PI and lab team to develop a research program that integrates omics-level analyses with existing expertise to evaluate the evolutionary dynamics of TSD within and across reptile species with differing patterns of sex-ratio response to developmental temperatures. Available lab resources include long-term data and tissues from a wild pedigreed population of turtles with TSD, as well as comparable resources from geographically distant populations. The research could thus include comparisons among years within populations (including across generations), across populations within species, as well as across taxa, to clarify proximate and ultimate mechanisms underlying observed plasticity in thermal reaction norms in reptiles with TSD.

The post-doctoral mentoring philosophy includes providing (1) opportunities for professional development and mentoring of student scholars, (2) time for independent project development, and (3) resources for outreach and activities that promote diversity, equity, and inclusion in STEM. The successful applicant(s) will be based at KBS, which hosts a vibrant group of resident faculty, post-docs, and graduate students along with multiple modern shared-use facilities, including a Molecular Ecology and Genomics (MEG) Lab, Pond Lab (experimental ponds, mesocosms, etc.), and Boathouse Research Facility (cutting-edge programmable walk-in environmental chambers and incubators). Opportunities for collaboration with MSU campus and other institutions are also available.

A PhD is required by the start of the appointment. Expertise with fieldwork, reptiles, or TSD is not required. More important will be (1) demonstrated scholarly excellence, (2) relevant skills wet lab/molecular biology experience, preparation of high-throughput sequencing libraries, bioinformatics capability related to omics data and (3) a strong desire to advance our conceptual understanding of phenotypic plasticity, including polyphenisms. Salary will be commensurate with experience.

Instructions for applying can be found here: https://careers.msu.edu/jobs/research-associate-fixed-term-hickory-corners-michigan-united-states-6866a4ac-7481-4d38-941f-afa10f3ce354 . Preferred start date by July 2026, although the specific start date is negotiable.

For further information, feel free to reach out to Dr. Janzen (janzenf1@msu.edu).

Fredric Janzen (he/him) Professor, W. K. Kellogg Biological Station Departments of Fisheries and Wildlife & Integrative Biology Ecology, Evolution, and Behavior Program Michigan State University 3700 East Gull Lake Drive Hickory Corners, MI 49060 USA

evoldir@evol.biology.mcmaster.ca

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MontanaStateU ComparativeBoneInnervation

Postdoctoral Researcher

Department of Earth Sciences/College of Letters and Science

The Deep Time Biology Lab (Montana State University, MSU) is looking for a new postdoctoral scientist to join our team. We are interested in candidates with expertise in comparative vertebrate development, neurobiology, bone biology, and macroevolution.

In collaboration with the Rashid Lab (MSU) and the Scheller Lab (Washington University), we seek to better understand the complex relationships between the nervous system and bone. This project provides a unique interdisciplinary environment that combines laboratory analysis with computational biology (phylogenetic comparative methods).

Duties & Responsibilities Include:

* *Tissue Sampling*: Execute the sampling and histological preparation and staining of bone from domestic sheep, domestic chicken, and African clawed frogs to characterize nerve fiber distribution. * *Immunohistochemistry: *Adapt and optimize multiple antibody stains for use on non-traditional model species like avian and amphibian sections. * *Gene Expression:* Conduct gene expression experiments on bone tissue samples * *Manage High-Resolution Imaging:* Perform light and fluorescent imaging across entire transverse bone sections, ensuring proper overlap for high-quality image stitching. * *Phylogenetic Comparative Methods: *Apply comparative data science methods to integrate results across species and differentiate between conserved and adaptive neural and vascular traits.

The position is based at Montana State University in *Bozeman, MT, USA*. Montana State is a research-active institution nestled in the Rocky Mountains, offering a vibrant academic community and unparalleled outdoor recreational opportunities. We maintain a close partnership with the *Museum of the Rockies*, a world-class institution and official repository for state and federal fossils.

For more information, visit the following resources:

* *Deep Time Biology Lab* < https://chrisorgan.github.io/ > * *The Neuroskeletal Biology Laboratory at Washington University* < https://sites.wustl.edu/schellerlab/ > * *MSU Department of Earth Sciences* < https://www.montana.edu/earthsciences/ > * *MSU Department of Microbiology and Cell Biology* < https://www.montana.edu/mbi/ > * *Museum of the Rockies Paleontology Team* < https://museumoftherockies.org/team/paleontology >

For complete job announcement and application procedures, click on:

https://jobs.montana.edu/postings/50520

In compliance with the Montana Veteran's Employment Preference Act, MSU provides preference in employment to veterans, disabled veterans, and certain eligible relatives of veterans. To claim veteran's preference, please complete the veteran's preference information located in the Demographics section of your profile.

Montana State University does not discriminate against any applicant on the basis of race, color, religion, creed, political ideas, sex, sexual orientation, gender identity or expression, age, marital status, national origin, physical or mental disability, or any other protected class status in violation of any applicable law.

Regards, Chris

Chris Organ 319D Leon Johnson Hall Department of Earth Sciences Department of Microbiology & Cell Biology (Affiliate Faculty) Museum of the Rockies (Research Associate) Montana State University, Bozeman, MT, 59717 Deep Time Biology Lab < https://chrisorgan.github.io/ > | organ@montana.edu | 406.994.6920

Chris Organ <organ@montana.edu>

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Montpellier ModellingRespiratoryVirus

Want your computations to matter before the next pandemic hits ? Build the next-generation methods that can shape public-health decisions in the first weeks of an outbreak when the data are heterogeneous in nature and quality, noisy, biased, incomplete... and everything depends on getting it right! We are recruiting a high-potential postdoc to join the PReViX project - Pandemic Prepared- ness for Respiratory Virus X -, a nationally funded flagship program (euro 1.4M) to help France respond optimally to future respiratory virus threats.

Please find more details in the following link:

https://www.normalesup.org/~sofonea/PReViX_Postdoc_JobOffer_2603.pdf Dr Mircea T. Sofonea, University of Montpellier & University Hospital of NÃmes (France)

"Mircea T. SOFONEA" <mircea.sofonea@umontpellier.fr>

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MontpellierU ComparativeGenomics

Postdoctoral Fellow in Genomics and Comparative Genomics

Environnement de travail (Work environment): The successful candidate will join a dynamic research group working on the ecology and evolution of host'parasite'environment interactions in non-model organisms, particularly snail vectors and its trematode parasites. She/He will conduct genomic analyses aimed at understanding host'parasite coevolution and the genetic architecture of resistance in the invasive snail Pseudosuccinea columella to the zoonotic parasite Fasciola hepatica. This thematic line is embedded within the regional scientific project InvaSnail financed by the ExposUM initiative from the Montpellier. The position is based in Montpellier, a vibrant scientific hub in Southern France internationally recognized for excellence in ecology and evolutionary biology. The IHPE laboratory provides a collaborative research environment with access to high-performance computing facilities, sequencing platforms, and strong interdisciplinary interactions across research institutions in the Montpellier area. University

Main mission:

Develop and implement strategies for whole-genome sequencing of non-model species Generate high-quality de novo genome assemblies using short- and long-read sequencing technologies Perform genome annotation and structural/functional characterization Conduct comparative genomic analyses across related species or populations Design and implement genome-wide association studies (GWAS) to identify loci associated with phenotypic or adaptive traits Integrate genomic, phenotypic, and environmental datasets Contribute to the development of reproducible bioinformatics pipelines

Activités (Activities):

Lead the genomic component of the research project High-molecular-weight DNA extraction optimization Long-read genome assembly (PacBio HiFi / ONT) Genome polishing and quality assessment (BUSCO, QUAST) Structural and functional annotation Variant discovery (SNPs, indels, SVs) Population genomic analyses (FST, demographic inference) Mixed-model GWAS accounting for structure Workflow development (Snakemake/Nextflow) HPC-based pipeline implementation Publish results in peer-reviewed journals Present findings at international conferences Collaborate with experimental and computational team members Contribute to project development Mentor graduate students when appropriate

Researcher profile :

The postdoctoral researcher will conduct genome sequencing, high-quality genome assembly, comparative genomics analyses, and genome-wide association studies (GWAS) to identify genomic regions involved in resistance. A PhD in genomics, evolutionary or computational biology, or a related field with strong experience in GWAS are required. Proficiency in scripting (e.g., Python, R, Bash), experience with bioinformatics tools for assembly, variant calling, and comparative analyses, experience handling and processing large-scale genomic datasets are aso required.

Strong publication record relative to career stage, excellent written and oral communication skills in English are a must. Autonomy, strong work ethic and team-playing, strong time-management skills and scientific creativity are expected, as well as the ability to structure and develop research directions

Contract: Starting Date: 1 June 2026; Duration : 2 years-contract (Full-time)

How to Apply: Candidates must send a CV (up to 3 pages), a cover letter containing a clear explanation of why the advertised postdoctoral position aligns with their interests and professional trajectory, an honest assessment of personal strengths and weaknesses, and what they hope to gain from this position and how it will support their long-term development as a scientist, a PDF of a first-author publication (published or in press), and 3 references to annia.alba-menendez@umontpellier.fr before April 20th, 2026

Lien du site internet de la structure (Website Link) : IHPE ≪ Interactions HÃÂtes-Pathogénes-Environnements ≫

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Annia ALBA MENENDEZ, PhD Researcher at CNRS Lab IHPE (UMR 5244), Montpellier University Place Eugéne Bataillon, BÃÂt 24 - CC 080 34095 Montpellier Cedex 5 MONTPELLIER, FRANCE

Annia Alba Menendez <annia.alba-menendez@umontpellier.fr>

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MontpellierU PopGenetics

2-year postdoctoral position in "Population Genomics of Sex Chromosomes in Jaera" with Christelle Fraïsse.

Start date: September 2026 (preferred but negotiable). Applications are welcome from now on until the position is filled.

Location: Institute of Evolutionary Science of Montpellier, Montpellier University (France). https://isem-evolution.fr/en/ ISEM is a research institution focusing on biodiversity origins, dynamics and the associated evolutionary mechanisms and processes. It hosts a total of ca. 250 scientists spread across 4 research departments. Montpellier is a vibrant university city located in the South of France.

Several stays in the Station Biologique of Roscoff, Sorbonne University (France). https://www.sb-roscoff.fr/en It is a marine biology and ecology laboratory with nearly 200 scientists working to study marine organisms and understand the functioning of complex and dynamic marine ecosystems. It is located in Roscoff, a maritime village on the north coast of Brittany in France.

Salary: Monthly net salary is ca. 2,300 euros, according to experience. The contract includes health insurance and 44 days of annual leave.

Context: ANR project "SexIsol" (2023-2028) led by Thomas Broquet. Evolution of sexual isolation in the species complex of Jaera albifrons crustaceans.

This project aims to test hypotheses about two complementary questions using an empirical study of the Jaera albifrons complex. How might sexual isolation have evolved? What exactly is the role of chromosomal rearrangements and sex chromosomes (ZW system), which have been pointed to in the development of sexual isolation?

Project: With that global aim, the post-doctoral candidate will first characterize, at the molecular level, the sex chromosomes across multiple species within the complex, including the degree of differentiation between the Z and W chromosomes, the extent of degeneration, chromosomal rearrangements, and patterns of dosage compensation. It will then reconstruct their evolutionary dynamics across the Jaera albifrons species complex. Next, the role of sex chromosomes as reproductive barriers to introgressive hybridization will be assessed through genome-wide scans and model-based inference. Gene expression data will also be analyzed to quantify sexual dimorphism in expression, interspecific expression divergence, and hybrid misregulation.

Profile: The candidate must hold a doctoral degree and have a strong background in population genetic and evolution. The ideal candidate should be motivated, have good communication skills, and be willing to work independently and collaboratively, integrating effectively into this collaborative project through active engagement with doctoral researchers and bioinformatics engineers.

Prior experience in any of the following areas will be an advantage: i) population genomics (short-reads and long-reads). ii) transcriptomics (short-reads). iii) programming skills (e.g. R, Python, bash, C). iv) experience with high-performance computing (e.g. slurm).

How to apply: i) motivation letter describing research interests, relevant experience and interest in the position (max. two pages). ii) CV, including a list of publications. iii) copies of academic diplomas. iv) names and email addresses of at least two references.

All applications must be sent to Christelle Fraïsse (christelle.fraisse@umontpellier.fr) and Thomas Broquet (thomas.broquet@sb-roscoff.fr) by email.

Christelle Fraisse <christelle.fraisse.rios@gmail.com>

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

QueenMaryU London ThermosensoryEvolution

Postdoc in Thermosensory Evolution Queen Mary University of London, UK

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About the Project:

How do sensory systems adapt to novel thermal environments? The postdoc will lead a research project to investigate the evolution of temperature perception and thermotaxis across Drosophila species. Like many animal taxa, Drosophilids inhabit diverse habitats and can adapt to diverse temperature environments. This project aims to understand how evolutionary changes in sensory neurons and thermoreceptors contribute to these adaptations. This project will use closely related species pairs (D. santomea/D. yakuba and D. takahshii/D. lutescens) in which parallel preferences for cool temperatures have evolved in parallel. The postdoc will develop neurogenic tools in these species and use them to study evolutionary changes in thermoperception and to relate the differences to beahvioural changes.

The position is for 4 years, supported by a Leverhulme Project Grant.

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About You:

Candidates will hold a PhD in neurobiology, genetics, evolution, biology, or a related field. Candidates will need to have experience in at least one of the following: fly genetics, transgenics/CRISPR approaches, neurophysiology, comparative/evolutionary biology.

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About the Lab:

The Arguello Lab (https://arguellolab.org) focuses on understanding the genetic and cellular bases of sensory evolution. What are the rapid changes that underlie differences in the way species perceive the world? Our approach is interdisciplinary and we combine wet and dry lab techniques to bridge evolutionary genomics, neurogenetics, and behavioural biology. The model organisms that we study are Drosophila species that come from diverse ecologies from around the globe.

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About QMUL:

Queen Mary University of London is a research-intensive university and a Russell Group member. The School of Biological and Behavioural Sciences is one of the UK's elite research centres, according to the 2021 Research Excellence Framework. It offers a dynamic multidisciplinary research environment and hosts approximately 180 PhD students working on projects in the biological sciences. Our students and postdocs have access to a variety of research facilities/platforms supported by experienced staff, as well as a range of support services.

Genomics is a particular focus within the School, with specific strengths in evolutionary genomics, population genomics, epigenomics, evo-devo, and functional genomics. The Biology Department hosts its own genomic facility and has recently developed a Research Centre on the theme: The Centre for Evolutionary and Functional Genomics (https://www.seresearch.qmul.ac.uk/cefg/).

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Contact & Application:

Informal inquires can be addressed to Roman Arguello: r.arguello@qmul.ac.uk

To see the full advert details and to apply formally, please go to: https://qmul-jobs.tal.net/vx/mobile-0/appcentre-ext/brand-4/candidate/so/pm/1/pl/3/opp/8717-Postdoctoral-Research-Associate/en-GB Roman Arguello Centre for Evolutionary and Functional Genomics School of Biological and Behavioural Sciences Queen Mary University of London Mile End Road, Fogg Building 6.14a arguellolab.org

Roman Arguello <r.arguello@qmul.ac.uk>

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Rennes France EvolutionFishReproduction

Postdoctoral position: The evolution of reproductive organs across fishes

INRAE - Fish Physiology and Genomics Institute (LPGP), Rennes, France

The group led by Dr. Florent Murat (https://florentmuratwebpage.wordpress.com/) is interested in the evolution of genomes and reproductive organs across vertebrates. Notably, teleost fish represent one of the largest and most diverse clades of vertebrates and exhibit an outstanding reproductive diversity. In this context, we are trying to better understand associated evolutionary patterns and underlying molecular mechanisms. To do so, we make an extensive use of large-scale comparative genomics and bioinformatics as well as single-cell techniques across various fish species.

Our group is hiring a postdoctoral researcher with expertise in bioinformaticsandinterested in evolutionary genomics and reproductive biology. Experienced in single-cell data analyses, the candidate will lead a project on the evolution of reproductive organs across fishes by analyzing gonadal single-cell and spatial transcriptomics datasets of various fish species showing contrasted reproductive features (already generated). The candidate will benefit from the great expertise of team members in bioinformatics, reproductive biology and evolutionary/comparative genomics.

Qualifications and interests: *Analysis of single-cell and spatial transcriptomics datasets *Evolutionary genomics *Molecular/Cell biology *Reproductive biology

Initial appointment will be for one year. The candidate must have spent at least 18 months outside France between May 1, 2021 and May 1, 2025. The candidate will be supported and encouraged to submit applications to prestigious postdoctoral fellowships (Marie Sklodowska-Curie, EMBO, ...) which would represent a strong asset for the next step of their career. The candidate will also be asked to present their results in international conferences.

In our group we attach great importance to a collaborative and friendly atmosphere. Our team is part of INRAE / LPGP (Fish Physiology and Genomics Institute) located in Rennes, a dynamic city in Brittany (France) surrounded by many outstanding sites (Saint-

Malo, Mont Saint-Michel, Normandy, English Channel, Atlantic Ocean, ...).

To apply, please send an email to Florent Murat (florent.murat@inrae.fr) with a full CV, a cover letter and the names and contact information of three references.

Contact: Florent Murat, PhD INRAE - Fish Physiology and Genomics Institute (LPGP) Campus de Beaulieu - Batiment 16A 35042 Rennes, France E-mail: florent.murat@inrae.fr Tel.: +33 (0)223485306

Link to the group website: https://florentmuratwebpage.wordpress.com/ Reference:

Murat, F., Mbengue, N., Boeg Winge, S., Trefzer, T., Leushkin, E., Sepp, M., Cardoso-Moreira, M., Schmidt, J., Schneider, Mï¿½ï¿½inger, K., Brï¿½ning, T., Lamanna, F., Riera Belles, M., Conrad, C., Kondova, I., Bontrop, R., Behr, R., Khaitovich, P., Grï¿½tzner, F., Pï¿½ï¿½bo, S., Marques-Bonet, T., Almstrup, K., Schierup, M.H. & Kaessmann, H. (2023) The molecular evolution of spermatogenesis across mammals. Nature, 613: 308-316.

Florent Murat <florent.murat@inrae.fr>

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RutgersU AlgalSeaWeedOmics

Postdoctoral Associate in algal and seaweed multi-omics and metabolic engineering - Rutgers University, NJ, USA

Apply and more info: https://jobs.rutgers.edu/postings/270143 Review of applications will begin immediately and continue until the position is filled. For additional information regarding the position, please contact Dr. Debashish Bhattacharya, Search Committee Chair, dbhattac@sebs.rutgers.edu

Ideal start by May/June 2026.

Summary: Rutgers, the State University of New Jersey is seeking a Postdoctoral Associate in the Department of Biochemistry & Microbiology within the School of Environmental and Biological Sciences. The Laboratory of Dr. Debashish Bhattacharya has an open Postdoctoral Associate position in the field of algal and seaweed multi-omics and metabolic engineering in support of multiple ongoing projects.

Under the direction of Dr. Bhattacharya the individual will be responsible for the independent conduct of a significant element of a larger research activity in algal and seaweed biotechnology, computational biology, and genetics aimed at developing platforms for generating valuable bioproducts from the brown seaweed Sargassum with a focus on bioprospecting using microbiome data. This Postdoctoral Associate will identify carbohydrate active enzymes to be used for downstream applications by collaborators and design and conduct highly specialized and technical research and aid graduate students with their research programs.

The Bhattacharya Lab at Rutgers University leverages many experimental approaches including multi-omics, physiology, live culture, and computational approaches to ask fundamental questions about algal and seaweed biology, adaptation, and conservation and algal plastid origin and evolution as well as algal extremophile biology. The candidate will have the opportunity to join a highly motivated and broadly trained laboratory that seeks to both generate basic knowledge and develop conservation tools.

Job Duties:

* Performs various research and technical operations independently or as assigned, relating to investigatory activities of a laboratory, followed by appropriate reports, recommendations and conclusions. * Assists and conducts independent research relevant to the interest and field of algal and seaweed multi-omics and biotechnological research with living and preserved samples. * Participates in the development of performance standards, selection of methodology and instrumentation and coordination of the analytical, biochemical, physiology, genetics, and instrumentation functions with the research areas to ensure conformance with the goals and objectives of the PI's lab. * Conducts a continuous program of research and development regarding the analytical and instrumentation functions of the laboratory, constantly evaluating existing procedures where required to keep methodology and procedures current. * Contributes to the supervision of the work performed by graduate and undergraduate students and other postdoctoral fellows.

Requirements: The individual must have completed a PhD in biology, biochemistry, molecular biology, or metabolic engineering with extensive computational research and lab experience.

A background in algal and or seaweed biology and genetics is preferred.

Erin Chille (she/her) Ph.D. Candidate | Bhattacharya Lab < https://bhattacharyalab.com/ > Graduate Program in Ecology and Evolution Rutgers University, New

Brunswick, NJ

email: erin.chille@rutgers.edu

My working hours are 9:00 AM to 6:00 PM Eastern. I do not expect you to read or take action on my emails outside of your normal working hours. Please expect a response from me within 48 business hours.

Erin Chille <eec72@sebs.rutgers.edu>

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Strasbourg France VariableDominanceAndAdaptation

Postdoctoral position in variable dominance and genomics of adaptation

(France)

As an assistant professor at the University of Strasbourg and a member of the HaploTeam (https://www.haploteam.org), I am currently seeking a motivated postdoctoral fellow to join our lab and contribute to research on the role of genetic dominance during adaptation to novel environments. The fellow will be appoited for one year with possible renewal for one more year. The position is funded through ANR (Agence Nationale de la Recherche) and is anticipated to start *1 September 2026* (negotiable).

Genetic dominance determines how mutations are exposed to natural selection and therefore strongly influences evolutionary dynamics. While traditionally treated as a fixed parameter in population genetics models, growing empirical evidence suggests that dominance can vary across genetic backgrounds and environments, with important consequences for adaptation and the maintenance of genetic variation.

To shed light on the role of variable dominance in contributing to the maintenance of adaptive variation, the project will combine empirical and theoretical approaches and leverage genomic and transcriptomic data from natural and experimental populations of Saccharomyces cerevisiae. Depending on the scientific interests of the postdoctoral fellow, she/he will analyse growth phenotypes and RNA sequencing data from controlled crosses, and model the evolution of dominance modifiers using computational tools as well as implement machine learning techniques to infer genomic regions under selection and variable dominance from empirical datasets. The postdoc will also be encouraged to develop independent research directions within the scope of the project.

Required qualifications - PhD (obtained or near completion) in evolutionary biology, population genetics, genomics, bioinformatics, or a related field - Excellent written and spoken English - Ability to work both independently and collaboratively in an interdisciplinary research environment

Preferred (but not mandatory) qualifications - Background in population genetics and/or evolutionary biology - Wet lab experience (depending on the work to be developed) - Prior experience with genomic and/or transcriptomic data analysis - Proficiency in at least one scripting language (e.g. Python, R, or similar)

Environment

The position will be based at the IGBMC, University of Strasbourg, France, within a dynamic and international research environment. The institute offers strong expertise in functional genomics, yeast genetics, and bioinformatics, with access to high-performance computing resources and state-of-the-art experimental facilities. The lab has generated large-scale multi-omic datasets from hundreds of natural S. cerevisiae isolates. This project sits at the interface of evolutionary theory, functional genomics, and quantitative genetics, and includes a collaboration with Prof. Claudia Bank (University of Bern), an expert in epistatic interactions and fitness landscapes. The postdoctoral researcher will have ample opportunities to work closely with both experimentalists and theoreticians.

Applications

Informal inquiries are welcome and can be addressed to Dr. Isabel Alves (itavaresalves@unistra.fr). Applications should include a CV, a brief statement of research interests, and contact information for 2-3 referees. Review of applications will begin in April and continue until June 1, 2026 or until a suitable candidate has been identified.

Isabel Alves Assistant Professor (MCF) Institut de Génétique et de BiologieMoléculaire et Cellulaire (IGBMC) IGBMC- CNRS UMR 7104 - Inserm U1258 1 rue Laurent Fries BP 10142 67404 Illkirch CEDEX France

itavaresalves@unistra.fr

Isabel <itavaresalves@unistra.fr>

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TempleU ComputationalGenomics

The Liberles Group is looking for a new postdoctoral scientist to join us, in the areas of computational/mathematical molecular evolution and comparative genomics. We are particularly interested in students with a joint background in mathematics (particularly probability theory and stochastic processes) and biology (particularly evolution and genetics). Those trained in math should have some formal training in biology and those trained in biology should have demonstrable quantitative expertise. We are also open to students from physics and other quantitative backgrounds who are grounded in biology.

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

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

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

David A Liberles <daliberles@temple.edu>

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UCalifornia LosAngeles DemogModelLandGenomics

UCLA Post-Doc Position in demographic modeling/landscape genomics

Dr. Victoria Sork in the Department of Ecology and Evolutionary Biology at UCLA invites applications for a full-time Postdoctoral Scholar position focused on demographic modeling and landscape genomics to understand climate maladaptation in oak populations under future climate scenarios and develop demographic models to evaluate the ecological consequences of that maladaptation. This position is a two-year appointment, contingent upon satisfactory performance after the first year, with start date between August-October 2026.

Supported by funding from the National Science Foundation, this collaborative project between theUniversity of California, Los Angeles, and the University of California, Santa Barbara integrates functional phenotypes, demographic modeling, and landscape genomics to study climate maladaptation in two California oak species: coast live oak (Quercus agrifolia) and valley oak (Quercus lobata). Working closely with Victoria Sork and a multidisciplinary team that includes ecophysiologist Lee Anderegg and plant ecologist Frank Davis, the postdoctoral scholar will participate in two complementary research aims. First, they will use growth and mortality data from common garden experiments to build demographic models that quantify the population-level impacts of maladaptation. Second, they will use common garden data to link fitness consequences with predictions from landscape genomic models of climate adaptation. The post-doc will also collaborate on other aspects of the project, including an analysis of the genetic basis of climate-associated phenotypes.

The ideal candidate will engage across all phases of the research program, from field sampling and laboratory work to genomic and statistical analyses, as well as manuscript preparation. The position offers opportunities for first-authored publications and co-authorship on collaborative papers. The postdoc will join a dynamic research community, interacting with postdocs and collaborators working on functional genomics, epigenetics, ecophysiology, plant ecology, and climate modeling to advance our understanding of how long-lived tree species respond to climate change.

Qualifications: - Ph.D. in biology, ecology, environmental science, evolutionary biology, geography, or conservation science with expertise in statistics, genomics, demographic modeling, and/or quantitative genetics. - Demonstrated computational and statistical experience relevant to the project. - Good writing skills with demonstrated record of peer-reviewed publications - Ability to work independently and collaboratively

Prospective candidates are encouraged to email Prof Victoria Sork at vlsork@ucla.edu with a paragraph stating reason for interest and a CV.

To apply, please submit application materials to UCLA Recruit position number JPF10896: https://recruit.apo.ucla.edu/JPF10896. Review of applications begins March 30, with final date May 1. 1) Cover letter that includes the following information: (i) short personal statement describing your motivation and relevant experience; (ii) specific computational or statistical skills relevant to research; (iii) contact information for three referees. 2) Curriculum Vita 3) Statement of research that includes specific research interests and conservation genomic expertise 4) Statement summarizing your efforts and interest to mentor and promote interest in the sciences broadly. 5) PDFs of 1-3 publications

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, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: UC Nondiscrimination and Affirmative Action Policy (http://policy.ucop.edu/doc/4000376/NondiscrimAffirmAct)

“Sork, Victoria” <vlsork@ucla.edu>

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UCaliforniaLosAngeles PopulationGenetics

The Goldberg lab at the University of California, Los Angeles is hiring one or more postdocs. Flexible start date. The position is fully funded from NIH and/or discretionary funds.

The Goldberg lab develops methods to study population genetics of humans, our primate relatives, and our pathogens. We integrate techniques from comparative & population genetics, ecology, and archaeology.

Students and postdocs may work on a range of projects in theoretical and empirical population genetics, disease ecology, and human-environment interactions. Much of our work is in humans and other primates, but study system is flexible.

Current projects include: - evolutionary genetics of malaria parasites from wild primates - adaptation and demography of admixed populations - genome-structure evolution in primates from long-read assemblies - the genetic basis of nonhuman primate phenotypes such as folivory and immunity

The lab combines theory and computational data analysis; interest in biological applications of programming, statistics, and/or mathematics is required.

Candidates should contact Amy Goldberg with a CV and brief statement of research interests. Please describe why they are interested in the Goldberg lab and their past research experience.

More information: https://www.goldberglab.org/join
Amy Goldberg <agoldberg701@gmail.com>

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UCanterbury NZ EvolutionOfResistance

Three year postdoc position exploring the evolution of pest and pathogen resistance in the group of Jason Tylianakis (University of Canterbury, New Zealand).

We are looking for an ecologist/entomologist/evolutionary biologist to address fundamental and applied questions on the evolution of resistance to natural enemies. The work will combine laboratory experiments to explore mechanisms (with a Drosophila-parasitoid system) and analyses of large host-parasitoid and plant-pathogen network datasets to scale up to community patterns.

More information about the group and position can be found at https://www.tylianakislab.org/vacancies.html. Applications close 29 March 2026, and must be submitted through the university portal linked on that page. Start date as soon as possible.

jason.tylianakis@canterbury.ac.nz

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UC London GeneticsEvolutionEcol

The Research Department of Genetics, Evolution and Environment, (GEE) at University College London (UCL) is organised into six Centres, with cross-cutting research interests, and close links with other organisations, including the Francis Crick Institute, the Natural History Museum, and The Zoological Society of London. The department has a long and rich history across many biological topics, a summary of which can be found here: https://www.ucl.ac.uk/life-sciences/gee GEE is grouped into six centres that are especially interested in the following research areas:

Institute of Healthy Aging: Ageing, age-related disease; interventions improving late-life health in model systems (e.g. cellular senescence); applying computational approaches to ageing and late-life disease (AI, big data, medical genomics).

Centre for Biodiversity and Environment Research: Evolution in response to environmental change; theoretical ecology/evolution; community or behavioural ecology (especially in plants, insects, fungi or microbes); biodiversity and its contributions to human health and well-being.

Centre for Life's Origins and Evolution: Centre for Life's Origins and Evolution: Origins and diversification of major groups of life; comparative genomics; evolution of cells and cell types; invertebrate palaeontology, plant and fungal evolutionary genomics, experimental evolution.

UCL Centre for Computational Biology: Big data and computation; computational genomics; computational phylogenomics.

UCL Genetics Institute: Computational approaches to biology or medicine; computational tool development and applying them to genomic data; high-throughput bioinformatics, statistical genetics; metagenomics.

UCL East People and Nature Lab: Cross-disciplinary solutions hub bringing together expertise from ecology, computer science, public health, built environment and social science to gather evidence on how we can best manage our natural resources for a sustainable and resilient future.

About the role

GEE invites Expressions of Interest from Early Career Researchers (ECRs) who wish to be sponsored to apply for external fellowships to establish an independent research group. GEE offers a world-class, interactive and supportive research environment within the Division of Biosciences at UCL. We are strongly committed to recruiting and supporting the most promising ECRs who choose to secure a Group Leader Fellowship as their route to becoming a Principal Investigator. This policy applies to senior fellowships such as Wellcome Trust Henry Dale, MRC CDA, BBSRC David Phillips, NERC IRF, Royal Society URF, CRUK, ERC Starting Grants and equivalent fellowships.

The deadline for this round is 30 April 2026

Important Salary is provided by the external award that is secured in future applications to the relevant fellowship schemes. UCL will not provide salary whilst the supported fellows apply for the fellowship schemes.

Applications need to be submitted via this link https://www.ucl.ac.uk/work-at-ucl/search-ucl-jobs/-apply?jobId=Q1KFK026203F3VBQBLO8M8M07-42816&langCode=en_GB About you

We are looking for candidates of the highest calibre, able to demonstrate an exceptional track record in relation to their career stage, and have the potential to submit competitive fellowship applications and secure external funding. Your initial application will be pre-assessed by several members of staff. We will also identify the researcher in GEE closest to your field, who will act as your sponsor and guide you through the selection process.

If selected as a suitable candidate following pre-assessment, you will be invited to deliver a research talk to present your recent work and fellowship plans. This is planned to occur in early June 2026. You will get the chance to meet our staff and students and view our facilities. In addition, you will get the opportunity to meet current GEE fellows, including those who have progressed to permanent positions within the department, and learn about the supportive and stimulating environment we offer. Where a visit is not possible, the discussion will be conducted online. Following a positive outcome of the visit, we will identify a sponsor(s) to support your fellowship application.

Eligibility:

Candidates should confirm their eligibility for specific fellowship schemes and will be required to provide evidence of eligibility to work in the UK before commencing any fellowship offered.

To apply, please ensure to attach the following:

1. Your CV that includes a list of publications (2 pages maximum).

2. A brief (2 pages maximum) document outlining your research proposal that will form your first fellowship application.

3. A list of fellowship schemes you are planning to apply for (the

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UCollegeLondon EvolutionaryGenomics

Postdoctoral Fellow in Evolutionary Genetics

Project: From eggs to live offspring: reconstructing an evolutionary pathway to novelty Location: University College London, UK Contract: 3 year initial contract with funding to extend, 1 year probation; start date flexible Salary: £45,103 - £48,679 depending on experience Closing date: 24-Mar-2026

We are seeking an enthusiastic early career researcher to design, develop, and work with a large population genomic dataset to study the pathway between egg-laying and live-bearing in Littorina snails. The project will be supported by a research technician.

Building on past work (https://www.science.org/doi/10.1126/science.adi2982), the Fellow will (i) use new genealogical methods (ARGs) to identify and (ii) date alleles that underpin the transition in reproductive mode and determine whether they act as primary barriers to gene flow between sympatric egg-laying and live-bearing species.

This position is funded by a Future Leaders Fellowship led by Dr. Sean Stankowski, in collaboration with project partners from the Sanger Institute (Dr. Joana Meier), the Institute of Science and Technology Austria (Dr. Nick Barton), The University of Gothenburg (Dr. Kerstin Johannesson and Dr. Erical Leder) and the University of Göttingen (Dr. Daniel Jackson). Please visit the project website for how this position fits in with the broader goals of this collaborative project.

What we offer - A fully-funded 3 -year position, with funds available to extend the position for several additional years. - The opportunity to collaborate and interact with members of the Littorina research community (https://littorina.at.biopolis.pt/home), and project partners at the Sanger Institute (Joana Meier), Institute of Science and Technology Austria (Nick Barton), University of Gothenburg (Kerstin Johannesson & Erical Leder), among others. - Funding to attend international conferences to build your scientific network - Space and encouragement to develop ideas that go beyond the original proposal - Active mentoring on publishing, grant writing, and career strategy - Opportunities to mentor research students - Support to apply for fellowships and build your independent research programme - Input and involvement in building the philosophy, structure, and core values of a new research group - Access to excellent resources and professional development opportunities - Support for internationally recruited employees with their transition - to work and live in the UK, including VISA and Immigration Health Surcharge costs

Who were hoping to recruit Youll likely be a great fit if you: - Have (or are close to completing) a PhD in evolutionary genomics or a related field - Have a demonstrated track record of communicating and publishing your research - Are comfortable analysing large genomic datasets and have experience working with tree sequences and/or ancestral recombination graphs - Have good coding skills and experience working with a HPC - Enjoy different aspects of being a biologist, not just bioinformatics - Use simulations to generate expectations and check intuition - Like thinking conceptually, not just technically - Have strong communication skills and like working as part of a team - Have the ability to develop and pursue independent research questions - You enjoy research and see it as your preferred career path

The research environment You will be a founding member of the new Speciation Research Group at UCL, one of the UKs leading research-intensive universities (https://www.ucl.ac.uk/research). You will be housed in the Department of Genetics, Evolution and Environment (GEE), which provides an internationally recognised research environment and environmental science, and an established culture of interdisciplinary collaboration.

Commitment to inclusive research We are committed to building an inclusive, supportive research environment and strongly encourage applications from candidates from groups historically under-represented in evolutionary biology.

How to apply Please apply via the UCL jobs website https://www.ucl.ac.uk/work-at-ucl/search-ucl-jobs/details?jobId=42298&jobTitle=Research+Fellow+in+Evolutionary+Genomics Informal enquiries very welcome! Email: s.stankowski@ucl.ac.uk

Sean Stankowski Senior Research Fellow

University College London

Sean Stankowski <s.stankowski@ucl.ac.uk>

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UCopenhagen ConservationGenomics

Postdoctoral position: University of Copenhagen - Conservation Genomics & Experimental Evolution

The Hologenomics Section, Globe Institute, University at Copenhagen, is looking for a dedicated and enthusiastic postdoctoral researcher to join our team. This position is part of the research project "Back from the Brink: experimental de-extinction in a model-organism to restore lost diversity". The project explores the potential of gene editing technologies for conservation using an experimental setting, the risks and consequences for the management of genetically vulnerable populations. Duration: one year.

About the position Gene editing has emerged as a promisingâstill largely unexploredâin some cases a last–resort tool to restore genetic diversity in populations on the brink of extinction. This potential however raises a fundamental question: can targeted genetic interventions help restore resilience in populations pushed beyond their natural adaptive limits, and if so, under what ecological conditions, practical constraints and risks? This project addresses this question empirically. It will experimentally push populations of Caenorhabditis elegans to the brink of extinction, edit genes and restore lost diversity in genetically impoverished populations. The main goal of this project is to benchmark the use of gene editing technologies for conservation. The ultimate aim is to assess whether gene editing can offer a viable complementary tool in conservation strategies.

Your job As a postdoctoral researcher, you'll work at the cutting edge of gene editing technologies, experimental evolution and conservation, maintaining, monitoring and analyzing highly replicated C. elegans populations. Responsibilities include maintaining several wild and lab–adapted strains and conducting bottleneck experiments, identifying and implementing genomic markers for targeted editing, as well as characterizing shifts in population genetic diversity over time. The work involves hands-on laboratory tasks, maintenance of nematode lines, large–scale DNA extractions, and CRISPR-based genome editing combined with data analysis. In addition to producing high–resolution experimental datasets, you'll apply computational and statistical approaches to measure genomic diversity, mutation load and selection using pooled datasets. You will contribute to benchmarking gene editing technologies for conservation. Beyond insights from experimental evolution, your work will advance theory and applied methods that connect gene editing outcomes with population–level evolutionary processes, opening new perspectives on the role of genetic interventions in restoring lost diversity and rebuilding resilience in collapsing populations.

Profile We are looking for a highly motivated scientist with the following competencies and experience: 1. Demonstrated experience in experimental evolution, including the design, execution, and maintenance of replicated populations. Comfortable operating large numbers of parallel experimental replicates 2. Demonstrated expertise in model–organism husbandry, preferably with C. elegans, encompassing sterile workflows, strain maintenance, including accurate population synchronization, ability to identify and troubleshoot unexpected problems, and refine protocols while preserving experimental validity 3. Practical experience with molecular biology workflows, including high–quality DNA extraction, PCR, and genotyping 4. A PhD in evolutionary biology, genetics, molecular biology, conservation genomics, or a related field 5. Strong communication skills and the ability to collaborate effectively in interdisciplinary research teams 6. Excellent written and spoken English

Desirable, but not mandatory skills: 1. Experience with CRISPR/Cas9 genome editing, including guide design, delivery methods, and screening of edited lines 2. Experience applying population genetics principles to real datasets, linking allele–frequency dynamics, selection regimes, drift, mutation, and demographic bottlenecks to understand genomic erosion and recovery potential in declining populations 3. Ability to work confidently on the command line, manage sequencing data, and run standard genomic analysis tools 4. Competence in computational and statistical analyses using R or Python, especially for assessing genetic diversity, mutation load, and evolutionary change through time

Place of employment You will be part of the Hologenomics Section at the Globe Institute. The Hologenomics section investigates how organisms and their associated microbiomes evolve, interact, and respond to environmental change. Our research combines genomics, metagenomics, ecology, and functional analyses to understand biodiversity from a truly integrative perspective. We work across temporal and biological scales, from contemporary ecosystems to

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UCork SalmonGenomicsFeralisation

Going feral: the evolutionary ecology of reverse domestication in an iconic fish species.

We are looking for an ambitious and competent postdoctoral fellow to work on the evolutionary ecology of feralisation and farm-wild interactions in Atlantic salmon (Salmo salar). The position is funded for 2 years as part of the Marine Institute Post-Doctoral Fellowship Programme. The Fellow will join the joint research groups of Dr Tom Reed and Prof. Philip McGinnity at University College Cork and be embedded within a wider team of fish biologists and geneticists. This exciting research project aims to tackle a series of fundamental questions concerning the genomic and epigenetic basis of "reverse domestication" processes, which occur when farmed salmon escape and establish potentially self-sustaining or admixed populations in the wild. The topic is also highly relevant to applied conservation issues pertaining to aquaculture escapes and fisheries management. We are looking for someone with a background in, and passion for, molecular ecology/conservation genetics, with strong bioinformatics/quantitative skills (e.g., the analysis of NGS data). The work will involve the analysis of archival biological material from past experiments and ongoing observational studies in the wild.

The fellow will work at the University of Cork, one of Ireland's largest and most successful universities. The research will be conducted in the School of BEES which consists of 30+ faculty, ca. 20 postdocs and 50 PhD students across Zoology, Ecology, Plant Sciences and Geology. Cork is situated on the south coast of Ireland, 2.5 hours from Dublin, is served by an international airport, has a population of about 200,000, and is on the doorstep of some of the most beautiful coastline in Europe.

Informal enquiries to: treed@ucc.ie

To apply formally for the position: Go to this website: http://ore.ucc.ie/ Search by reference number: 095413

Thomas Reed <treed@ucc.ie>

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UFlorida InsectRNAi

Postdoctoral Associate in RNAi-Based Insect Pest Management

University of Florida, Department of Environmental Engineering Sciences Gainesville, Florida

A postdoctoral associate position is available in the lab of Dr. Elizabeth Cash at the University of Florida. The successful candidate will contribute to a CAMTech < https://www.iucrc-camtech.org/ >-funded project focused on developing RNA interference (RNAi)-based control strategies for pest and invasive ants and cockroaches. The project will combine comparative genomics, molecular biology, and insect bioassays to identify and prioritize RNAi target genes, design and synthesize dsRNA constructs, optimize oral delivery formulations, and evaluate effects on gene expression, survival, and behavior.

Initial funding is available for one year, with the possibility of renewal for a second year based on progress and funding availability. The anticipated starting salary is $58,656, consistent with the current University of Florida minimum for postdoctoral associates; a higher starting salary may be considered in limited cases based on qualifications and available funding. The position may begin as soon as feasible following the hiring process, with a latest possible start date of July 1, 2026.

This position is based in the Department of Environmental Engineering Sciences and offers opportunities for collaboration across the University of Florida, including strong connections with Entomology and Nematology. The project sits at the intersection of insect molecular biology, genomics, chemical ecology, and sustainable pest management and is especially well suited for applicants who enjoy integrating laboratory and bioinformatic approaches. Current focal systems include Argentine ants, carpenter ants, leaf-cutter ants, and German cockroaches, with two focal species to be prioritized based on project needs and industry guidance.

Applicants must have a Ph.D. in biological sciences (e.g., entomology, molecular biology, evolutionary biology, ecology, or a closely related field) by the start date.

Preferred qualifications include:

* Evidence of research productivity * Strong written and oral communication skills * Experience mentoring undergraduate researchers * Experience in one or more relevant areas: * molecular biology, functional genetics, genomics, transcriptomics, bioinformatics, insect husbandry, behavioral assays, and quantitative data analysis.

For full details and application instructions, please see the University of Florida job posting at: https://explore.jobs.ufl.edu/en-us/job/539093/postdoctoral-associate-in-rnaibased-insect-pest-management Review of applications will begin on April 6, 2026 and will continue until the position is filled.

Questions may be directed to Dr. Elizabeth Cash at e.cash@ufl.edu.

Additional information about Dr. Cash's research program is available at https://www.elizabethcash.com/.

Elizabeth Cash, Ph.D. Research Assistant Scientist Engineering School of Sustainable Infrastructure & Environment University of Florida 265F Weil Hall Gainesville, FL 32611

"Cash, Elizabeth I." <elizabeth.cash@essie.ufl.edu>

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UGottingen EvolutionOfBiomineralStructures

The group of Professor Daniel J. Jackson in the Department of Geobiology at the University of Göttingen (Germany) is offering the following position:

Full time Post-doctoral position (100% TV-L 13)

The application deadline is 6 April, 2026.

The position is a fixed term position available for 3 years (starting June 2026).

The molecular mechanisms by which metazoans construct biomineralised structures are of great interest to a variety of scientific disciplines (evolution, materials science, cellular biology, development), however little is known about the details of these processes. A postdoctoral position is available within the research group of Professor Daniel J. Jackson to identify and characterise the molecular mechanisms that fabricate these structures, pigment and pattern them. We primarily use the molluscan model system Lymnaea stagnalis to investigate the process of shell formation, and are actively developing methods to better understand the functional genetics and evolution of this process.

This position requires an individual with strong molecular biology skills and familiarity with the analysis of large computational datasets such as transcriptomes and whole genomes. Lab skills (such as RNA extraction, cloning and in situ hybridization) and bioinformatic skills (for example the ability to write Perl, Python, R and shell scripts, to install and use command line programs and use high performance computing clusters) are highly desirable. Familiarity with maintaining (and repairing) aquarium systems and working with live aquatic animals is also highly desirable. Familiarity with the maintenance and operation of liquid handling robots would be an advantage.

The applicant will also have the opportunity to teach undergraduate and Masters level courses within the framework of a degree in “Ecosystem Management”. A teaching portfolio that can be adapted to this theme would be advantageous. Ideally, the individual will have experience with teaching the application of molecular and bioinformatic tools to the characterisation and management of natural populations. The supervision of Bachelor, Masters and PhD students is also expected.

Candidates should hold a doctorate in evolution, cell biology, developmental biology, molecular biology, or a related field. In addition to their academic qualifications, candidates should have excellent communication, record keeping, organisational and team-working skills, be committed to the topic and to working in a dedicated, interdisciplinary research environment.

The working language of the group is English, and applicants from abroad are encouraged to apply. For international applicants a willingness to learn German should be demonstrated.

All applications should be made in English, and must include the following 3 items (incomplete applications will not be considered):

1. A full academic CV including any published or unpublished academic work.

2. A 1-2 page letter outlining the candidate’s research interests and motivation for applying to this position.

3. Letters of reference and the contact details of 2-3 referees (ideally previous supervisors).

Applications must be made via the University job portal at:

https://obp.uni-goettingen.de/en-us/OBF/Index/-76291 For more information about the Jackson group see:

http://www.uni-goettingen.de/en/102705.html “Jackson, Daniel” <djackso@gwdg.de>

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UHawaii BioinformaticsBiocontrolGenomicTools

Please apply directly on the RCUH website to be considered for the position. HCSU POSTDOCTORAL RESEARCH ANALYST (BIOINFORMATICS/BIOCONTROL GENOMIC TOOLS) - ID# 226172.

CLOSING DATE: March 31, 2026, or until filled. Job postings are removed from the RCUH Job Openings site once the recruitment process has ended.

INQUIRIES: Lori Bufil 808-932-7977 (HawaiÊ≫i). Regular, Full-Time, RCUH Non-Civil Service position with the Hawai’i Cooperative Studies Unit (HCSU) at the University of Hawaiâat Hilo (UHH) in collaboration with the United States Geological Survey Pacific Island Ecosystems Research Center (USGS PIERC). Work location is in the USGS PIERC office in HawaiâVolcanoes National Park on the island of Hawaiâ. Continuation of employment is dependent upon program/operational needs, satisfactory work performance, availability of funds, and compliance with applicable Federal/State laws. MONTHLY SALARY RANGE: $5,833 - $6,250/Mon.

DUTIES: Contributes to genomic-based research efforts to advance biocontrol tools for landscape-scale suppression or eradication of invasive species, and analyzes population genomic datasets applicable to conservation of native species in the Pacific Basin. Applies bioinformatics techniques to model population demographics, characterize gene expression datasets (RNA-seq), perform gene annotations, and evaluate genomic features. Assists in the development of datasets to inform biocontrol efforts that might be enacted in the future, including synthetic biology approaches for invasive species or disease control. Coordinates with state, federal, and/or international agencies and researchers to collect additional specimens, and processes tissue samples in the lab (dissection, DNA extraction, next-generation library preparation, sequencing, and analysis). Carefully documents analysis, computational pipelines, and performs data management and database archiving. Reviews relevant literature and works with the research team leads and collaborators. Authors or co-authors scientific manuscripts related to the development of landscape-scale biocontrol tools for invasive species, conservation genomics of native species, and related topics. Assists with preparing all research products for the United States Geological Survey (USGS) policy and quality reviews, such as Fundamental Science Practices (FSP). Edits and formats scientific manuscripts. Produces project summaries and data visualizations to routinely communicate progress to research team members, and prepares reports and project summaries for internal or general distribution at scientific meetings, workshops, and presentations, including outreach products for different audiences.

PRIMARY QUALIFICATIONS: EDUCATION PhD from an accredited college or university in Bioinformatics/Genomics, Ecology, Biology, Zoology, Fisheries/Wildlife, or other related field.

EXPERIENCE One to three (1-3) years of experience working or conducting research in the field of genomics, bioinformatics, and applied statistics or data analysis. Includes experience with study design, scientific writing, and publishing peer-reviewed scientific papers.

KNOWLEDGE Must have proficiency in molecular biology, high-performance computing, and commonly used bioinformatic programs for analysis of high throughput sequencing data. Must have familiarity with population genomics analysis pipelines and ability to perform statistical analysis. ABILITIES & SKILLS Must possess strong bioinformatics, molecular biology, data management, and quantitative analytical skills. Ability to prepare written reports of study results and analyses with good grammar and proficiency. Ability to evaluate and analyze existing techniques and procedures. Demonstrated excelled oral and written communication skills. Ability to work independently to manage, analyze, and interpret written reports and data. High degree of attention to detail, high level of organization, and problem-solving skills. Ability to work effectively as part of a multidisciplinary team. Post Offer/Employment Condition: Must be able to complete the UH Title IX training within 30 days from date of hire, and re-certify annually. Must be able to complete the Workplace Violence Prevention training within 30 days from date of hire, and re-certify annually. Must be able to complete the UH Information Security Awareness Training (ISAT) within two (2) weeks from date of hire, and re-certify every twelve (12) months.

POLICY/REGULATORY REQUIREMENT As a condition of employment, employee will be subject to all applicable RCUH policies, procedures, and trainings and, as applicable, subject to University of Hawaiâ's and/or business entity's policies, procedures, and trainings. Violation of RCUH's, UH's, or business entity's policies and/or procedures or applicable State or Federal laws and/or regulations may lead to disciplinary action (including, but not limited to possible termination of employment,

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UHawaii Manoa StatisticalPhylogenetics

Postdoctoral Researcher in Statistical Phylogenetics and Computational Genomics Pipes Laboratory, Pacific Biosciences Research Center University of Hawai'i at Manoa

The Pipes Laboratory is seeking a Postdoctoral Researcher to drive innovation in analyzing ultra-large evolutionary trees. We are looking for a candidate who sits at the intersection of statistical inference, algorithm design, and evolutionary biology.

The Role This position focuses on developing scalable algorithms and high-performance computing solutions to solve complex phylogenetic placement and inference problems. The researcher will work on environmental and public health surveillance projects (e.g., wastewater surveillance, microbial ecology).

Key Responsibilities

Design and optimize scalable statistical phylogenetic methods (Maximum Likelihood, Bayesian) for massive datasets.

Engineer novel algorithms for phylogenetic placement and ancestral state reconstruction on trees with tens of thousands of tips.

Implement highly efficient, parallelized analysis pipelines (C/C++, HPC) for processing large-scale environmental sequencing data.

Apply rigorous statistical modeling (e.g., substitution models, continuous-time Markov chains) to extract evolutionary insights.

Qualifications

Education: PhD in Computational Biology, Statistics, Computer Science, or a related quantitative field. A

PhD in Biology is accepted if accompanied by a strong thesis in computational phylogenetics or algorithm development.

Experience: 1 to 3 years of experience developing computational algorithms or statistical models for evolutionary analysis.

Skills: Proficiency in C/C++ (preferred) or Rust. Strong theoretical understanding of phylogenetic statistics (likelihood theory, Bayesian MCMC, coalescent theory) and graph algorithms.

Compensation

Monthly Salary: $6,250 to $7,000 USD/month.

Full-time position with benefits.

How to Apply Interested candidates should email Dr. Lenore Pipes (lpipes@hawaii.edu) directly with the following:

-CV / Resume -Cover Letter

Inquiries Dr. Lenore Pipes lpipes@hawaii.edu

lpipes@hawaii.edu

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USDA Arizona FungalCompetition-TranscriptomicsGenomics

An ORISE Postdoctoral Fellowship is available to work in the U.D. Department of Agriculture-Agricultural Research Service's Aflatoxin Biocontrol lab in Tucson, Arizona, USA. Initial appointment is for 1 year and will be extendable.

Research Project: Aflatoxin, a mycotoxin produced by Aspergillus flavus and closely related fungi, contaminates crops and is a threat to food and feed safety. The overall research goal of the lab is to develop, improve, optimize, and disseminate aflatoxin biocontrol technologies to growers. The goal of the current project is to elucidate genetic and genomic traits associated with enhanced displacement of aflatoxigenic fungi by non-aflatoxigenic Aspergillus in soils and on crops that can be used for selection of superior biocontrol strains. Specifically, you will help utilize transcriptomics to identify changes in gene expression during competition between aflatoxigenic A. flavus and non-aflatoxigenic A. tamarii that are associated with different competitive outcomes under a variety of biotic and abiotic conditions. Anticipated outcomes of the project include criteria for selection of fungal genotypes that will be developed into new biocontrol products for mitigation of crop aflatoxin contamination.

Eligibility: Participant should have (or be close to finishing) a Ph.D. which includes genomic or transcriptomic analysis. Knowledge of mycology or plant pathology is helpful but not required. This position is limited to U.S. citizens who have received their Ph.D. within 5 years of starting the position.

Application process: Applications should be made through ORISE's Zintellect platform: https://www.zintellect.com/Opportunity/Details/USDA-ARS-PWA-2026-0138 Kenneth Callicott, Ph. D. Research Molecular Biologist Pest Management and Biocontrol Research Unit U.S. Arid Land Agrictural Research Center

Agricultural Research Service 416 W Congress Ave, Tucson, Arizona 85716 w: (520) 848-4652 c: (520) 301-6887 Ken.callicott@usda.gov

"Callicott, Ken - REE-ARS" <ken.callicott@usda.gov>

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USDA-ARS HiloHawaii InsectSexChromosomeEvolution

The USDA Agricultural Research Service (ARS) Tropical Pest Genetics and Molecular Biology Research Unit (TPGMBRU) is seeking a POSTDOCTORAL RESEARCH ASSOCIATE to be stationed in Hilo, Hawaii for a TWO-YEAR APPOINTMENT

Ph.D. is required. Starting salary is $75,640 per annum plus benefits. Citizenship restrictions apply.

The incumbent will investigate the structure, function, and epigenetic control of genes on the X and Y chromosomes of fruit flies in the insect family Tephritidae which are major agricultural pests of specialty crops. Using full-length transcriptome sequencing and ATAC-Seq, the incumbent will explore chromosome-scale genome assemblies to evaluate changes in gene content on the X and Y chromosomes across taxa. The goal of this project is to better understand sex chromosome evolution in Tephritidae and apply knowledge of sex-specific gene function to pest management.

The incumbent will be responsible for guided experimental design, data analysis, and manuscript preparation. To support the research and training of the postdoctoral research associate, the research unit has expertise in arthropod genomics and houses a multi-million-dollar genomics laboratory highlighted by a suite of high-throughput sequencing platforms (PacBio Revio, Oxford Nanopore Promethion, and Element Aviti) for which the researcher can gain hands on experience with library preparation and sequencing if desired.

Additionally, high-performance compute infrastructure is available, including hardware focused on AI approaches which can be utilized by this project,including training and professional development opportunities in bioinformatics and data science and a large network of scientists and postdoctoral research fellows as your peers.

The ideal candidate for this position will have:

PhD in Biology, Evolution, Genetics, Entomology or related field with degree conferred at the time of hiring Demonstration of excellent written and oral communication Experience with population genomic analysis Comfort with high-throughput sequence data analysis Comfort with BASH, R, and command-line usage on an HPC environments Comfort with Python3, Git, and workflow management Experience in entomological systems

This role is not remote. Projected start date is flexible and contingent on background clearance. Send application materials and references to Dr. Sheina Sim by e-mail (sheina.sim[at]usda.gov).

USDA/ARS is an equal opportunity provider and employer.

Sheina Sim Research Biologist U.S. Pacific Basin Agricultural Research Center

Agricultural Research Service 64 Nowelo Street, Hilo, HI, 96720 p: (808) 932-2175 | c: (808) 896-0561

"Sim, Sheina - REE-ARS" <sheina.sim@usda.gov>

UStockholm Modeling EvoDevo

Postdoctoral Positions in Mathematical Modeling of Development and Evolution - Stockholm University, Sweden

Link & details: https://su.varbi.com/en/what:job/jobID:906238/ *Contact*: lisandro.milocco@zoologi.su.se

What: Two 2-3 year postdoctoral positions in group of Lisandro Milocco (Stockholm University & SciLifeLab, DDLS program). Research focuses on mathematical and computational modeling of developmental and evolutionary dynamics.

Projects include: (1) Data-driven inference of dynamical systems from high-dimensional biological time-series data. (2) Modeling developmental constraints in phenotypic evolution using low- dimensional structure and phylogenetic comparative methods.

The work is computational/mathematical (no lab work).

Who: PhD in quantitative biology, applied mathematics, physics, computational science, statistics, or related field, with strong quantitative training and interest in evolution and development.

Where: Stockholm, Sweden

Keywords: evolution, evo-devo, prediction, systems biology, developmental biology, dynamical systems, phylogenetics, dimensionality reduction

Deadline: March 31st, 2026

Informal questions are welcome!

Lisandro Milocco Assistant Professor & DDLS Fellow Department of Zoology, SciLifeLab, Stockholm University Tomtebodavägen 23A, Gamma 7, SE-171 65 Stockholm, Sweden Email: lisandro.milocco@zoologi.su.se Website: https://lisandromilocco.github.io/ Lisandro Milocco <lisandro.milocco@zoologi.su.se>

UTennessee Knoxville EvolutionaryBiomechanics

University of Tennessee Knoxville: Post-Doctoral Research Associate Position in Evolutionary Biomechanics

Applications will be reviewed on a rolling basis beginning April 17 and will continue until the position is filled.

An employment application must be submitted through the UTK HR system for full consideration

https://fa-ewlq-saasfaprod1.fa.ocs.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1/job/7273 . Job Description:

The Evolutionary Mechanics Lab (https://eeb.utk.edu/people/michael-granatosky/) in the Department of Ecology and Evolutionary Biology (EEB) at the University of Tennessee, Knoxville, led by Dr. Michael Granatosky, is seeking a motivated postdoctoral research associate to conduct comparative biomechanical and evolutionary research. The successful candidate will contribute to broad research themes in the lab, including the evolution of locomotor strategies, the neuromuscular and musculoskeletal mechanisms that underlie movement, and the ways animals meet novel biomechanical challenges in both natural and experimental contexts. Current efforts in the lab explore locomotor trade-offs across species, behavioral and mechanical strategies of injury compensation, and the anatomical and functional bases of performance. Additional information about ongoing work can be found on Dr. Granatosky's EEB profile (link above) and ResearchGate page:

https://www.researchgate.net/profile/Michael-Granatosky The preferred start date for this position is August 1, 2026. Funding is available for an initial one year, and the position may be renewed for up to one additional year (maximum of two years total), contingent upon performance and the availability of funding. Extensions beyond two years would require the acquisition of additional external funding. Salary will be competitive and commensurate with experience.

Responsibilities:

The position will involve experimental design, data collection and analysis, manuscript preparation, and participation in the development of external funding proposals. The postdoc will provide mentorship to undergraduate and graduate researchers in the lab and contribute to maintaining a collaborative, productive research environment. Research in the Evolutionary Mechanics Lab combines controlled laboratory experiments with opportunities for data collection at zoos and international field sites, and emphasizes broad training in biomechanics, anatomy, neuromuscular physiology, and comparative approaches.

This position requires full-time, in-person work, with occasional evening or weekend effort during experiments or outreach events. Responsibilities may also require travel to zoos, field sites, or partner institutions for data collection and outreach.

Qualifications:

A PhD in organismal biology, biomechanics, comparative anatomy, evolutionary biology, or a closely related field.

Applicants who are ABD will be considered, provided that all PhD requirements are completed by the start date (e.g., degree in hand by August).

Knowledge of comparative biomechanics, evolutionary biology, and statistical/computational approaches relevant to biomechanical datasets.

Skill in data collection and processing, including the use of high-speed videography, force plates, electromyography, metabolic systems, or morphometric methods.

Ability to design reproducible experiments and analyze complex data using coding environments such as R, Python, or MATLAB.

A strong record of publication demonstrating the ability to bring projects to completion.

Ability to mentor student researchers and contribute to a collaborative laboratory environment.

Ability to contribute to the development of external funding proposals.

Preferred knowledge of advanced biomechanical modeling methods (e.g., musculoskeletalmodeling, multibody dynamics, finite element analysis).

Preferred knowledge of imaging techniques such as CT/Ã, ultrasound, or XROMM.

Preferred skill in working with live animals, especially bats or small vertebrates, and supporting data collection at zoos or field sites.

To Apply:

Please attach the following materials to the online application https://fa-ewlq-saasfaprod1.fa.ocs.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1/job/7273, and subsequently send them to Dr. Michael Granatosky (mgranato@utk.edu):

Curriculum vitae

A statement of research (up to 3 pages, single-spaced, 12-point font, 1-inch margins) that includes:

the candidate's educational background and prior research experience,

current research focus and future research goals,

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UTuebingen GeneticDiversity

Postdoctoral Researcher in Genetic Diversity (m/f/d, E13 TV-L, 100%)

Institute of Evolution and Ecology, University of Tübingen

The Institute of Evolution and Ecology at the University of Tübingen invites applications for a postdoctoral researcher in genetic diversity. The position is available as soon as possible and is limited to two years, with a possible extension depending on funding availability.

The successful candidate will develop and test cross-species metrics of genetic diversity using both empirical and simulated genetic data. These metrics will be applied to a unique large-scale dataset on plant genetic diversity in grasslands and forests. The position is part of the collaborative project "BEGenDiv", conducted with partners at the Universities of Freiburg and Marburg and the Helmholtz Centre for Environmental Research (UFZ) in Halle, within the DFG-funded Biodiversity Exploratories. The postdoc project is jointly supervised by Oliver Bossdorf and Henri Thomassen.

We are looking for a highly motivated researcher with strong analytical skills and a keen interest in genetic biodiversity. Applicants should have a background in population genetics/genomics, molecular ecology, biodiversity informatics, or a related field. Experience with large-scale data analysis is essential. Additional experience in macrogenetics, population genetic simulations, or data synthesis is advantageous.

We offer a supportive and collaborative research environment within an internationally recognized research network. The University of Tübingen is one of Germany's leading universities, and Tübingen is a beautiful university town with a high quality of life. The successful candidate will benefit from close links to the two newly funded Clusters of Excellence GreenRobust and TERRA (incl. the new TERRA Molecular Biodiversity Lab), with additional opportunities for exchange and collaboration in genetic diversity research.

The University of Tübingen is committed to equity and diversity and actively promotes equal opportunities. Applicants with disabilities will be given preference in the case of equal qualification. The university aims to increase the proportion of women in research and teaching and therefore particularly welcomes applications from women.

Please submit your application, including a motivation letter, CV, and contact details of at least two referees, as a single PDF to eve-office@biologie.uni-tuebingen.de.

For informal inquiries about the project or the position, please feel free to contact oliver.bossdorf@uni-tuebingen.de or henri.thomassen@uni-tuebingen.de.

Application deadline: 30 April 2026

– Prof. Dr. Oliver Bossdorf University of Tübingen Plant Evolutionary Ecology oliver.bossdorf@uni-tuebingen.de

GROUP: www.uni-tuebingen.de/plantevoeco HERBARIUM: www.uni-tuebingen.de/herbarium PUBLICATIONS: https://scholar.google.com/citations?user=hAPepaEAAAAJ "Boßdorf, Oliver" <oliver.bossdorf@uni-tuebingen.de>

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UVermont GrassChillingToleranceEvol

POSITION Post-doc in grass chilling tolerance evolution.

DESCRIPTION: The Preston lab in the Department of Plant Biology at the University of Vermont is hiring a postdoctoral scholar to work on a National Science Foundation-funded project investigating convergent origins of chilling tolerance in C4 grasses (see https://www.nsf.gov/awardsearch/showaward?AWD_ID=3D2514613 for details of the award).

The position will primarily involve generation of plant phenotypic and transcriptomic data, bioinformatic and statistical analysis of data in a phylogenetic framework, mentoring of junior researchers, and manuscript preparation. The candidate will be responsible for supporting general laboratory oversight, including but not limited to ordering, equipment maintenance, and lab safety. In addition to appropriate safety training, the candidate will be encouraged to develop side projects and participate in professional development activities as a basis for development of an independent career.

QUALIFICATIONS: Applicants should have a PhD in Evolutionary Biology, Developmental Biology, Genomics/Genetics, or a related field, and preferably experience analyzing large transcriptomic and phenotypic datasets.

APPLICATIONS: To electronically apply, upload a resume and/or CV and cover letter to www.uvmjobs.com under Posting #S5969PO by the 14th of March. The anticipated start date is May 2026 but this is somewhat flexible. The initial appointment is for one year with expected renewal contingent on performance. General questions about this position should be directed to Jill.Preston@uvm.edu.

The University of Vermont 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, protected veteran status, or any other category legally protected by federal and state law.

Jill Preston <Jill.Preston@uvm.edu>

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ZurichU ChemicalPlantDiversity

Postdoctoral research assistant 80%: Chemical Diversity of Amazonian Plants

A Postdoctoral position in the Cámara-Leret groupat the Department of Systematic and Evolutionary Botany, University of Zurich, is available from 1 June 2026. The position is for one year, with the possibility of extension for an additional year following a positive evaluation.

Reporting to Prof Rodrigo Cámara-Leret, the postdoctoral researcher will work within the SNSF Starting Grant project INDIGENOMICS, which investigates the diversity and distribution of plant chemical traits and their relationships with human use. The project aims to document and explain patterns in the chemical diversity of plants used by people, with a particular focus on tropical regions. By integrating metabolomics, biodiversity data, and ethnobotanical information, the project seeks to better understand how plant chemical diversity underpins the benefits that biodiversity provides to societies and how these resources can be conserved and used sustainably.

The Cámara-Leret lab offers a collaborative research environment with high-quality supervision and a vibrant international team. The successful candidate will actively collaborate across disciplines and project partners, including Prof. Lauren Raz (Instituto de Ciencias Naturales, Universidad Nacional de Colombia, Bogotá), Prof. Laurent Bigler (Department of Chemistry, UZH), and Dr. Mathieu Perret and Dr. Fred Stauffer (Conservatoire et Jardin botaniques de Genève), among others.

Responsibilities

The post holder will conduct research and provide technical support in metabolomics, including laboratory analyses, data processing, interpretation, publication, and supervision of team members. Key responsibilities include:

Performing metabolite extractions and LC-MS analyses (positive and negative ionisation) of a large set of 3,000 botanical samples. Managing and processing large LC-MS datasets, including feature detection, annotation, quality control, and multivariate statistical analyses. Interpreting results and contributing to the scientific direction of the project. Contributing to manuscripts for peer-reviewed journals and to presentations and reports. Providing technical support to MSc and PhD students in laboratory procedures and data processing workflows.

Essential selection criteria

Hold a PhD in chemical ecology, biology, chemistry, or a related discipline. Specialist knowledge in untargeted metabolomics. Demonstrated ability to manage own academic research and associated activities Track record of high-quality publications in peer-reviewed journals. Excellent communication skills, including the ability to work effectively within international research teams. Proficient in spoken and written English and Spanish.

About the Department of Systematic and Evolutionary Botany

Our Department of Systematic and Evolutionary Botany houses modern molecular and ecological labs, an herbarium comprising 3,000,000 plant specimens (United

Herbaria of UZH and ETH, the 15thlargest herbarium in the world), and a Botanical Garden with 8,000 species. The mission of the Department is to “increase the knowledge of plant diversity, the processes and patterns of plant evolution, the relationships between plants and other organisms and aspects of plant conservation.”Our collaborators at the Department of Chemistry have state-of-the-art instruments for screening plant metabolomes, computational facilities with databases of natural products, and structure elucidation software. The University of Zurich has a broad research coverage of organismal and molecular biology. The city of Zurich offers excellent quality of life and attractive surroundings for outdoor sports.

Interested applicants should send me an email (rodrigo.camaraleret[at]uzh.ch) by April 1st2026with:

1.Motivation letter (2 pages maximum), summarising your research experience, interests, and plans to link chemical traits to ethnobotany beyond previous research (e.g., any publication at https://rcamaraleret.com/-publications.html)

2. CV (2 pages maximum)

3. e-mail of two academic referees

Please send all documents in a single pdf file.

Dr. Rodrigo Cámara Leret

Assistant Professor in Tropical Plant Diversity and Ethnobotany Department of Systematic and Evolutionary Botany | University of Zürich Zollikerstrasse 107 | 8008 Zürich | Switzerland http://rcamaraleret.com Rodrigo Camara Leret <rodrigo.camaraleret@uzh.ch>

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Cambridge UK ScalableGenomicsAndPangenomics Oct11-16

Dear colleagues,

It's our pleasure to invite you to Scalable Genomics and Pangenomics workshop hosted by Wellcome Connecting Science.

Where: Wellcome Genome Campus, Hinxton, Cambridge, UK When: 11. - 16. of October 2026 Confirmed teachers: Kathrine Janike, Kamil S. Jaron, Vikram Shivkumar, Richard Durbin & Antoine Limasset with a guest lecture by Gene Myers

Large-scale sequencing projects now investigate variation across populations and species, often involving hundreds or thousands of genomes. This expansion creates new opportunities to study structural variation, gene content diversity, and evolutionary processes, while demanding analytical approaches that remain efficient and robust at scale.

In this course you will learn:

k-mers as a foundation for genome analysis and comparison

Genome profiling and reference-free quality assessment

Limitations of linear references and introduction to pangenome concepts

Representing genomic diversity using graph-based and comparative frameworks

Strategies for comparing multiple genomes efficiently at scale

Considerations for computational performance, indexing, and workflow design

Applications and more details: https://coursesandconferences.wellcomeconnectingscience.org/event/scalable-genomics-and-pangenomics-20261011/ Application deadline: 22 June 2026

On behalf of the organising committee, Kamil S. Jaron

The Wellcome Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is Wellcome Sanger Institute, Wellcome Genome Campus, Hinxton, CB10 1SA.

Kamil Jaron <kj11@sanger.ac.uk>

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IntroductionToR May15-Jul31

The Computational Biology Core at the University of Connecticut is hosting in-person data science workshops this summer! We still have space available in our Introduction to R Workshop (10 weeks, in person - May 15-July 31).

This hands-on workshop will introduce participants to the core principles of R for data analysis and visualization. You'll learn how to import and organize data, work with common data structures, wrangle and tidy datasets using the tidyverse, build functions and pipelines, create effective visualizations, and run basic statistical analyses using real datasets and widely used R packages.

No prior programming experience is required. We will start with the basics and build skills week by week.

Learn more & register here: https://bioinformatics.uconn.edu/cbc-workshops/ WHERE: UConn Storrs Campus (room TBD) WHEN: Fridays, 1:00-2:00 PM EST COST: $500 (UConn affiliates) / $600 (External participants)

Registration is first come, first served.

Questions? E-mail: cbcsupport@helpspotmail.com

"Lambert, Karelyn" <zsc25001@uconn.edu>

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Oeiras Portugal EMBO-CellularEvol Jun2-5

10 days left to submit abstracts (deadline: March 19)

EMBO Workshop: The rules of the game: biophysical and molecular principles in cellular evolution Oeiras, Portugal | 2-5 June 2026 | Hybrid meeting

Interested in the interface between biological physics, evolution, and cell biology? Consider submitting an abstract.

Many contributed talks will be selected from submitted abstracts, and travel grants are available, particularly for early-career researchers.

More information and application: https://meetings.embo.org/event/26-cellular-evolution

Please feel free to share this announcement with colleagues and trainees who may be interested.

Best,

"The Rules of the Game" Organizers: Marco Fumasoni (Gulbenkian Institute for Molecular Medicine) Andrea Giometto (Cornell University) Liedewij Laan (Delft University of Technology)

Confirmed speakers: Alexandre Bisson, Brandeis University Agathe Chaigne, Utrecht University Andrea Giometto, Cornell University Andrew Murray, Harvard University Arvind Murugan, University of Chicago Aude Bernheim, Institut Pasteur Ines Anna Drinnenberg, Institute Curie Kabir Husain, University College of London Kerry Samerotte, Arizona State University Liedewij Laan, Delft University of Technology Marco Cosentino-Lagomarsino, IFOM ETS - The AIRC Institute of Molecular Oncology Marco Fumasoni, Gulbenkian Institute for Molecular Medicine M?nica Bettencourt-Dias, Gulbenkian Institute for Molecular Medicine Mukund Thattai, National Centre for Biological Sciences Sergey Kryazhimskiy, University of California San Diego

Marco Fumasoni <marco.fumasoni@gimm.pt>

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Online AI Coding EvolutionaryGenomics

Hello EVOLDIR members

Last chance - Explore how autonomous AI agents can revolutionize your research by streamlining complex analytical tasks. Agentic Data Analytics: Automating Research Workflows is a 2-day seminar livestreaming March 24 and 27 with Peter Gruber (Faculty of Economics, USI Universitï¿½ della Svizzera Italiana). This seminar introduces Agentic AI, a powerful approach for automating complex scientific workflows, which can be invaluable for researchers handling large evolutionary or genetic datasets. Participants will learn to apply these methods to automate tedious tasks such as data cleaning, statistical analysis in R/Python, and generating publication-ready visualizations or reports relevant to their studies. By using tools like Google Antigravity for local execution, researchers can ensure data privacy for sensitive genetic or population data while building reproducible analytical pipelines.

Sign up today (https://instats.org/seminar/agentic-data-analytics-automating-resear) to secure your spot, and please share this opportunity with colleagues and students who might benefit!

Best wishes

Michael Zyphur Professor and Director Instats | instats.org

mzyphur@instats.org

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

Online BioinformaticsSpringSchool Jun8-12

We are pleased to announce our upcoming Spring School in Bioinformatics (9th edition), which will take place online from 8-12 June.

Course website: (https://www.physalia-courses.org/courses-workshops/course68/)

This five-day course will introduce participants to the fundamentals of Next Generation Sequencing (NGS) data analysis, combining conceptual lectures with extensive hands-on practical sessions. Participants will learn how to assess sequencing quality, assemble and annotate genomes, perform RNA-seq and differential gene expression analyses, and explore phylogenomics using NGS data. While the course will primarily focus on Illumina data, it will also cover the opportunities and requirements of long-read technologies such as Nanopore and PacBio.

Throughout the week, participants will also gain practical experience with the Linux command line, as well as with Docker and software containers, which are widely used in bioinformatics to ensure reproducible analyses.

The course is designed for researchers with a biological background who would like to gain practical experience in handling and analysing genomic and transcriptomic data. By the end of the training, participants will have a solid understanding of the strengths and limitations of NGS approaches and the tools commonly used in modern bioinformatics workflows.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-course68/)

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/)

Online BioinformaticsWithPython Mar-Jul

Dear all,

If you want to strengthen your Python skills, we have three upcoming online courses designed for researchers in bioinformatics and life sciences:

1. Advanced Python for Data Science and Bioinformatics - Online, 23-26 March(https://www.physalia-courses.org/courses-workshops/advanced-python/) Build intermediate to advanced Python skills with hands-on coding exercises, focusing on typical workflows in biology and data science.

2. Genomic Data Visualisation with Python - Online, 22-24 June(https://www.physalia-courses.org/courses-workshops/genomic-data-viz-python/) Learn to create publication-quality visualizations for genomics data, including volcano plots, Manhattan plots, phylogenetic trees, and pangenome graphs.

3. AI-Powered Python for Bioinformatics - Online, 1-2 July(https://www.physalia-courses.org/courses-workshops/ai-powered-python/) Discover practical strategies to integrate AI coding tools (ChatGPT, Copilot) into Python workflows, including writing, debugging, and optimizing scripts for genomics and data analysis.

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

Best regards, Carlo

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Online ComparativeMethodsInR Jun15-19

Dear all,

We are pleased to announce the upcoming online Physalia course “Phylogenetic Comparative Methods in R” (6th edition), taking place from 15-19 June.

Course website: (https://www.physalia-courses.org/-courses-workshops/course44/)

This five-day hands-on course is designed for advanced students, researchers, and professionals interested in applying phylogenetic comparative methods to investigate trait evolution, diversification rates, and historical biogeography. Participants will work with ultrametric (time-calibrated) phylogenies and real datasets, gaining practical experience in generating chronograms, reconstructing trait evolution, and interpreting results in an evolutionary context.

Each day combines lectures with practical tutorials in R, covering topics such as: Generating and manipulating ultrametric trees Bayesian and likelihood approaches for dating and trait evolution Phylogenetic independent contrasts, phylogenetic PCA, and ancestral state reconstruction Modelling diversification, adaptive radiations, and historical biogeography Students will work on instructor-provided datasets and are encouraged to bring their own data for guidance on setting up analyses. The course assumes basic knowledge of molecular evolution and some familiarity with R, though guidance will be provided throughout.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-course44/)

Best regards, Carlo

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Online DeepLearningForComplexDatasets Mar25

Hello EVOLDIR members

We invite you to explore an upcoming seminar that offers advanced methods for analyzing intricate research data. Deep Learning for Complex Datasets with AI 3.0 is a 1-day seminar livestreaming March 25, led by Nikolay Oskolkov (Group Leader (PI) at LIOS). This workshop explores deep learning techniques for analyzing complex biological datasets, offering methods to uncover intricate patterns and hidden structures. Participants will learn to apply convolutional and recurrent neural networks to genomic and time-series data, and integrate multi-omics datasets using tools like R, Python, TensorFlow, and ChatGPT. These skills will enable researchers to develop advanced analytical approaches for their own evolutionary and genetic studies.

Sign up today (https://instats.org/seminar/deep-learning-for-complex-datasets-with-4) to join the livestream, and please pass this along to colleagues and students who may find it useful!

Best wishes

Michael Zyphur Professor and Director Instats | instats.org

mzyphur@instats.org

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Online EvolutionaryMacroecologyR Jun8-12

Dear evoldir members,

Transmitting Science is offering the live online course "Evolutionary Macroecology in R: Exploring Biodiversity Patterns at Large Scales" (2nd edition).

Learn more and register here: https://www.transmittingscience.com/courses/ecology/macroecology-in-r-exploring-biodiversity-patterns-at-large-scales/ This course combines historical components of geographic patterns, phylogeny, and ecology to provide a comprehensive overview of evolutionary macroecology.

The course has a strong practical component in R. Students will learn to manipulate large geographic databases in R, grid-map biodiversity in various forms, conduct analyses of biogeographic regionalization incorporating evolutionary history, and estimate phylogenetic turnover and historical dispersal in geographic space. The practical sessions also cover common metrics in community phylogenetics and diversification, focusing on large geographic scales.

If you have any questions do not hesitate to contact us at courses@transmittingscience.com

Best regards,

Haris

Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com [1]

Links:

[1] http://www.transmittingscience.com "haris.saslis@transmittingscience.com"

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

Online GeneticDataAnalysis Oct2-Nov13

Genetic Data Analysis Course and Workshop: "ConGen-2026" Online

Theme: Applications of next-gen sequencing data in conservation, ecology, & evolution.

*Instructors include Eric Anderson, Ellie Armstrong, Chris Funk, Matthew Desaix, Marty Kardos, Brenna Forester, Will Hemstrom, Gordon Luikart, Angel Rivera-Colon, Rena Schweizer, Arun Sethuraman, Robin Waples, and more TBA (*subject to change).

Course Objective: To provide training in conceptual and practical aspects of data analysis for understanding the population and evolutionary genomics of natural and managed populations. The course covers concepts and methods including the coalescent, Bayesian, and likelihood-based approaches. Emphasis is on next-generation sequence data analysis (RADs, whole genome sequence analyses, etc.) and the interpretation of output from important statistical approaches, pipelines, and software programs with >12 leaders in population genomics. Activities include taking raw reads through to genotype calling (de novo and with reference), genome assembly, and analyses such as estimation of effective size (Ne), inbreeding from runs of homozygosity (RoH), selection detection (landscape genomics), assignment tests, and more. Past course lecture videos by experts on other topics will be available (e.g., gene expression, epigenetics, landscape genetics, etc.).

Who should apply: Advanced undergraduates, M.S. & Ph.D. students, post-docs, faculty, agency researchers, and population biologists who have taken a course in population genetics.

If you have little experience with R or Linux, we bring you up to speed the first few lectures (see below).

Where: Online via Zoom. Lectures are video recorded to allow asynchronous participation (e.g. from overseas).

When: Monday, Wednesday and Friday, 8-10 AM, Oct. 2nd - Nov. 13th (>15 lectures by >10 expert instructors). The full day between lectures gives students time to master the material.

For details on ConGen-2026, see: www.umt.edu/congen/ <and see lecture titles below>

Past course overviews or review publications: Andrews & Luikart 2014: http://onlinelibrary.wiley.com/doi/10.1111/mec.12686/abstract Benestan et al. 2016: http://onlinelibrary.wiley.com/doi/10.1111/mec.13647/full Hendricks et al. 2018: https://onlinelibrary.wiley.com/doi/full/10.1111/eva.12659 Rena Schweizer et al. 2021: https://doi.org/10.1093/jhered/esab019 Schiebelhut, L. 2023: Guidance in conservation genomics. doi.org/10.1111/1755-0998.13893 Hemstrom et al. 2024: Next-generation data filtering... doi: 10.1038/s41576-024-00738-6.

Registration & Costs include all lectures (live and recorded) by at least 12 expert instructors, online Q&A sessions during hands-on exercises with worksheets and dummy datasets, copies of lecture PowerPoint slides, along with ConGen Swag. The course materials (datasets, lectures, etc.) will remain available online for years. $US 890 if payment is before June 30th.

Sponsors: American Genetic Association (AGA), Journal of Heredity, National Aeronautics and Space Administration (NASA), PacBio, NanoPore. [cid:image001.jpg@01DCA80C.B878CA30]

Lecture topics/titles: The role of genomics in conservation - an overview

Pop genomics: Concepts & tools to answer eco-evo questions

The fastq file format and basics of Next-gen sequence data

Basic R & Linux. Introduction to Next-gen sequence data analysis

Probability, Bayesian stats, MCMC, genotype likelihoods

The Coalescent: theory and applications

Raw sequence reads to genotype calls with versus without a reference genome

Filtering (QC) best-practices, effects of F choices on downstream analyses (Hemstrom et al. 2024)

Inbreeding and runs of homozygosity (RoH)

Genome sequencing & assembly: Conceptual and practical aspects

Inferring population structure and conservation units using genetics & omics

Effective population size estimation

Assignment tests for ecology, conservation, and forensics (WGSassign, GeneClass)

Detecting local adaptation (Landscape Genomics)

Phylogeny and phylogenomics

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

Final Discussion: Future research directions, career advice, and publishing a ConGen Review.

Other Lectures (or breakout groups) possible if students request them: Relatedness, kinship, & parentage assignment Gene flow estimation (current and historical via BayesAss and Migrate) Hybridization detection, quantification, and testing for adaptive invasive alleles GWAS Genome wide association testing (or GWAA) Population abundance estimation, e.g., Close-Kin Mark-Recapture (CKMR), non-invasive sampling

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

Online GenomicDataAnalysis Sep24-Nov13

Genomics Data Analysis Course: ConGen 2026

Theme: Applications of genomics in ecology, evolution, and conservation. see: www.umt.edu/congen/ Course Objective: To provide training in conceptual and practical approaches using genomic data to address key research questions. You will learn the coalescent-, Bayesian-, and likelihood-based approaches. We emphasize next-generation sequencing data analysis (RAD-seq, DNA-capture, whole genomes) and the interpretation of output from important statistical approaches, pipelines, and software, taught by 15 + expert instructors. You'll learn R and Linux and take raw reads through to genotype calling, assemble a genome, estimate pop effective sizes (Ne), inbreeding, detect selection (landscape genomics), estimate gene flow & dispersal rates, parentage, & more.

Who should apply: Advanced undergraduates, M.S. and Ph.D. students, post-docs, faculty, and PIs with a basic understanding of population genetics. We teach R and Linux skills the first weeks to ensure your success. Overseas participation is common, strongly encouraged, and facilitated by video-recordings of lectures.

Where: Online (Zoom). Lectures are video-recorded for asynchronous participation (e.g., by overseas participants).

When: Monday, Wednesday & Friday, 8-9:50 AM (Mountain time, USA), Sept 24th - Nov. 13th (20 + lectures)

Instructors: Eric Anderson, Ellie Armstrong, Chris Funk, Marty Kardos, Brenna Forester, Will Hemstrom, Paul Hohenlohe, Gordon Luikart, Rena Schweizer, Arun Sethuraman, Bruce Rannala, Steve Spear, Robin Waples, Schuyler Liphardt, and more...

For more details and to Apply see: www.umt.edu/congen/ <and see lecture titles below>

Registration: costs $890 and includes all lectures and video-recorded Q&A sessions for later viewing, hands-on exercises with worksheets & genomic datasets, PowerPoint slides, recommended readings, and individual advice from instructors on your research.

Course credit: 3 course credits are available through The Univ of Montana (BIOB 595 Pop Gen Data Analysis).

Selected lecture topics: see www.umt.edu/congen/ .The history and role of genomics in population genetic and conservation - a thorough overview! Pop genomics: Concepts and tools to answer eco-evo questions R & Linux basics, FastQ file format for next-generation sequencing data Scripting, data handling, & organizing bioinformatics projects Probability, Bayesian statistics, MCMC, and genotype likelihood calculations The Coalescent: Theory and applications Raw sequence read filtering and genotype calling (with and without a reference genome) Filtering (QC) best practices, and effects of Filtering choices on downstream analyses Inbreeding and runs of homozygosity (RoH) Genome sequencing and assembly: Conceptual and practical aspects *PacBio, and Nanopore representatives will present recent technologies and services Inferring population structure and conservation units Effective population size estimation Assignment tests for quantifying gene flow, dispersal, and forensics testing (WGSassign, GeneClass) Gene flow estimation (BayesAss - a new version) Hybridization quantification (IM models) Detecting local adaptation and adaptive loci (Landscape Genomics) Phylogeny and phylogenomics eDNA Metabarcoding applications (biodiversity monitoring, diet analysis, microbiomes, etc.)

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

*We teach a similar course in Ecuador in Jan. 2028 (with optional trip to the Galapagos Islands, & a cloud forest field station)

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Online GWAS May18-22

Dear all,

We are pleased to announce the upcoming Physalia online course "Introduction to Genome-Wide Association Studies (GWAS)", which will take place 18-22 May.

Course website: (https://www.physalia-courses.org/courses-workshops/course49/)

This five-day course provides a practical introduction to the full GWAS workflow, guiding participants from study design and data preparation to statistical analysis and interpretation of results. Through a combination of lectures, discussions, and hands-on exercises, participants will learn how to perform GWAS analyses and integrate the different steps into a coherent and efficient pipeline.

The course combines conceptual lectures with practical sessions using R and Linux command-line tools. Participants will explore key topics such as linkage disequilibrium, linear and logistic regression models, exploratory data analysis, genotype imputation, statistical power, multiple testing, and the construction of reproducible GWAS pipelines. The final sessions will introduce post-GWAS analyses and alternative approaches.

The course is intended for students, researchers, and professionals with a background in biology or genetics who wish to gain practical experience with GWAS. Prior experience with GWAS is not required.

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

Best regards, Carlo

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Online IntroAnalysisSpatialProteomics Jun1-5

Introduction to Processing and Analysis of Spatial Multiplexed Proteomics Data (SPMP02) https://prstats.org/course/introduction-to-processing-and-analysis-of-spatial-multiplexed-proteomics-data-spmp02/ Dates:1-5 June 2026 Format:Live online, 5 days Ã 5.5 hours per day Fee:450 (standard) Time zone:UK (GMT); all sessions are recorded and made available for 30 days

Why This Course Matters Spatial multiplexed proteomics techniques such as CODEX, CycIF, and MxIF/MACSIMA are revolutionising how we understand tissue microenvironments, cellular interactions, and spatial heterogeneity in biological systems. However, converting raw multiplexed imaging data into actionable biological insight requires expertise in image processing, spatial statistics, phenotyping, and bioinformatics pipelines. SPMP01bridges that gap. Over five intensive days, you will learn both the theoretical foundations and the hands-on computational skills needed to process, analyse, and interpret spatial multiplexed proteomics data. Whether your work lies in basic biology, cancer immunology, neuroscience, or spatial systems biology, this course equips you to handle complex image-based proteomics datasets.

What You’ll Learn Participants will move from foundational concepts to applied workflows across these core topics:

Overview and comparison of spatial multiplexed imaging platforms (CODEX, CycIF, MxIF / MACSIMA)

Image processing workflows: tile stitching, illumination correction, alignment, and region-of-interest generation

Handling multi-resolution image formats (e.g., .tif, .ome.tif, .ome.zarr), and visualization strategies

Single-cell segmentation: algorithms (e.g. Cellpose, Stardist, Mesmer), mask QC, and error diagnostics

Feature extraction and cell phenotyping (marker intensity gating, clustering, annotation)

Spatial neighbourhood and cell-cell interaction analysis: quantifying local and global neighbourhood statistics

Batch processing and scalable workflows (using Nextflow pipelines such as MCMICRO)

Best practices for reproducibility, data storage, workflow modularity, and integration with R/Python pipelines

Through guided coding sessions and worked examples, you will apply these methods to real multiplexed imaging datasets and gain experience interpreting spatial proteomics results.

Format & Support

Each day blends lectures, demonstrations, and hands-on practical work

Participants are encouraged to bring their own data for discussion (time permitting)

All course materials, scripts, and datasets are shared with attendees

Livestream sessions are recorded and made available the same day

Post-course email support is offered for 30 days to assist with implementation and troubleshooting

Who Should Attend This course is aimed at researchers, computational biologists, bioinformaticians, and technical scientists who work with or plan to work with spatial omics and proteomics imaging data. Prior experience with R or Python is advantageous. Basic knowledge of statistics and familiarity with image data (microscopy) will help, but are not strict prerequisites. A comfortable level of computing literacy (e.g. command line use) is expected.

Instructors Dr Victor Perez Meza an expert in fluorescence microscopy, image artefact correction, and multiplexed imaging workflows MSc Miguel Angel Ibarra Arellano specialist in reproducible bioimage analysis, neighbourhood spatial statistics, and spatial omics tools Their combined experience ensures a mix of methodological insight and practical, cutting-edge implementation.

Who Will Benefit (Use Cases) Participants in SPMP01 will be better equipped to:

Process and clean raw multiplexed imaging datasets

Segment individual cells reliably and assess segmentation quality

Assign cell phenotypes and derive per-cell morphological or marker statistics

Quantify spatial relationships and neighbourhood structure in tissue

Develop reproducible pipelines for spatial proteomics workflows

Integrate processed spatial data into downstream statistical or machine learning analyses

In fields such as cancer microenvironment analysis, immunology, neuroscience, and developmental biology, these capabilities are invaluable for linking cellular spatial patterns to functional and phenotypic insights.

Registration & Details Spaces are limited to ensure a high-quality interactive experience. Standard registration is 450. Visit the course page for full schedule, registration, and further details: https://prstats.org/course/introduction-to-processing-and-analysis-of-spatial-multiplexed-proteomics-data-spmp02/ Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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

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Online LandscapeGenomics Jul13-17

Dear all,

We are excited to announce the upcoming Physalia Landscape Genomics course, scheduled from 1317 July, designed to introduce the fundamentals and practical applications of this powerful approach to studying genetic variation across space.

Course website: (https://www.physalia-courses.org/courses-workshops/course17)

In this course, we will explore how genetic diversity is shaped by spatial and environmental factors, and attendees will:

learn to obtain and process environmental data from public databases using GIS

explore genetic data acquisition and analyze population structure in R

apply statistical methods for local adaptation, including Sambada, latent factor mixed models (LFMM), and redundancy analysis (RDA)

interpret and validate results, and plan robust landscape genomics experiments (e.g., sampling design) By the end of the course, participants will be equipped to integrate environmental and genomic data to uncover adaptive patterns in natural populations.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/course17)

Best regards, Carlo

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Online MachineLearningForPopGenomics Mar23-26

Dear all,

You can still join The Physalia online course on applying Machine Learning and Deep Learning to Population Genomics and Phylogeography.

Dates: 23-26 March (online)

Course website: (https://www.physalia-courses.org/courses-workshops/deep-learning-in-popgen/)

This 4-day course introduces modern machine learning and deep learning approachesparticularly Convolutional Neural Networks (CNNs)to extract information from genetic data for population genomic and phylogeographic inference. The course combines essential theory with guided practical sessions, using real research case studies.

Participants will learn how to:

Simulate genetic data under competing demographic scenarios

Apply Approximate Bayesian Computation (ABC)

Use machine learning and deep learning methods for evolutionary inference

Detect selective sweeps in genomic data using CNNs The course is structured around lectures, interactive discussions, and hands-on exercises, ensuring participants gain both conceptual understanding and practical skills.

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

Best regards, Carlo

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Online MachineLearning RandPython

Learn how to apply modern machine learning methods to ecological time-series data in our live online course Machine Learning for Time Series Using R (METR01).

https://prstats.org/course/machine-learning-for-ecological-time-series-metr01/ This applied R training is designed for scientists who want practical skills for analysing, modelling, and forecasting time-series data using reproducible workflows. Participants will work through hands-on examples to understand how machine learning approaches can be used to detect patterns, make predictions, and interpret complex ecological dynamics. The course covers:

Preparing and structuring time-series data

Supervised and unsupervised machine learning approaches

Model training, validation, and performance assessment

Forecasting trends and dynamics

Interpreting machine learning outputs

The training is delivered via recordings available 30 days before the course and supported by 5 x live Q and A sessions from 13-17 April. You also have access for 30 days after the course to revisit any materials.

Course details Dates: 13’17 April 2026 Duration: 5 days, approximately 7 hours per day Format: Recorded sessions with live Q&A Fee: pounds 450 This course is suitable for postgraduate students, researchers, consultants, and professionals working with ecological monitoring data, population time series, sensor data, or environmental datasets who want to apply machine learning techniques in R.

Full details and registration: https://prstats.org/course/machine-learning-for-ecological-time-series-metr01/ Email oliver@prstats.org with any questions

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Oliver Hooker PhD.

PR stats

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Build practical deep learning skills in Python with our live online course Deep Learning Using

Python(DLUP01). https://prstats.org/course/deep-learning-using-python-dlup01/ This intensive two-day workshop provides a structured introduction to deep learning and its implementation in Python using PyTorch. Participants learn both the theoretical foundations of neural networks and how to build modern deep learning models through hands-on coding exercises. The course covers:

Foundations of artificial neural networks and deep learning

Training networks using backpropagation and optimisation methods

Building multilayer perceptrons in PyTorch Convolutional neural networks for image data

Transformer architectures and minimal GPT-style models

Using pre-trained models with the Hugging Face Transformers library ()

Delivered live online with recordings available, participants receive course materials, datasets, and post-course support.

Course details Dates: 14-15 April 2026 Duration: 2 days, approximately 6 hours per day Format: Live online Fee: 300 This course is suitable for researchers, data scientists, and professionals who are comfortable with Python and want a clear, practical introduction to neural networks, CNNs, and transformer models for real research problems. ()

Full details and registration: https://prstats.org/course/deep-learning-using-python-dlup01/ Email oliver@prstats.org with any questions

–

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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Online MarineGenomics May25-29

Dear all,

We are excited to announce that our Marine Genomics course, originally planned in-person, will now be fully online to foster international participation!

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

Over five days (25-29 May), this course offers hands-on training in:

Genome assembly assessment and variant calling

Population genomics analyses with marine datasets

Integrating genomic and environmental data for seascape genomics

Interpreting results for ecology, conservation, and fisheries The course combines lectures, discussions, and practical exercises using real marine datasets. It is designed for graduate students, postdocs, and researchers working in marine and population genomics.

For the full list of our courses and workshops, please visit: Course website: (https://www.physalia-courses.org/courses-workshops/marine-genomics/)

Best regards, Carlo

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Online MetaAnalysisInR May11-14

Dear all,

It is still possible to join us for the 2nd edition of our course “Meta-Analysis in R”, taking place 11-14 May (online).

This hands-on course provides a complete and practical introduction to evidence synthesis, covering both systematic reviews and meta-analysis. You will learn how to move from question formulation and literature search to effect size calculation, meta-analysis, meta-regression, and result interpretation, with a strong focus on heterogeneity and publication bias.

We keep the group small to ensure interaction and support, and a few seats are still available: (https://www.physalia-courses.org/courses-workshops/metain-r/)

All sessions are highly practical and conducted in R, using widely adopted tools such as metafor and orchaRd. You will work with real datasets and receive fully reproducible workflows and scripts.

The course is designed for researchers in ecology, evolution, and related fields, with a basic understanding of statistics and some familiarity with R.

If you would like to join, feel free to reply to this email or register via our website.

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

Best regards, Carlo

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Online ModelBasedBiogeography Oct12-16

Dear colleagues,

Transmitting Science is offering a new edition of the live online course “Model-Based Statistical Inference in Evolutionary Biogeography”.

Course webpage: https://www.transmittingscience.com/courses/evolution/model-based-statistical-inference-evolutionary-biogeography-2/ This course offers a structured, hands-on introduction to methods for inferring historical biogeography using phylogenetic and spatial data. Participants will learn how to estimate ancestral geographic ranges, compare probabilistic models, and interpret biogeographic patterns using real data.

The course moves from introductory training in R, phylogenies, and BioGeoBEARS, through likelihood-based model testing and visualisation, to advanced topics such as trait-dependent dispersal, state-dependent diversification models, and large-scale analyses using PhyBEARS.jl in Julia. It also incorporates the integration of GIS and paleogeographic data (e.g., via GPlates), equipping participants with a comprehensive toolkit for studying lineages across space and time.

For any questions, please write to courses@transmittingscience.com

Best regards,

Haris

Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com [1]

Links:

[1] http://www.transmittingscience.com Haris Saslis - Transmitting Science <haris.saslis@transmittingscience.com>

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Online MultivariateDataAnalysis May4-7

Dear all,

registration are now open for the online Physalia course on Multivariate Data Analysis with R and vegan, 4-7 May, and gain practical skills to analyse and interpret complex multivariate datasets using R and the vegan package.

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

This hands-on course covers ordination methods (PCA, CCA, RDA, PCoA), PERMANOVA, and permutation-based inference with applications to ecological and high-throughput data such as shotgun sequencing (metabarcoding) and metagenomics.

Participants should be familiar with RStudio and have some fluency in programming R code, including being able to import, manipulate (e.g. modify variables) and visualise data. There will be a mix of lectures, and hands-on practical exercises throughout the course.

Format: fully online, 14:00-20:00 Berlin time, mixing lectures, discussion, and exercises.

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

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>

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Online Palaeogenomics Jun3-9

Dear evoldir members,

Transmitting Science is offering the live online course "Introduction to Palaeogenomics" (6th edition).

Learn more and register here: https://www.transmittingscience.com/courses/genetics-and-genomics/introduction-to-palaeogenomics-concepts-methods-and-applications-of-ancient-dna-data/ This course covers concepts, methods and applications of ancient human and non-human DNA data.

In a combination of interactive lectures and hands-on practical sessions, the course will provide a theoretical overview of molecular biology laboratory techniques for the retrieval of aDNA from ancient samples from different species and an introduction to the bioinformatic pipelines for the analysis of palaeogenomic data.

We will introduce the standard bioinformatic methods often used in palaeogenomic projects for the analysis of aDNA data. We will also consider and discuss the practical problems of ancient DNA recovery, the theoretical problems associated with the interpretation of palaeogenomic data, and the ethical implications embedded in this type of research.

If you have any questions do not hesitate to contact us at courses@transmittingscience.com

Best regards,

Haris

Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com [1]

Links:

[1] http://www.transmittingscience.com

Haris Saslis - Transmitting Science <haris.saslis@transmittingscience.com>

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Online RegressionAnalysis Mar23-25

Hello EVOLDIR members

Last chance - Explore how to effectively use regression analysis, Stata, and AI in your research endeavors. Regression with ChatGPT and Stata 2.0 is a 2-day seminar livestreaming March 23 and 25 with Tor Georg Jakobsen (Norwegian University of Science and Technology). This workshop introduces fundamental regression analysis techniques, including OLS and multivariate models, which are crucial for quantifying relationships between genetic variants, phenotypic traits, or environmental factors in evolutionary studies. Participants will learn to implement these methods using Stata, a widely used statistical software, and leverage ChatGPT to efficiently generate code and interpret complex statistical outputs relevant to their research questions. By mastering these skills, evolutionary biologists and geneticists can enhance their ability to model complex biological systems, test hypotheses about selection pressures, and analyze population dynamics with greater precision.

Sign up today (https://instats.org/seminar/regression-with-chatgpt-and-stata-20) to secure your spot, and please share this opportunity with colleagues and students who might benefit!

Best wishes

Michael Zyphur Professor and Director Instats | instats.org

mzyphur@instats.org

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Online RNA-seq Mar23-25

Hello EVOLDIR members

Last chance - This seminar offers essential skills for processing and analyzing high-throughput sequencing data effectively. RNA-seq: From FASTQ to Counts is a 2-day seminar livestreaming March 23 and 25 with Estefania Mancini (Josep Carreras Leukaemia Research Institute). RNA sequencing provides critical insights into gene expression dynamics, essential for understanding evolutionary processes like adaptation, speciation, and population-level genetic variation. Participants will learn to retrieve public FASTQ data, run community-standard nf-core Nextflow pipelines to generate read count matrices, and interpret quality control reports, which are directly applicable to comparative genomics or identifying genetic markers of environmental adaptation in their own evolutionary research. By mastering these workflows, researchers can ensure their RNA-seq analyses are reproducible and publication-ready, providing a solid foundation for drawing accurate conclusions about gene regulation and its role in evolutionary biology.

Sign up today (https://instats.org/seminar/rna-seq-from-fastq-to-counts) to join before enrollment closes, and please pass this to colleagues and students who may be interested!

Best wishes

Michael Zyphur Professor and Director Instats | instats.org

mzyphur@instats.org

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Online SingleCellRNAseq Mar24-26

The Computational Biology Core at the University of Connecticut is hosting a virtual Single Cell RNA-seq workshop this spring! We still have space available in our Single Cell RNA-seq Workshop (3 days, virtual - Mar. 24-26).

This hands-on workshop will introduce participants to the core principles of single-cell RNA-seq analysis. You'll learn about experimental design considerations for single-cell RNA-seq experiments, converting raw sequencing data into count or expression matrices, dataset quality control, clustering cells (UMAP, t-SNE), identifying cluster-specific markers and annotating cell types, integrating datasets across conditions, and performing trajectory analysis to study cell differentiation.

Participants will gain practical experience working through commonly used tools and approaches in single-cell transcriptomics.

Learn more & register here: https://bioinformatics.uconn.edu/cbc-workshops/ WHERE: Virtual (MS Teams - live sessions, recordings distributed) WHEN: March 24-26, 10:00 AM - 2:00 PM EST COST: See website for registration details

Registration is first come, first served. No prior bioinformatics experience needed!

Questions? E-mail: cbcsupport@helpspotmail.com

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Online SpatialOmicsWithBioconductor May18-20

Dear all,

We are excited to announce our upcoming online course: Spatial Omics in R/Bioconductor, taking place 18-20 May.

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

In this course, attendees will learn to:

Understand spatial omics concepts and differentiate imaging vs. sequencing methods

Explore various spatial omics technologies and practical experimental design

Tackle challenges in spatial data analysis using R/Bioconductor

Apply 'tidy' data principles for efficient analysis

Interpret and extract meaningful insights from spatial omics datasets Course schedule (9.30 AM - 1.30 PM Berlin time, online):

Day 1: Introduction & spatial analyses of sequencing data (SpatialExperiment, Seurat)

Day 2: Tidyomics & spatial analyses of imaging data (tidySpatialExperiment, MoleculeExperiment, Seurat)

Day 3: Advanced spatial analyses (spatial differential expression, cell-neighbour analysis, pixel-based deconvolution, multi-modality integration)

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/spatial-omics-1)

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>

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Paris EVOGEM 2026

We are pleased to announce that applications are now open for the 2nd year of Master program EvoGEM (Evolution of Genomes, Populations, and Species: Data and Models).

This interdisciplinary and inter-institutional master provides a comprehensive foundation in evolutionary genetics, with a strong focus on modelling, mathematics, bioinformatics, and genomics.

EvoGEM is taught by researchers and professors in the Parisian area from Muséum National d’Histoire Naturelle, Paris Sciences & Lettres (ENS/EPHE), Sorbonne Université, Université Paris-Cité, and Université Paris-Saclay, offering a theoretical and methodological training in computational and mathematical modelling approaches to interpret evolutionary mechanisms from genomic data.

Key Features:

- Six specialized teaching units: Evolution, Statistics, Applied Mathematics, Population Genetics, Quantitative Genetics, and Comparative Phylogenetic Analysis - Tutored project in labs during the first semester - Fully taught in English

We invite interested students to apply and encourage you to share this opportunity with potential candidates in your network. For more information and application details, please visit [https://evogem.fr/] . Henrique Teotónio Experimental Evolutionary Genetics Institut de Biologie Ãcole Normale Supérieure 46 Rue d’Ulm 75005 Paris, France https://www.ibens.ens.fr/?rubrique28 Henrique Teotónio <teotonio@bio.ens.psl.eu>

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Paris Tartu Reykjavik SLiMEvolModeling May-Aug

Hi folks!— I’m re-posting about three SLiM workshops this summer, since there are still a few seats available for them.——As background: SLiM is a software package for creating evolutionary models/simulations that are individual-based and genetically explicit. It is scriptable, flexible, fast, free, open-source, and includes an interactive graphical modeling environment.— You can read more about it on its home page (https://messerlab.org/slim/).

The workshops currently scheduled:

- Paris, France, May 18-22, 2026, at the Musee de l’Homme near the Eiffel Tower - Tartu, Estonia, June 15-19, at the University of Tartu - Reykjavik, Iceland, August 17-21, at the University of Iceland

The Paris workshop is full, but I can add you to a waitlist.— The Tartu and Reykjavik workshops still have seats free, so if you want to be sure to get into a workshop, I would advise going for one of those.— They will probably be full soon too, so don’t delay too much.— :->

More details are at: https://groups.google.com/g/slim-announce/c/XpgfrF98M-4 . Cheers, -B.

Benjamin C. Haller Messer Lab Cornell University

PythonTraining ForDataScience

Python Training for Data Science and Machine Learning

Develop practical Python skills for data analysis, machine learning, and modern scientific computing through our series of Python training courses. These courses are designed for researchers, analysts, and professionals who want to apply Python to real-world datasets using widely adopted libraries and workflows.

Live Online Courses

Python for Data Science and Statistical Computing (PYDS01) Learn Python for data science and statistical computing. Build practical skills using NumPy, Pandas, and data visualisation tools across two days of hands-on training. https://prstats.org/course/python-for-data-science-and-statistical-computing-pyds01/ Deep Learning Using Python (DLUP01) An intensive introduction to deep learning using Python and PyTorch. Learn neural networks, convolutional neural networks, and transformer models through practical coding exercises and real datasets. https://prstats.org/course/deep-learning-using-python-dlup01/ Machine Learning for Time Series (MLTP01) Learn how to model, analyse, and forecast time series data using machine learning methods in Python, with practical workflows for real-world datasets. https://prstats.org/course/machine-learning-for-time-series-mltp01/ Advanced Python for Ecologists and Evolutionary Biologists Take your Python skills further by learning object-oriented programming, testing, optimisation, and best practices for building robust scientific and bioinformatics workflows. https://prstats.org/course/advanced-python-for-ecologists-and-evolutionary-biologists/ Recorded Courses

Machine Learning using Python A practical introduction to machine learning using Python, covering supervised and unsupervised learning, neural networks, and applied model building with libraries such as scikit-learn and TensorFlow. https://prstats.org/course/machine-learning-using-python/ Machine Vision using Python Apply deep learning and computer vision techniques using Python, OpenCV, and TensorFlow to classify images and analyse visual datasets, including ecological and environmental applications. https://prstats.org/course/-machine-vision-using-python/ On-Demand Learning

All courses are also available ason-demand recordings, allowing you to learn at your own pace and revisit material whenever needed. Recorded courses are ideal for busy schedules or different time zones, enabling participants to pause, review, and work through examples while retaining full access to course materials.

Emailoliver@prstats.orgwith any questions

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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UConnecticut RNAseq

The Computational Biology Core at the University of Connecticut is hosting a virtual RNA-seq (de novo) workshop this spring! We still have space available in our RNA-seq (de novo) Workshop (3 days, virtual - Mar. 17-19).

This hands-on workshop will introduce participants to the core principles of de novo transcriptome analysis using RNA-seq. You'll learn how to design RNA-seq experiments, process raw sequencing data, assess data quality, assemble transcriptomes de novo, and perform differential expression and functional enrichment analyses using R and the Linux command line.

Participants will gain practical experience working through the workflow using commonly used tools and approaches in transcriptomics.

Learn more & register here: https://-bioinformatics.uconn.edu/cbc-workshops/ WHERE: Virtual (MS Teams - live sessions, recordings distributed) WHEN: March 17-19, 10:00 AM - 2:00 PM EST COST: $500 (UConn affiliates) / $600 (External participants)

Registration is first come, first served.

Questions? E-mail: cbcsupport@helpspotmail.com

"Lambert, Karelyn" <zsc25001@uconn.edu>

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YosemiteNatlPark Symbiosis Apr17-19

The 14th Annual Yosemite Symbiosis Workshop 2026

DEADLINE SOON AND SPOTS REMAINING

An integrative meeting of biologists focusing on symbiosis research April 17-19, 2026 New location: Yosemite Bug Rustic Mountain Resort

Register here:https://snri.ucmerced.edu/form/-symbiosis-workshop-2026 KEYNOTE SPEAKER: John McCutcheon, Arizona State University

Why: Our goal is to better integrate scientists who focus on symbiosis research, including researchers that study animal-microbe and plant-microbe systems, as well as broader topics related to microbiomes, cooperation, and mutualism. This will be our 14th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

Who: The meeting is small and intimate by design (45 participants). We typically cover a range of symbiosis topics from ecology and evolution to molecular mechanisms in different model and non-model systems. We are limiting registration to four people per lab, with priority for graduate students, postdocs, and PIs (undergraduate students are welcome to attend if we have space).

What: The meeting will consist of two half-days of talks and one poster session. Other than the keynote (˜1 hour), talks are 15 minutes long (including time for questions). Posters are flexible for size, but the ideal poster should be no larger than ˜4 feet square. When you apply for the meeting, you will provide your preference for a talk or poster. We usually strike a good balance but were a bit poster heavy in 2025, so talks are encouraged.

When: A welcome party will occur for everyone arriving on the evening of Friday April 17th. The talks and poster sessions will be held Saturday and Sunday April 18-19, 2026.

Where: This is the best part! The meeting takes place at the Yosemite Bug, a comfortable rustic resort located outside the Highway 140 entrance to Yosemite Valley, near the Merced River. The resort has a spa and easy access to hiking trails.

What will it cost? Thanks to generous support from the Moore Foundation, this meeting is free for graduate students and postdocs –! We charge $300 for PIs and other types of participants (e.g. industry/foundation/journalist). PIs must pay a registration fee of $300. The registration deadline is March 15, 2026.

We ask that graduate students and postdocs plan to present their work. Everyone who registers on time gets to present a talk or poster (your choice). What does registration include? Registration includes lodging Friday and Saturday nights, dinner Friday night, all meals on Saturday, and breakfast and lunch on Sunday. Dietary offerings will include meat, vegetarian/vegan/dairy-free, and gluten-free options.

The registration also includes spa tickets! Accommodations are in dorms and heated tent cabins with shared, dorm-like rooms and bunk beds. There are no single rooms. Please don't register unless you are comfortable with the idea of staying in a rustic cabin or sharing a room. For questions about travel or lodging, please feel free to email Carolin Frank (cfrank3@ucmerced.edu).

Thinking of bringing a guest? If you want to bring a guest, we kindly ask that you book their accommodations directly with the Yosemite Bug. For questions about travel or lodging, please feel free to email Carolin Frank (cfrank3@ucmerced.edu). Please fill out the registration form below.

https://snri.ucmerced.edu/form/symbiosis-workshop-2026 If you are a PI, you need to pay the registration fee in order for your registration to be complete. Payment is by credit card only. Cancellations are not allowed, but in the event that we need to cancel the workshop (e.g. due to weather), you will get a refund.

Joel Sachs <joel.sachs@ucr.edu>

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