
E v o l D i r

June 1, 2024

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

Foreword

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

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ASN Asilomar

AcceptingProposalsSymposia Jan3-7

Accepting Proposals for Symposia at The American Society of Naturalists stand-alone meeting in Asilomar 2025 (Due July 15, 2024)

The American Society of Naturalists will be going back to Asilomar in Pacific Grove, California, to hold our stand-alone conference - Asilomar 2025 - on 3-7 January 2025!

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.

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

(michelle.afkhami@miami.edu) no later than midnight Eastern Time on July 15, 2022. Send your proposal as a single pdf attachment, under subject heading "ASN Asilomar 2025 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. Further, we especially encourage early career researchers to propose sessions as organizing symposia can advance their careers through building broader scientific networks and a record of scientific leadership.

Additionally, 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 August 2025. In cases of financial hardship, requests for assistance to allow participation in symposia can be made to the American Society of Naturalists and will be evaluated on a case-by-case basis.

Michelle Afkhami ASN Symposium Committee Chair Department of Biology University of Miami michelle.afkhami@miami.edu

Michelle E. Afkhami, Ph.D.

*Associate Professor & *UM Greenhouse Director* University of Miami Department of Biology Coral Gables, FL *michelleafkhami.wordpress.com* she/her/hers

Michelle Afkhami <michelle.afkhami@gmail.com>

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Bristol GenomeScience Jul16-18

We have extended Early Bird registration to Genome Science UK 2024, Bristol. Early Bird registration will now close on 24th May. Anyone who registered at full price over the weekend will be refunded the difference between Early Bird and Full rates.

The Abstract Submission deadline is also approaching on the 24th May.

Register now at <https://bristol.genomescience.org.uk/register/> —

Join us at Genome Science UK 2024, the ever-popular gathering for genomics researchers, clinicians, and industry leaders in the UK. Taking place in the vibrant city of Bristol, July 16th-18th, this three-day conference offers a unique opportunity to hear from world-renowned leaders in the field such as Professor Deborah Williamson (UKHSA), Prof Richard Durbin (University of Cambridge), Dr Lucy Burkitt-Grey (UK Biobank) and Prof Matt Brown (Chief Scientific Officer, Genomics England).

The conference covers the latest advancements across various priority areas, including Evolving Technologies, Human & Clinical Genomics, Evolutionary Genomics, Plant and Animal Genomics, Microbes and Microbiomes, Epigenetics, Bioinformatics & Machine Learning in Genomics, Spatial and Single-Cell Genomics, and Genome Engineering. Discover the latest technologies and solutions shaping the future of genomics at our dedicated exhibitor booths.

Genome Science UK 2024 promises to be an unforgettable event. Register now at <https://bristol.genomescience.org.uk/register/>. Limited early-bird registration discounts are available until 24th May. Students early bird registration \ddot{i} $_{\frac{1}{2}}$ 225, delegates early bird \ddot{i} $_{\frac{1}{2}}$ 260, industry attendees \ddot{i} $_{\frac{1}{2}}$ 400.

Jordi Paps Montserrat <jordi.paps@bristol.ac.uk>

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DurhamUK EvolMedicineSociety Aug6-9 DiscountedRegistrationEnding

Just two more days to get the early registration discount for ISEMPH 2024, Aug 6-9 in Durham UK! This 9th annual meeting of the International Society for Evolution, Medicine, and Public Health is a must for anyone interested in evolutionary applications in medicine and public health. <https://isemph.org/ISEMPH-2024> The full program of 161 presentations is now posted at <https://airtable.com/app7lujEgWxAHWU9P/shr0rQ9wbenL0kviO> This will be a terrific meeting! Special thanks to Molly Fox and the Program Committee and Gillian Bentley and the Hosting Committee for creating it!

nesse@umich.edu

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Heidelberg HumanAncientGenomics Sep17-20

Dear all,

Our EMBO | EMBL Symposium 'Reconstructing the human past: using ancient and modern genomics' is open for registrations. It is a multi-disciplinary meeting on studies of the human past using archaeogenomic methods to reconstruct the landscape of human genetic variation over time. Submit your abstract now and join us in September 2024!

Important information: 'Reconstructing the human past: using ancient and modern genomics' Dates 17 - 20 September 2024, EMBL Heidelberg and Virtual

Abstract submission deadline: 18 June 2024 On-site registration deadline: 6 August 2024 Virtual registration deadline: 10 September 2024

About the symposium The available dataset of genome-wide data from present-day and archaic humans has risen exponentially since the first EMBO 'Reconstructing the

human past' meeting in 2019. This has drastically enhanced our ability to carry out further large-scale studies on both global and local scales across deeply sampled time transects, making it now possible to ask and answer questions that were simply impossible to address before, in addition to motivating the development of new analytical methods. Critically, with new frontiers in data generation and analyses, questions on ethical practices in paleogenomics need to be considered.

Furthermore, the reconstruction of ancient pathogen genomes and metagenomic analysis of the oral and gut microbiomes provides us with molecular fossils to study microbial evolution through time. The potential of ancient DNA data to reconstruct genomic variation of human-associated animals and plants to understand the process of domestication and their evolutionary trajectory is equally promising to such studies in humans.

This meeting will involve scientists from population genetics, bioinformatics, microbiology, anthropology, archaeology and history and will strengthen future interactions in this young research field that is already changing the way we think about our past and will shape how we study genetic variation in the future.

Keynote speaker We are pleased to announce that Nobel Laureate Svante Pääbo from Max Planck Institute for Evolutionary Anthropology (Germany) will be the keynote speaker at 'Reconstructing the human past: using ancient and modern genomics'.

Organisers Scientific organisers Johannes Krause (Max Planck Institute for Evolutionary Anthropology, Germany), Ida Moltke (University of Copenhagen, Denmark), Maanasa Raghavan (University of Chicago, USA), and Pontus Skoglund (The Francis Crick Institute, UK) have put together an excellent programme and are ready to welcome you in September!

Session topics §Our closest living and extinct relatives §Detecting patterns of selection §Reconstructing the genetic history of human populations §Ethical considerations and research practices in paleogenomics §Integrating genetic and historical evidence §Evolution of human pathogens, microbiome, and health §New methods and avenues for ancient genomic data analysis

Find out more and submit your abstract via EMBL Events website: <https://www.embl.org/about/info/-course-and-conference-office/events/ees24-09/> Thank you! Kind regards, Mayra Sanchez

Marketing Trainee mayra.sanchez@embl.org (+49) 6221 3878 109 Advanced Training Centre | A0702 European Molecular Biology Laboratory Course and Conference Office Meyerhofstr. 1 D-69117 Heidelberg Germany

Visit www.embl.org/events for a list of all EMBL events and subscribe to our newsletter (<http://www.embl.org/events/newsletter/signup>).

Mayra Gabriela Sanchez Ponce
<mayra.sanchez@embl.de>

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Heidelberg Two Jul4-5-Oct8-11

Dear all, Our EMBL 50th Anniversary Scientific Symposium 'From atoms to ecosystems' a new era in life sciences is open for registrations. The symposium will take place at EMBL Heidelberg and is open to EMBL staff and alumni. Registration for the onsite event is only via the link in the invitation email. The option to join virtually is open to all. To take part in the symposium virtually please register via the button on this link.

<https://www.embl.org/about/info/course-and-conference-office/events/lab24-01/> Important information: 'From atoms to ecosystems' a new era in life science' 4 - 5 July 2024, EMBL Heidelberg and Virtual Registration deadline: 27 June 2024 About the conference

In 2024, EMBL will celebrate its 50th anniversary with a historic two-day scientific symposium. This colloquium, 'From atoms to ecosystems' a new era in life sciences', will be held both virtually and in-person at Heidelberg on Thursday 4 - Friday 5 July 2024. The event will celebrate EMBL from the moment of its inception, in 1974 when the proposal to bring a world-class life sciences laboratory to Europe was ratified, through to the exciting and vibrant organisation that EMBL represents today.

The symposium will explore the foundational scientific research, service, technology and innovation that EMBL has fostered over the past 50 years. It will showcase EMBL's inspiring and pioneering scientific contributions and highlight how these still continue to evolve to address topics of global importance. The programme will encompass both a historic perspective and a forward look to the cutting edge science that EMBL is bringing to the life sciences of the future.

The symposium sessions will include presentations from current and former EMBL group leaders, as well as former EMBL pre- and postdoctoral fellows. The first

day will be focused on research from cells to tissues, spanning genome biology, developmental biology, as well as protein structures and complexes. The second day will focus on digital biology and the current EMBL research programme, 'Molecules to Ecosystems', as well as technological advances past and present. The symposium will conclude with a panel on "The past, the present and the future. A discussion with EMBL's global community".

Session topics * Genome biology

- * Protein structures and complexes
- * From cells to tissues
- * Developmental biology
- * Molecules to ecosystems
- * Bioinformatics * EMBL's technology highlights * Alumni: celebrating EMBL and its community Panellist We are pleased to announce that Ana Boskovic EMBL Rome (Italy), Edith Heard EMBL Hiedelberg (Germany), Jan Kosinski EMBL Hamburg (Germany), Paul Nurse The Francis Crick Institute (UK), Christian Nüsslein-Volhard Max Planck Institute of Biology (Germany), Oliver Stagle EMBL Heidelberg (Germany), and Flora Vincent EMBL Heidelberg (Germany) will be the panellist at the symposium

Find out more and register via EMBL Events website: <https://www.embl.org/about/info/course-and-conference-office/events/lab24-01/> Thank you!
Kind regards, Mayra Sanchez Marketing Trainee
mayra.sanchez@embl.org (+49) 6221 3878 109 Advanced Training Centre | A0702 European Molecular Biology Laboratory Course and Conference Office Meyerhofstr. 1 D-69117 Heidelberg Germany

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(https://www.youtube.com/user/emblmedia/playlists?sorti=&viewP&shelf_id=4) | EMBL Events Blog (<https://blogs.embl.org/events/>)

Dear all, Our EMBO Workshop Molecular mechanisms in evolution and ecology is open for registrations. The workshop series aims to highlight the latest technological advances, amplify scientific and societal focus on

biodiversity, and showcase studies on the vital role of microbes in planetary ecosystems.

Important information: 'Molecular mechanisms in evolution and ecology' 8 - 11 October 2024, EMBL Heidelberg and Virtual Abstract submission deadline : 10 July 2024

— / —

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>

IndianaU MidwestPopGenetics Aug9-10

Dear colleagues,

Registration is now open for the 9th annual Midwest Population Genetics meeting, to be held here at Indiana University, Bloomington. The conference will begin at noon on Friday, August 9th and run through ~5 pm on August 10th, with a conference dinner Friday night.

There will be the opportunity to give 20-minute talks, as well as a poster session. This is a trainee-oriented meeting, with largely students and postdocs presenting their work. Mike Wade will be the keynote speaker.

If you would like to attend, please register here by June 1st (or until we run out of room):

<https://docs.google.com/forms/d/1GH2W6xP6P5KFFYQOtRO4vcqAsR4-7rsHQupkfNpjvyo> We will notify people interested in giving a talk as to whether their abstract has been selected by July 1.

There are many places to stay in and around campus. If you'd like to stay in the on-campus hotel (<https://imu.indiana.edu/hotel/index.html>) you will get a 10% discount by using the code MWPG24.

Matt

Matthew Hahn (he/him) Distinguished Professor Department of Biology and Department of Computer Science Indiana University 1001 E. 3rd St. Bloomington, IN 47405 <https://hahnlab.sitehost.iu.edu/> "Hahn, Matthew" <mwh@indiana.edu>

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Montreal DispersalAdaptation Jul26-30

Dear colleagues,

We are excited to announce a symposium during the joint Evolution conference in Montreal, scheduled for July 26-30, 2024. The theme of the symposium is “The interplay between dispersal, plasticity, and adaptation in coping with changing environments”. You can find more details about the symposium below and information about the conference and abstract submission process here.

We hope you will consider joining us!

Title: The interplay between dispersal, plasticity, and adaptation in coping with changing environments

Organizers: Inês Fragata: irfragata@gmail.com. cE3c - Faculdade de Ciências da Universidade de Lisboa (PT)

Elvira Lafuente: elafuentemaz@gmail.com. Instituto Gulbenkian de Ciência (PT)

Abstract: In response to environmental changes organisms can move, adapt, or adjust. These three strategies have been extensively studied across various species, providing a solid basis to our understanding of the separate contribution of dispersal, adaptation, and plasticity to the maintenance of biodiversity. However, the possible synergies between them and how prevalent they are in the response to stressful environments remains largely unexplored.

This symposium aims to bring together researchers working on the interplay between dispersal, adaptation, and plasticity to bridge connections and synergies between these different strategies (e.g. evolution of dispersal or plasticity, dispersal or evolution via plasticity) and build a framework that integrates the contribution of all three. Ultimately, exploring the interconnections between these three strategies can help us to better understand how natural populations cope with changing environments.

Relevance: Studying the response of natural populations to changing environments is of great importance in the face of unprecedented global challenges. Genetic variation, phenotypic plasticity, and dispersal all play important roles in allowing populations to cope with those challenges. While these strategies are frequently

studied in isolation, they are intricately connected and their prevalence and relevance in nature often relies on those interconnections.

This timely symposium will bring together researchers that are working at the interface between the three strategies. By doing so, we can address existing discrepancies and foster new synergies between them. Ultimately, this symposium aims to build a framework that integrates knowledge from these three different fields and their interactions to provide a more comprehensive and realistic view of how natural populations cope with environmental changes.

Warm regards,

Inês Fragata and Elvira Lafuente

Inês Fragata <irfragata@ciencias.ulisboa.pt>

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Montreal QuestforOrthologs Jul17-18 DeadlineMay14

PLEASE FORWARD THIS ANNOUNCEMENT!

Quest for Orthologs meeting (QfO8) - July 17-18, 2024 - Montreal, QC, Canada.

LAST CALL : abstract submissions for Talks and/or Posters.

DEADLINE EXTENSION TO : May 14, 2024

Webpage: <https://event.fourwaves.com/qfo8> Confirmed Invited Speakers : Fiona Brinkman (Simon Fraser University), Elena Kuzmin (Concordia University), Markus Hecker (University of Saskatchewan), Christine Orengo (University College London).

Scope: The QfO Consortium addresses a key challenge in molecular evolutionary biology and strives to develop large-scale methods for inferring orthology among fully sequenced genomes, and to reconstruct the complement of protein-coding genes in common ancestral genomes across the tree of life. The QFO meetings aim to bring together disparate groups around the world that work in the field to accelerate progress through sharing of ideas, methods and research findings. The particular aim of this QfO8 meeting is to gather an even more diverse set of end-users and to connect different research communities that are rooted in orthology.

Travel and Caregiver Fellowships: Authors of accepted talks/posters will be eligible for travel and caregiver fellowships to attend the conference. The procedure for application will be communicated to the relevant people in the talk/poster acceptance email.

ISCB members can receive a 15% discount on registration rates.

Further information on abstract submission deadline and guidelines can be found here: <https://event.fourwaves.com/qfo8/submission> PLEASE FORWARD THIS ANNOUNCEMENT!

Aïda Ouangraoua
<Aida.Ouangraoua@USherbrooke.ca> Ouangraoua

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Online ESEB InternalConflictsSTN May14

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 May 14th at 15:00 UTC. Our speakers for this seminar are:

Clément Lafon Placette (Charles University): Genomic imprinting, involved in parental conflict? Insights from gene regulatory networks in the plant species **Arabidopsis arenosa**. Graeme Keais (University of British Columbia): Meiotic drive of an X chromosome through both sexes in **Drosophila**.

In addition, we will host breakout discussion groups on two goals of the STN for which we are soliciting feedback: (1) generating an atlas of internal conflicts, and (2) establishing an online journal club/reading group. These discussions will take place after the presentations and associated questions and discussion. We expect the meeting to take approximately 1.5 hours.

Meeting details: Link: <https://georgetown.zoom.us/j/92437298472> Date: May 14th, 2024. Time: 15:00 UTC.

If you would like to get on our mailing list and take part in our upcoming events, please sign up (HERE < <https://docs.google.com/forms/d/e/>

1FAIpQLSeJjKjGDxh76JYjqxLS035D_Zhpo3IG00HHD8G5o6wrzivvGviewform?usp=sf_link >) or visit our website (<https://internalconflictsstn.wordpress.com/>) for more information.

Sincerely, The Internal Conflicts and Organismal Adaptation STN Martijn Schenkel, Arvid Ågren, Manus Paten, and Nina Wedell

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 SociallyTransferredMaterials May7

Dear colleagues,

Our ESEB-funded special topic network “Social Transfer Network” is organising a number of online and in-person workshops (Social Transfer Evolution Workshops, aka STEWs) on topics around socially transferred materials. The next one is our second online Bring-Your-Own-Fluid Seminar on 7 May 2024 at 12:00 (Amsterdam time); BYOF refers to either the social fluid you might study or your cup of coffee or tea in hand.

The BYOF session will last for one hour, where we will have 3 short 7-min talks on different social transfers, socially transferred materials, and relevant techniques followed by discussion. Our intention with this is to build an interdisciplinary community on this topic, to learn from one another and to advance research across the study of social transfers.

Topic: Bring Your Own Fluid Seminars (7 May) Time: May 7, 2024 12:00 PM Amsterdam, Berlin, Rome, Stockholm, Vienna <https://vu-live.zoom.us/j/94238053625?pwd=-ZGRaZWZ2Qk1lbUIwYUpLZGg0V0Z0Zz09> 7
May Programme:

Seize or share? Quantifying eusocial (re-)distribution of nutrients in carpenter ant colonies - Pranas Grigaitis (Amsterdam Institute for Life and Environment, Vrije Universiteit Amsterdam, NL)

Plasticity and evolution in the metabolic division of labour in burying beetle families - Eleanor Bladon (De-

partment of Zoology, Cambridge, UK)

Hypodermic injection of socially transferred materials - Joris Koene (Amsterdam Institute for Life and Environment, Vrije Universiteit Amsterdam, NL)

We will organise at least 4 more BYOF seminars in 2024. If you are interested in speaking or helping to organise please attend and get in touch. The next planned seminar will be on June 12th. Fall dates and times will be announced in the summer. The next in-person event will be our symposium at Evolution2024 in Montreal this summer.

If you would like to stay in touch, please join the Social Transfer Network: <https://forms.gle/-cJG3gBUMAHMBviUr5> We look forward to seeing you there!

The Social Transfer Network organising committee:

Adria LeBoeuf, Sanja Hakala, Rebecca Kilner, Katharina Gapp, Joris Koene (joris.koene@vu.nl)

Dr. Joris M. Koene Associate Professor at Vrije Universiteit Amsterdam <http://www.joriskoene.com> Ecology & Evolution Amsterdam Institute for Life and Environment (A-LIFE) Vrije Universiteit Visiting address: De Boelelaan 1108, 1081HZ, Amsterdam Mail address: Van der Boechorststraat 3, 1081 BT, Amsterdam THE NETHERLANDS tel: +31 (0)20 5987095 joris.koene@vu.nl <https://vu.nl/en/about-vu/-faculties/faculty-of-science/departments/a-life> <https://research.vu.nl/en/persons/jm-koene> “Koene, J.M. (JM)” [<joris.koene@vu.nl>](mailto:joris.koene@vu.nl)

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PuertoVallarta SMBE GENHIST Jul7

Dear colleague,

If you're going to SMBE, consider registering for the Genomic History Inference Strategies Tournament (GENHIST) kickoff event. The event will be the afternoon of the first day of the conference, Sunday at 2:00 pm.

In population genomics, there are a dizzying array of potential data analysis approaches to infer population history, aspects of natural selection, or other evolutionary properties from data. Although methods developers try to evaluate their approaches, those evaluations can

be unconsciously biased or may not reflect the experiences of real-world users. GENHIST aims to create an annual forum in which the community can test inference approaches in an unbiased fashion. Each year, the GENHIST organizers will release simulated population genomic data sets and host a competition to infer various aspects of the processes that generated those data. From the submissions, the community will learn what approaches perform well or poorly in particular circumstances.

This year will be the first GENHIST competition. We will have 4 tasks, ranging from simple to complex. In the simplest task, competitors will be given a Variant Call Format (VCF) file of data from a population that was simulated to undergo a collapse in size. They will be asked to infer the timing and magnitude of that collapse. More complex tasks will involve multiple populations, migration from ghost populations, and/or background selection. Competitors who perform well will be asked to join as authors on the publication describing the year's competition.

At the kickoff event, we will walk you through accessing the competition data, briefly analyzing it with *dadi* and/or *MSMC*, and submitting your first results! We expect this event and the overall competition to be great for trainees, to get experience with population genomic inference.

For questions, please contact Ryan Gutenkunst [<rgutenk@arizona.edu>](mailto:rgutenk@arizona.edu), chair of the Organizing Committee for GENHIST

rgutenk@arizona.edu

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Reading UK Systematics Jun19-21

Abstract & Registration deadline for upcoming Systematics Association Biennial Conference (19th - 21st June).

Dear colleagues, Our upcoming Biennial Conference, to be held in Reading, United Kingdom on 19th-21th June, has extended the deadline for abstract submission and registration for the final time in preparation of the upcoming conference.

NEW DEADLINES: (i) Abstract submission Friday 24th May (ii) Registration deadline Friday 31st May.

Find out more details about abstracts and registration on our webpage: <https://systass.org/events/biennial/>
 Scope: This is the Systematics Associations 11th Biennial conference. The Biennial is our flagship conference and we have planned an exciting programme of talks, workshops, and social activities throughout the conference. We have 2 fantastic plenary speakers with Erica McAlister (NHM) and Sandy Hetherington (University of Edinburgh). We will run 3 symposia with invited speakers as well as an open symposia, where you can submit for full or flash talks. This is a great opportunity to present research relating to taxonomy, systematics, and phylogenetics to a friendly and supportive audience.

For more details on the Programme and Workshops see our website: <https://systass.org/events/biennial/-programme/> We hope to see you in Reading in June!

Best wishes, Biennial organising team

(Contact us at biennial@systass.org for any queries)

peter.mulhair@biology.ox.ac.uk

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Tahoe California GenomicTechnologies Oct6-9

Register & submit abstracts by Saturday, June 1st!

AGA2024 President's Symposium – Genomic Technologies & the Future of Conservation

<https://www.theaga.org/agatwentytwentyfour> AGA President Beth Shapiro, Chief Scientific Officer at Colossal Biosciences, has focussed the 2024 Symposium on exploring DNA and other biotechnologies, including cloning and de-extinction, for biodiversity conservation.

The meeting will take place at Granlibakken Resort, Tahoe City. It begins on Sunday, Oct 6, with an opening reception and Key Distinguished Lecture by Scott Edwards. The following two days of invited talks, poster session, and field trip will examine present-day conservation challenges and delve into innovative solutions.

All registrants may submit poster abstracts, with a limited number to be selected for oral presentations. Students with accepted abstracts will receive a refund of the \$200 registration fee.

We can only accommodate 100+ participants, so register soon! Registration is anticipated to close on June 1st.

Invited speakers: Scott Edwards, AGA Key Distinguished Lecturer Herni, $\frac{1}{2}$ n Morales Elinor Karlsson Carlos Garza Joanna Kelley Caren Helbing Moi Esposito-Alonso Rachel Meyer Teal Brown Zimring Eli Ilano Bridgett vonHoldt Klaus-Peter Koepfli Anna Keyt Andrew Pask Allison Miller

contact: Anjanette Baker, Symposium Coordinator
theaga@theaga.org

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Alaska Halibut DNA methylation

A 2-year MSc level graduate student project is available in January of 2025 or earlier involving the development of a genome-wide DNA methylation-based method for aging Pacific halibut as an alternative to current traditional aging methods. This project will be the basis of a graduate thesis that the student will conduct towards the completion of a MSc degree in Environmental Science at Alaska Pacific University (APU) in Anchorage, AK (http://catalog.alaskapacific.edu/-preview_program.php?catoid=17&poid=1148&returnto=501). The student will be jointly supervised by faculty at APU and scientists at the International Pacific Halibut Commission (IPHC; <https://www.iphc.int/>) in Seattle, WA and the Auke Bay Laboratories/Alaska Fisheries Science Center in Juneau, AK (<https://www.fisheries.noaa.gov/about/-auke-bay-laboratories>), to develop and validate an epigenetic clock and high-throughput genomic methods for age estimation that will inform the Pacific halibut stock assessment. The specific objectives of this grant-funded project involve: 1) developing an age estimation method based on the generation of a high-resolution DNA methylation map for Pacific halibut tissue (fin clips) by leveraging the high-quality reference genome (Jasonowicz et al., 2022; <https://doi.org/10.1111/1755-0998.13641>) and extensive transcriptomic data available for Pacific halibut generated by the IPHC; 2) developing predictive age models comparing age determinations by traditional (i.e. otolith annuli reading) and genome-wide DNA methylation-based methods; and, 3) developing error estimation methods and conducting sensitivity analyses. MSc course requirements will be done at APU in Anchorage and laboratory and bioinformatic work will be conducted primarily at the IPHC office in Seattle.

Ideal candidates will have a BSc in Fisheries, Marine Biology, Ecology or related field and programming ex-

perience in one or more modern scripting languages (eg. R, Python, etc.). Knowledge of using Command Line Interfaces (CLI) such as Linux, Unix and or Bash shell is strongly desired. Experience in analyzing genomic data is preferred but not required.

To apply, please send 1) a cover letter summarizing research interests and experience, 2) a current CV containing a list of publications (if applicable), 3) a copy of the latest academic transcript, and 4) the names and contact information for three professional references to Dr. Nathan Wolf at Alaska Pacific University (nwolf@alaskapacific.edu). Review of candidates will begin immediately, but the position will remain open until a suitable candidate is found.

Josep Planas, Ph.D. Biological & Ecosystem Science Branch Manager 2320 West Commodore Way, Suite 300 Seattle, WA 98199 USA +1-206-552-7687 josep.planas@iphc.int www.iphc.int Josep Planas <Josep.Planas@iphc.int>

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Bar Ilan U Sexual Conflict

PhD student position in Bar Ilan University, Israel: Drivers and reducers of sexual conflict in utero

Sexual conflict can develop if alleles affect traits in both sexes in an opposite manner, promoting fitness in one sex while decreasing fitness in the opposite sex. Although mainly studied in adults, the processes that give rise to sexual conflict likely start in utero, thus shaping the organism's entire life trajectory. This fascinating process has yet to be elucidated, with a key question remaining unresolved: What factors during fetal development underly sexual conflict? Here we seek to answer this question by providing a mechanistic understanding of sexual conflict during ontogeny, starting in gestation.

We will focus on the hypothalamic-pituitary-gonadal (HPG) axis and its components, such as testosterone (T). This axis exhibits sex differences in optimal levels and in the mediation of morphological, physiological, and behavioral processes throughout life, paving the way for sexual conflict. Sexual conflict may be affected by environmental factors, such as steroid transfer between fetuses in litter-bearing mammals. It may also involve a genetic component. In the case of the HPG axis, if its components are heritable, then sex different genetic architecture (from mother only to daughter and father only to son) may reduce sexual conflict. We here propose a holistic approach to testing the contribution of the environmental and genetic effects and their interactions to sex differences in the HPG axis before birth. Our preliminary results on T show sex differences that may be indeed compensated by sex different genetic architecture, which may serve to reduce sexual conflict.

Our in utero study will take advantage of the annual culling of hundreds of free-ranging nutrias (*Myocastor coypus*) in Agmon Hula Park, Israel, which will afford us access to many large litters with validated maternity and widespread within-litter multiple paternity. It will further offer a unique opportunity to test a complete, large, natural dataset that includes variability beyond that of model laboratory animals. We will integrate data collected from different tissues and in different developmental stages, including circulating T in fetal and maternal hair, T in amniotic fluid, and gene expression levels of HPG axis components in fetal gonads and brain areas involved in sexual dimorphism in quantitative morphological and behavioral traits. Then, we will evaluate the contribution of environmental vs. genetic effects, assess sexual conflict using quantitative genetics tools, and test whether there is a differential genetic architecture within and between sexes, in different developmental stages. We will also map the expression of HPG axis genes at different developmental stages (trimesters) and in specific tissues and determine whether there is a relationship between levels of HPG axis gene expression. The interaction between the environmental and genetic effects will be explored in a unified statistical model that will partition the variance of sex differences that can account for sexual conflict. This naturally controlled experiment, where the environment is contained within the mother, is expected to yield a clearer understanding of the environmental-heredity interplay driving sexual conflict. Understanding the contribution of environmental vs. genetic effects on sex differences in HPG axis components is expected to shed light on the mechanisms behind sexual dimorphism in other fitness-related traits.

This four year position includes tuition, a full scholar-

ship, salaried teaching opportunities, and conference travel funds.

We are looking for a bright, highly motivated scholar who has completed an MSc in the fields of Zoology, Ecology, Behavioural Ecology, Endocrinology, and/or Computational biology. An experience in field work, dissections, molecular techniques, and computational skills are an asset. Interested candidate should send a CV and a statement of interests, in addition to proof of MSc or transcripts to Dr. Lee Koren (lee.koren@biu.ac.il).

Lee Koren <Lee.Koren@biu.ac.il>

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JagiellonianU Poland TardigradeEvolution

PhD studentship in sex and tardigrade evolution

Fully funded 4-year PhD studentship in tardigrade evolution at the Jagiellonian University in Krakow (Poland) in the team of Prof. ukasz Michalczyk, in collaboration with Prof. Mark Blaxter (Wellcome Sanger Institute, Cambridge, UK).

The main goal of the project is to take a unique advantage of applying cutting-edge methodology of genome sequencing to a fascinating model, tardigrades, in order to answer one of the fundamental questions in life sciences: why are some asexual lineages able to persist over long evolutionary time, whereas the majority of them seem to be evolutionary dead ends? Given that genetic recombination seems to be the key to evolutionary success, the prediction is that ancient asexual lineages exhibit genomic signatures of recombination, whereas most recent asexuals do not. In other words, the project will provide first large scale, systematic comparative analysis of the genomic architecture of ancient and recent asexuals.

The PhD studentship presents a great and unique opportunity to answer one the fundamental questions in life sciences using a fascinating model and cutting edge methods. Importantly, the position also offers additional training in genomics and transcriptomics in one of the world's leading institutions in genomics, the Wellcome Sanger Institute in Cambridge, UK. Prof. Mark Blaxter, Head of the Tree of Life Programme at Sanger, is a formal and the key collaborator on the project.

Although the evolution of sex and tardigrades are the central project aims, the system provides potential for a dedicated student to explore their own ideas on other topical tardigrade biology and evolutionary questions. A dedicated student will have a great chance not only to learn a range of transferable skills, but also to build a sound publication record which will help them to get an attractive PostDoc or industry position in the future.

The successful candidate will be involved in will be involved in field work (sample collection), tardigrade identification, culturing, DNA extraction, genome & transcriptome sequencing and assembly, as well as in phylogeny reconstruction. The PhD Student will be also required to prepare first drafts of some manuscripts and will be involved in the promotion of results at seminars and conferences.

The PhD programme in Biology at the Jagiellonian University is run entirely in English and it includes some obligatory and facultative classes. The programme is open to all nationalities and there are no tuition fees.

The PhD stipend is 5 —500 —PLN per month (typically, cost of life in Krakow for a PhD student is ca. 4 —000 PLN/month).

Deadline for applications: 6th of June 2024.

More information on the project, university, our team and the application procedure is available here: <http://tardigrada.edu.pl/PhD.htm> Prof. ukasz Michalczyk LM@tardigrada.net

ukasz Michalczyk <LM@tardigrada.net>

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KLI Austria WritingUpFellowships EvolBiol

Call for Writing-Up Fellows in Morphometrics in Evolutionary or Developmental Biology

The Konrad Lorenz Institute for Evolution and Cognition Research (KLI) in Klosterneuburg, Austria, is an international center for advanced studies in the life sciences, with a focus on conceptual, philosophical, historical, and mathematical approaches in evolutionary biology and biomedicine. Embedded in a vibrant research community in the Vienna area, the KLI typically hosts about 20 fellows, visiting scholars, faculty, and students. The KLI announces up to four Writing-Up

Fellowships for students who are in the late stage of their PhD project involving geometric morphometrics, biological image analysis, or computational anatomy to address questions in evolutionary and developmental biology or biomedicine. Candidates are expected to have finished their data collection phase so that they can focus on analysis, conceptual integration, and writing up of their PhD project during the fellowship. At the KLI, the fellows will be advised by Barbara Fischer and Philipp Mitteroecker. The duration of the fellowship is six months, starting either in spring or in fall 2025. The gross stipend is EUR 2,500.- monthly (before tax and social insurance). https://www.kli.ac.at/content/en/the_kli/open_calls Call for Writing-Up Fellows in Evolutionary Medicine

The Konrad Lorenz Institute for Evolution and Cognition Research (KLI) in Klosterneuburg, Austria, is an international center for advanced studies in the life sciences, with a focus on conceptual, philosophical, historical, and mathematical approaches in evolutionary biology and biomedicine. Embedded in a vibrant research community in the Vienna area, the KLI typically hosts about 20 fellows, visiting scholars, faculty, and students. The KLI announces up to four Writing-Up Fellowships for students who are in the late stage of a PhD project addressing topics in evolutionary medicine. Research approaches can involve conceptual, historical, and theoretical methods as well as data-driven, computational, or experimental work. The call is open to all medical topics, including evolutionary psychiatry. Candidates are expected to have finished their data collection phase so that they can focus on analysis, conceptual integration, and writing up of their PhD project during the fellowship. At the KLI, the writing up fellows will be advised by the staff of the institute. The duration of the fellowship is six months, starting either in spring or in fall 2025. The gross stipend is EUR 2,500.- monthly (before tax and social insurance). https://www.kli.ac.at/content/en/the_kli/open_calls Dr. Barbara Fischer

Barbara Fischer <barbara.fischer@kli.ac.at>

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Liverpool Raptor Conservation Genomics

Announcement for a PhD thesis at Liverpool John Moores University, Liverpool, UK

Title:

Conservation Genomics to assist in the conservation and management of vulnerable raptor species

Funding notes:

The selected applicant will be applying for the 2025 LJMU Vice-Chancellor PhD Studentship competition (<https://www.ljmu.ac.uk/research/phd-studentship-application>). If successful, the applicant will start in February 2025 and will receive three years funding covering tuition fees, UKRI-standard student stipend and research support. This competition is open to both UK and International students. Applications from candidates from under-represented ethnic minority backgrounds are encouraged.

Project description:

The impact of global climate changes on patterns of biodiversity and species distributions is a major current topic in Biology. However, we are only beginning to develop tools and model systems to examine how species have responded and adapted to large-scale perturbations in the past. Past demographic patterns and adaptations leave a footprint on the genomes of individuals, providing insights into past population sizes and periods of hybridization or genetic introgression from other populations or species. Analyses of genomic data can therefore throw light on the effects of past environmental changes, allowing development of predictive models for future scenarios.

This project involves use of Illumina whole genome sequencing and machine learning tools to identify the main processes that have led to the present distribution of genetic diversity within several endangered raptor species (eagles and harriers). The findings will inform the conservation management strategy of the studied populations/species

The PhD will involve analyses of genomic data at three levels:

1) Demographic histories among species at evolutionary and ecological times. The Spanish imperial eagle

Aquila adalberti, the Eastern imperial eagle *A. heliaca*, the steppe eagle *A. nipalensis*, and the tawny eagle *A. rapax* form a clade within the Aquilagroup. These species are all considered vulnerable or endangered by the IUCN. The study will try to disentangle questions on divergence times, gene flow and changes in effective population sizes (N_e) to understand the current patterns of the distribution of genetic diversity. This understanding will be informative for the management of the species in the wild.

2) Genomic analyses among populations within a species. Western European populations of the hen harrier, *Circus cyaneus*, will be studied. Several European countries have reported recent declines in this species suggesting a possible more extended decline for this vulnerable species. The study will provide the first data on the population genetics of this species, its levels of genetic diversity and whether the populations are connected by gene flow.

3) Diversity within a population. This will focus on a founding population of hen harriers from a captive breeding project that intends to repopulate the South-Western corner of the UK. A pedigree of the captive population will be established from whole genome data and provide a basis for genomic monitoring of the captive population and released individuals. The aim is to maintain high levels of genetic diversity in the captive population while avoiding increased genetic load.

Supervisory team

The PhD student will join our School of Biological and Environmental Sciences (BES) at the Liverpool John Moores University and work under the supervisory team of Dr Begonia Martínez-Cruz, Dr Gareth Weedall and Prof Richard Brown from BES. The PhD will require use of established genomic and machine learning tools and therefore require previous experience of Bioinformatics/computational statistics and background in genomics. Good communication skills, ability to meet deadlines and an ability to work both independently and with the supervisory team is essential. Please explain in your cover letter and evidence in your CV how your experiences meet the criteria.

How to apply

To apply email a CV and covering letter detailing your suitability for the project and contact details of two referees to Dr Begonia Martínez-Cruz (b.martinezcruz@ljmu.ac.uk). The deadline for applications is the 15th of June. Applicants must be available for an interview (by video if necessary) at the end of June and able to start in February 2025.

Additional notes

The Faculty of Science and its three Schools: Biological & Environmental Sciences, Pharmacy & Biomolecular Sciences, and Sports & Exercise Science, have dedicated Diversity and Inclusion (DI) Groups. The individual School Diversity & Inclusion Coordinators and the Faculty Associate Dean for Diversity & Inclusion lead collective action to promote and embed a culture of equality, diversity and inclusivity. All Schools

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LundU Evolutionary Conservation Genomics

PhD project in conservation genomics

A PhD position is available in the lab of Tobias Uller at Lund University. The aim of the project is to study causes and consequences of genomic diversity in sand lizards (*Lacerta agilis*). For more information about the research group, see <https://feiner-uller-group.se>. THE PROJECT: Intensive forestry, agriculture and urbanization reduce the habitat for many species. As populations become small and isolated, genetic diversity is lost and inbreeding and mutation load can make populations succumb to an 'extinction vortex'. The project aims to establish the consequences of habitat fragmentation and loss for the Swedish sand lizard (*Lacerta agilis*) - an indicator and umbrella species for open habitats with many other red-listed species. With the help of genomic analyses, it is possible to reveal historical changes in population demography, identify features of the landscape that promotes functional connectivity between locations, and establish to what extent purging of harmful genetic variants enables small populations to persist. The findings of the project can be used to identify effective conservation strategies for the sand lizard.

The project is situated at the interface of evolutionary genomics and conservation biology. The research is mainly based on genomic analyses of a large number of individuals from isolated and fragmented populations. The student will be encouraged to develop the project in a direction that they prefer, such as genome evolution, population genomics, or conservation biology. The

project includes field work to collect data, laboratory work, bioinformatics analyses of whole-genome data, and methods and statistics for spatial analyses.

THE CANDIDATE: Applicants should have an MSc in evolutionary biology, ecology or a closely related area. They must have demonstrated ability for proactive and independent work and practical experience in analysis and interpretation of genomic data. A driver's license is a requirement.

In addition to the mandatory requirements, documented experience in the following areas will be considered as strong merits: Good knowledge and experience in data processing and statistical analyses; Practical experience in molecular laboratory methods; Experience in field work; Experience in spatial analysis and GIS.

For more information and how to apply, see <https://-lu.varbi.com/en/what:job/jobID:721487>. The deadline for applying is May 27 and the expected starting date is September. For informal enquiries, please contact Tobias Uller (tobias.uller@biol.lu.se).

Tobias Uller Professor of Evolutionary Biology

Lund University Department of Biology
www.biology.lu.se/tobias-uller www.feiner-uller-group.se Tobias Uller <tobias.uller@biol.lu.se>

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MainzU Fourteen EvolGeneRegulation

PhD Programme "Gene Regulation in Evolution" 14 funded PhD positions on offer in Mainz, Germany

Thinking of doing a PhD at the interface of Molecular & Evolutionary Biology?

The Research Training Group 2526 "Gene Regulation in Evolution" (GenEvo), which is funded by the DFG (German Research Foundation), is offering projects on all levels of organismic complexity, from changes in genes and proteins to the evolution of symbiotic and parasitic behaviour. As a GenEvo PhD student, you will join a community of passionate scientists who are applying a broad spectrum of methods on model and non-model organisms.

Programme Themes are: * Epigenetics * Evolution * RNA Biology * Ageing * Computational Biology *

Bioinformatics * Ecology * Behaviour * Paleogenomics
* Speciation * Structural Biology

What we offer: * Exciting, interdisciplinary projects in a vividly international environment, with English as our working language * Advanced training in scientific techniques and professional skills * Access to state-of-the-art Core Facilities and their technical expertise * 14 funded PhD positions (employment contract) * A lively community of 34 PhD students supported by 28 Principal Investigators * Collaboration with the International PhD Programme (IPP) at IMB with more than 200 PhD students from 40 different countries

Requirements: * Master or equivalent * Motivation to contribute to the forefront of science in molecular and evolutionary biology * Interactive personality & good command of English * 2 letters of reference

Within the programme the Faculty of Biology of Mainz University (JGU) and the Institute of Molecular Biology (IMB) collaborate both modern research institutions located on the bustling campus of Mainz University in Germany. With a population of 210,000, of which about 40,000 are students, the city of Mainz is charming and open-minded and within easy reach of cosmopolitan Frankfurt and its international airport, the Rhine valley region with its castles, vineyards, and nature reserves, and the equally picturesque cities of Wiesbaden and Heidelberg.

Are you an ambitious, young scientist looking to push the boundaries of research while interacting with colleagues from multiple disciplines & cultures? Then joining GenEvo is your opportunity to give your scientific career a flying start!

Application deadline: 15 July 2024 Interview date: 9-10 September 2024 Starting date: 1 January 2025

For more details on the 14 different projects offered and how to apply, please visit <https://www.genevo-rtg.de/-application> GenEvo <GenEvo@uni-mainz.de>

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MainzU Two AntEvolution

PhD Position JGU, Mainz, Germany Epigenetic Regulation of Division of Labor in Ants Supervisor: Susanne Foitzik Co-Supervisors: Peter Baumann, Susanne Gerber, Hanna Kokko

Project Overview:

Join an exciting PhD project focused on uncovering the molecular mechanisms regulating division of labour in the ant *Temnothorax longispinosus*. This project aims to identify epigenetic processes and their impact on gene networks, exploring how external and internal signals influence task-specific behaviours. You will delve into the roles of histone acetylation, transcription factors, and odorant receptors in shaping worker specialization.

Key Techniques and Skills:

Behavioural genomics and evolutionary biology Behavioural observations and field ant collection Epigenetic molecular techniques: CUT&TAC, RNAseq, microRNA, RNAi Bioinformatics analysis and mathematical modelling

Qualifications:

Candidates should hold a Master's or 4-year Bachelor's degree in biology, molecular biology, or bioinformatics. Knowledge of bioinformatics, molecular genetics, and behavioural or evolutionary biology is a plus. Experience with mathematical modelling and social insect biology, especially ants, is beneficial but not mandatory.

Publications:

Caminer et al., 2023 - Communications Biology; Kohlmeier et al., 2023 - Biology Letters, Libbrecht et al., 2020 ' Iscience, Kohlmeier et al., 2019 - Molecular Ecology, Kohlmeier et al., 2018 - PLOS Biology

Apply now to be part of groundbreaking research at the intersection of evolution and epigenetics! This project is part of the international PhD training program Gene regulation in Evolution <https://www.genevo-rtg.de/>. In GenEvo, scientists are working together on the core question of how complex and multi-layered gene regulatory systems have evolved. Experts in the field of molecular & evolutionary biology support & train our PhD students in their interdisciplinary research as well as their personal development. Offered position will be located at the Faculty of Biology of JGU in Mainz. All PhD students will become a member of the International

PhD Programme (IPP).

Mainz is a history lively city with a large student population, located at the river Rhine.

Application webpage: <https://www.genevo-rtg.de/-application> Registration deadline: 15 July 2024 Interviews: 9-10 September 2024 Starting date: 1 January 2025

Prof. Dr. Susanne Foitzik Institute of Organismic and Molecular Evolution Johannes Gutenberg University Mainz Biozentrum Hanns Dieter Hüsch Weg 15 D-55128 Mainz Germany Tel: +49 (0) 6131 39 27 840 Fax: +49 (0)6131 39 27 850 Email: foitzik@uni-mainz.de

“Foitzik, Susanne”

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PhD Position JGU, Mainz, Germany Molecular manipulation of host phenotype via regulatory interference

Supervisor: Susanne Foitzik Co-Supervisors: Peter Baumann, Joan Barau Project Overview:

Explore the fascinating world of parasitic manipulation with a PhD project focusing on the molecular mechanisms used by the parasitic cestode *Anomotaenia brevis* to alter the phenotype of its ant host, *Temnothorax nylanderii*. This project investigates how the parasite interferes with host gene regulation through epigenetic processes, aiming to understand the transcriptional and epigenetic changes that lead to altered host behavior, physiology, and extended lifespan. Key Techniques and Skills:

• Evolutionary biology with a focus on parasite-host interactions

• Epigenetic molecular techniques: CUT&TAG, Bisulfite sequencing, RNAseq, microRNA, RNAi

• Bioinformatics analysis and scripting

• Ant colony collection and behavioral studies Qualifications:

Applicants should have a Master's or 4-year Bachelor's degree in biology, molecular biology, or bioinformatics. Knowledge of bioinformatics, molecular genetics, and evolutionary biology is important. Experience with social insect biology and parasitology is advantageous but not required.

Publications: Seistrup et al., 2023 - Molecular Ecology, Hartke et al., 2023 - Molecular Ecology,

Sistermanns et al., 2023 - Molecular Ecology, Beros et al., 2021 - Royal Society Open Science,

Beros et al., 2015 - Proceedings of the Royal Society B

Apply now to contribute to cutting-edge research on the molecular manipulation of host phenotypes by parasites!

This projects is part of the international PhD training program Gene regulation in Evolution <https://www.genevo-rtg.de/>. In GenEvo, scientists are working together on the core question of how complex and multi-layered gene regulatory systems have evolved. Experts in the field of molecular & evolutionary biology support & train our PhD students in their interdisciplinary research as well as their personal

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Marseille Marine Zooplankton

I obtained a funding for a PhD salary for three years in France (Marseille) cosupervised by myself (CNRS, IMBE) and Pr Delphine Thibault (Aix marseille Univ, MIO). A few keywords : “marine zooplankton, larvae, life history traits, metabarcoding, temporal survey, connectivity, global change”

The persons to contact are Anne Chenuil (anne.chenuil@imbe.fr) and Delphine Thibault (delphine.thibault@univ-amu.fr).

It is very urgent (I should send the candidate CV until may 17th, although I will try to extend this delay). Below is a link describing the PhD topic and the candidate profile (but the contact persons and the deadline are obsolete): <https://www.univ-amu.fr/fr/public-actualites/appels-doffres-de-theses-et-postdocs-ocean> Anne Chenuil-Maurel <anne.chenuil@imbe.fr>

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Montpellier Adaptation Wheat Wild Relatives

Applications are invited for a fully funded 3-year PhD fellowship based at INRAE Montpellier (France), aiming at characterizing the genetic bases of adaptation in wheat wild relatives.

Start date autumn 2024, deadline to apply 5 July 2024.

Candidates should have an interest to work at the interface among population genetics, genomics, phylogenetics, and bioinformatics.

More information about the subject and the application procedure can be found at the following link:

https://umr-agap.cirad.fr/content/download/7560/68385/version/1/file/PhD_triticeae_GE2pop_AGAP.pdf For informal inquiries, please, contact: Concetta Burgarella (concetta.burgarella@inrae.fr) Nathalie Chantret (nathalie.chantret@inrae.fr) Vincent Ranwez (vincent.ranwez@supagro.fr)

Best regards,

Concetta Burgarella

Concetta Burgarella INRAE, Equipe Génétique Évolutive et Gestion des Populations UMR AGAP Biologie Arcad 10 rue Arthur Young 34090 Montpellier concetta.burgarella@inrae.fr www.inrae.fr Concetta Burgarella <concetta.burgarella@inrae.fr>

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Montpellier Sexual Selection Plants

A fully-funded three-year position is opened to work on sexual selection in plants with a special focus on pollen-pistil interactions, under the supervision of Dr. Jeanne Tonnabel (<https://isem-evolution.fr/membre/tonnabel/>) in the context of the SEXIPLANTS project funded by the ERC.

Project goals ? Sexual selection is generally thought to apply to all sexually reproducing organisms and should

therefore include plants. Yet, general predictions from sexual selection theory remains untested for the plant kingdom. This PhD aims at testing the most fundamental predictions of sexual selection theory, including female choice models (Fisherian and good-genes models) with a special focus on pollen and pistil traits. The PhD will benefit from a unique material developed for plants: the output of experimentally evolved lines of Brassica rapa 'fast plants' which have been maintained for 18 generations in monogamy vs. polygamy. The PhD candidate will study the evolution of pollen and pistil traits in these experimental evolution lines, but also paternity biases induced by those traits and the genetic correlations between them through quantitative genetics.

For whom? We are looking for candidates with a MSc degree in biology (or equivalent) with strong motivation both for understanding and testing general concepts in evolutionary biology and for conducting experimental work. Knowledge on sexual selection and/or plant evolution and experience on experimental evolution/quantitative genetics/paternity analyses would be an advantage but is not required.

Where? The PhD student will join a stimulating working atmosphere comprising enthusiastic researchers working on sexual selection in plants in the context of the SEXIPLANTS project with high collaboration opportunities. The PhD student will work at the Institut des Sciences de l'Évolution

de Montpellier (ISEM, UMR 5554). Montpellier offers a stimulating scientific environment for evolutionary biologists with many seminars and opportunities

to interact with many renowned scientists. The working language will be English but some notions of French will come in handy in the daily life.

Working contract? The PhD contract will consist three-year contract funded by the ERC SEXIPLANTS led by Jeanne Tonnabel. The gross monthly salary is around 2 135 euros. The contract includes health insurance and 44 days of annual leave.

When? The ideal starting date of PhD would be September 1 st 2024 but starting date is negotiable.

How to apply? All applications must be sent by email to Jeanne Tonnabel (jeanne.tonnabel@umontpellier.fr) and in parallel submitted to the CNRS platform (<https://emploi.cnrs.fr/Offres/Doctorant/UMR5554-JEATON-005/Default.aspx>) before June 1st. Applications should include 1) a motivation letter describing research interests, relevant experience and motivation for applying to this PhD position, 2) a CV and 3) contact information for two referees.

Jeanne Tonnabel <jeanne.tonnabel@umontpellier.fr>

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ing@mcmaster.ca)

NTNU Museum Systematics

The Norwegian University of Science and Technology's Department of Natural History at the University Museum has an opening for a PhD Candidate in Dark Taxon Science.

The NTNU University Museum is seeking a passionate and qualified candidate to specialize in the integrative study of dark taxa, which are diverse yet poorly understood groups often characterized by small body sizes and complex taxonomy. This project will utilize advanced methodologies to systematically investigate a designated dark taxon, with a primary focus on refining our understanding of its systematics and ecology within an evolutionary context. Given the challenges posed by the Anthropocene and climate change, understanding dark taxa dynamics is vital for biodiversity preservation and informing conservation strategies. The successful candidate will utilize the department's resources, including natural history collections, molecular laboratories, and computational tools, to advance our knowledge of dark taxa and their evolutionary adaptations. The successful candidate will develop and employ innovative and multidisciplinary techniques to the study of species at scale. Novel approaches could include the use of robotics, artificial intelligence or machine learning, integration of novel data sources for species delimitation, or revolutionary approaches to species description.

NTNU is an internationally oriented university with a main profile in science and technology, with headquarters in Trondheim, Norway. It is Norway's biggest university, with over 43,000 students (approximately 10% international).

Deadline: 1 June 2024

For more information and to apply for this position: <https://www.jobbnorge.no/en/available-jobs/-job/261542/phd-candidate-in-dark-taxon-science> Contact: Associate Professor Emily Hartop emilydothar-topatntnu.no

Emily Hartop <emily.hartop@ntnu.no>

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ing@mcmaster.ca)

Potsdam-Berlin Modelling Symbioses

Project Title: Modelling context-dependent shifts in the forms of symbioses

Project Description: Symbiotic interactions - representing prolonged physical associations of several species - are common in natural systems and can determine population dynamics, species persistence and ecosystem functioning, as demonstrated for example in coral reefs and plant-pollinator networks. Symbiotic interactions can take different forms including parasitism, mutualism and competition. Depending on the underlying costs and benefits of the symbiotic interaction, the form of symbiosis may shift between different types of species interactions, e.g. mutualism and predator-prey interaction (see figure). While recent work has shown that the costs and benefits of symbioses depend on the densities of the symbiosis partners, we currently lack an understanding of how the form of symbioses depends on species traits and the overall food web context. This is particularly important as individuals and populations may adapt their traits to altered environmental conditions and as the food web structure may strongly vary across time and space. Hence, we want to improve general theory in community ecology by accounting for context-dependent changes in the form of symbiosis including the species' potential to adapt to altering conditions in a food web context.

The project is embedded into a network of experimental and theoretical working groups across Germany, conducting regular workshops and meetings promoting international networking. The prospective PhD student will join the working group of Prof. Dr. Ursula Gaedke, jointly supervised by Dr. Toni Klauschies. The prospective PhD candidate has the opportunity to closely interact with an experimental PhD student addressing the same overarching topic in our working group and related research groups on Campus. They can join the Potsdam Graduate School (PoGS) allowing for a broad interdisciplinary training of soft skills and early career development. The unique location of our campus in Park Sanssouci is part of a historical place in Potsdam providing a fruitful scientific environment and good working atmosphere.

Your qualification: MSc degree in Ecology or other relevant subjects such as Physics, Mathematics or Environmental Science. We are seeking enthusiastic and

committed candidates who enjoy ecology and applied mathematics with a solid background in ecology and ecological modelling. The successful candidate is expected to implement and analyze numerically differential equation models with a modern programming language such as Python, MatLab or Mathematica. Very good English writing and communication skills are expected, German is an asset but not essential.

Application: To apply, please send the following documents as a single PDF to gaedke@uni-potsdam.de (the position is open until it is filled)

- * Cover letter, including a statement of motivation and from when on you would be available
- * Detailed curriculum vitae including a description of your pre- knowledge in (theoretical) ecology, programming and former research activities
- * Certifications of education
- * If possible, provide letters of recommendation from previous supervisors

Ursula Gaedke <ursula.gaedke@uni-potsdam.de>

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Sydney PollinationMatingSystems

The Hawkesbury Institute for the Environment (HIE) is offering two research scholarships to highly motivated PhD candidates to study pollinator abundance, diversity and behaviour in native seed production areas, and how pollinators influence plant mating patterns and seed quality. The project is co-funded by Greening Australia, Western Sydney University's Graduate Research School, and the Ian Potter Foundation.

Addressing Australia's challenges of biodiversity loss and climate change is hampered by limited availability of good quality native seed. Regional Seed Production Areas (SPAs) are thus required to produce stocks of resilient, healthy seeds suitable for a changing climate. Consequently, we also need to know how different horticultural practices and planting designs influence seed yield and quality in SPAs. Given the importance of pollinators to the yield and genetic quality of SPA-produced seed, it is essential to investigate pollinator visitation and performance on key plant species in SPAs. This project will use innovative fieldwork techniques (plantings, exclusions) and technologies (eDNA, cam-

eras) to understand which animals pollinate selected Australian native plants and how SPA design influences their pollination, seed yield and seed quality.

Shortlink: <https://tinyurl.com/2snw929c> Please share with potential candidates and email to discuss. Regards Paul

Dr Paul Rymer | Associate Professor Hawkesbury Institute for the Environment Western Sydney University Hawkesbury Campus Locked Bag 1797 Penrith NSW 2751 Australia P: +612 4570 1094 | M: 0415 963 139

https://www.westernsydney.edu.au/hie/-people/researchers/doctor_paul_rymer <https://scholar.google.com.au/citations?user=-cRzWkkAAAAAJ&hl=en> westernsydney.edu.au

Paul Rymer <P.Rymer@westernsydney.edu.au>

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SZN Naples EvolutionConservation

Fully funded international PhD position in Biological Sciences at Stazione Zoologica Anton Dohrn (Naples, Italy) The evolution of range shifts: understanding and predicting species' responses to changing environments Application deadline: June 21st 2024 12.00 CET

A PhD studentship (3 years) is available from October 2024 under the supervision of Francesca Raffini, Fabio Crocetta, and Roger Butlin in the Department of Biology and Evolution of Marine Organisms, Stazione Zoologica Anton Dohrn (Naples, Italy).

Why do some populations fail to survive changing environmental challenges (e.g., extinctions) while others thrive and even spread outside their historical range (e.g., biological invasions)? Can we predict whether a population facing a new environment will contract, move, or expand? If you are passionate about climate change, biodiversity, evolution, genomics, and conservation, join us as a PhD student at the Stazione Zoologica Anton Dohrn to explore the evolutionary processes underlying range shifts in a cool marine snail.

We're offering a fully funded position in the Stazione Zoologica Anton Dohrn & Open University (SZN-OU) PhD program. You will be part of a broad international and transdisciplinary team of researchers with excellent training and contributing opportunities.

More information about the position and the application procedure can be found at the following link: <https://raffinifrancescalab.weebly.com/join.html> Please contact us if you have any questions or would like to discuss the position further (Francesca Raffini, francesca.raffini3@gmail.com, <https://raffinifrancescalab.weebly.com>)

Francesca Raffini <francesca.raffini3@gmail.com>

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TennesseeTechU Metabarcoding

Graduate Student Opportunity Environmental DNA Metabarcoding for Assessing Cave Biodiversity

A graduate student opportunity (MS) is available through the Department of Biology (<https://www.tntech.edu/cas/biology/>) at Tennessee Tech University in Cookeville, Tennessee; the starting date is flexible (Fall 2024 or Spring 2025 preferred).

This study will use a combination of traditional and molecular-based survey methods to investigate the effect of bat activity on animal biodiversity and ecosystem function. This study will utilize eDNA metabarcoding, a non-destructive and efficient tool for biodiversity assessment, as well as traditional, morphology-based sampling techniques. Applicants should have a BS in biology or a related field and have an interest in both molecular tools and fieldwork. For more information, please contact Dr. Carla Hurt (churt@tntech.edu). We are looking for highly motivated candidates with a degree in biology or closely related field and a strong academic record. A GPA of at least 3.5 is required. The successful candidate should demonstrate an interest in conservation and molecular genetics. The student will need to possess an aptitude for data analysis and careful research in a molecular genetics laboratory as well as an ability to conduct field work. Previous experience working in a molecular laboratory is preferred but exceptional applicants without experience will be considered. Financial support (stipend and full tuition waiver) will be provided through a teaching and research assistantships and will be renewable annually contingent upon satisfactory performance. Interested students are encouraged to e-mail me (churt@tntech.edu). Please include a short description of your academic background, research interests, and your CV. Screening of applicants

will begin immediately. This position is open until filled.

Carla Hurt, Ph.D. Professor of Biology Tennessee Tech University P.O. Box 5063 Cookeville, TN 38505 931-372-3143 churt@tntech.edu

“Hurt, Carla” <churt@tntech.edu>

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TorontoMetU PlantBiosignals

We are excited to announce a funded PhD position in the Department of Chemistry & Biology at TMU (Toronto Metropolitan University) with a focus on interpreting plant biosignals as a tool for predicting plant response to environments (acclimation, phenotypic plasticity, and reaction norms). The position offers a stipend of \$27,000/year for up to 4 years. The anticipated start date is September 2024, with some flexibility on the starting date.

This project aims to explore the mechanisms of plant communication, specifically how plants use electrochemical signals to respond to environmental challenges such as nutrient stress, insect attacks, and pollination processes. By integrating machine learning algorithms with plant biosignal data, this research will seek to decode and manipulate these signals to enhance plant acclimation and productivity.

Prospective candidates should have a background in evolution, plant physiology, bioinformatics, or a related field. Experience with data analysis tools (Python, MATLAB) and an interest in interdisciplinary research combining plant sciences with technology are highly desirable.

Research Overview:

• $\frac{1}{2}$ Investigate the electrochemical signatures associated with different plant communication processes.

• $\frac{1}{2}$ Employ machine learning techniques to predict plant responses and improve management practices.

• $\frac{1}{2}$ Participate in the development and testing of new tools for real-time plant monitoring.

The successful candidate will be co-supervised by Dr. Lesley Campbell (<https://www.torontomu.ca/chemistry-biology/our-people/lesley-campbell/>) and Dr. Habiba Bougherara (Department of Mechanical, Industrial and Mechatronics Engineering, TMU). Opportunities for experimental research in controlled environments

will also be available. Candidates may also contribute to ongoing collaborations with ag-technology firms.

Interested applicants should submit a CV, unofficial transcripts, and a one-page cover letter detailing their interest and qualifications for the project to Lesley.g.campbell@torontomu.ca by July 15th, 2025.

Lesley Campbell <lesley.g.campbell@torontomu.ca>

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Toulouse Forest Adaptation

Ph.D. Position in Eco-evolutionary response of forests to climate change (M/F)

Thesis subject description

The objective of this thesis will be to combine macro-evolutionary and spatio-temporal data analyses to understand how adaptive potential of plant species is driving their range shifts, community reshuffling and/or productivity in face of climate change. First, the candidate will infer the adaptive potential of forest plant species using a macro-evolutionary approach. For instance, the evolution rate of the climatic niche of plant species could be estimated using a phenotypic evolution model reconstructing the evolution of climatic tolerances and optimum along the plant phylogeny. Second, the effect of the adaptive potential (in combination with other traits implied in species' persistence and migration) on species range shift, community reshuffling and/or productivity will be tested using different datasets (BioShift, NFI data, ...).

The thesis will be supervised by Romain Bertrand (Biodiversity and Environment Research Center; CRBE lab in Toulouse) and will benefit from the expertise of and collaboration with Jonathan Rolland (CRBE), GaeÅÅ Grenouillet (CRBE) and Xavier Morin (CEFE). Strong interactions with the international BioShift working group are also expected.

Work Context The proposed thesis topic is part of FREEvol project aiming to study the eco-evolutionary mechanisms underlying the response of the forest ecosystem functioning in face of climate change. The candidate will be hosted at the Biodiversity and Environment Research Center (CRBE) located in Toulouse on the campus of the University of Toulouse 3 - Paul Sabatier. The candidate will be affiliated with the SEVAB doc-

toral school at the University of Toulouse.

Expected skills The candidate should have strong knowledge in evolutionary, functional and global change ecology, as well as proficiency in statistical analysis tools (notably used to study phylogeny and big database) in the R environment. Previous experience with the plant biological model will be advantageous for the application. The candidate may potentially participate to field sampling of the FREEvol project in a mountainous context (Pyrenees) and must be in good physical condition for missions in challenging terrain.

Contract information

Type of Contract: Fixed-term doctoral contract
Contract Duration: 36 months
Ph.D. Start Date: October 1, 2024
Workload: Full-time
Remuneration Monthly gross flat rate of 2135 euros

How to apply?

Applications should include a detailed CV (2 pages max), a letter of motivation demonstrating your skills for the accomplishment of the PhD, transcripts of Master's grades, and at least two references (persons likely to be contacted). The candidate will include the thesis of his M2 internship if possible.

All required documents need to be uploaded here: <https://emploi.cnrs.fr/Offres/Doctorant/-UMR5300-ROMBER-001/Default.aspx?lang=EN> The deadline for applications is 14/06/2024. Contact: romain.bertrand2[at]univ-tlse3[dot]fr

Jonathan Rolland <jonathan.rolland@yahoo.fr>

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Toulouse Human Palaeogenomics

I am recruiting a PhD student to work on my ERC project anthropYXX.

Website for application details: <https://euraxess.ec.europa.eu/jobs/232339> Keywords: Palaeogenomics, bioinformatics, gender archaeology

Short description: The PhD project, as part of the ERC-funded project anthropYXX, will examine differences in women and men in the past, regarding their health, life history traits, mobility, epigenetics and more, by combining ancient DNA data with other lines of evidence, especially archaeo-anthropological data and stable iso-

tope data. The project involves mainly the development and application of computational pipelines and statistical methods to analyze NGS data obtained from ancient human individuals from France and dated from the Neolithic to the Bronze Age.

Andaine Seguin-Orlando

Andaine Seguin <andaine.seguin@univ-tlse3.fr>

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Tromso Norway Arctic eDNA

We are recruiting a PhD student to be a part of the Norwegian Centre for Arctic Ecosystem Genomics (ArcEcoGen) at the Arctic University Museum, UiT, Tromso, Norway and “Changing Arctic” transdisciplinary Research School at the UiT.

UiT Aurora Center- ArcEcoGen: <https://uit.no/research/arcecoegen> Website for the research school: <https://uit.no/research/changingarctic> More about the PhD project: <https://uit.no/research/changingarctic/-project?pid=837314> ArcEcoGen centre focuses on the combined effect of humans, climate, and biota on northern ecosystem dynamics in the past, present, and future using environmental DNA (eDNA) techniques.

The largest impact of climate change currently seen on arctic vegetation is the northwards expansion of shrub tundra. However, shrubs may be impacted by a range of factors such as herbivory, snow cover, moisture, and temperatures, and the long-term impact are not well known. Ancient DNA has recently revolutionized our understanding of effect of past climate changes as it provides a local vegetation signal of high taxonomic resolution. Unfortunately, the dominant shrub genera, birch (*Betula*) and willow (*Salix*), are rarely distinguished to the species level in ancient DNA studies. This PhD will focus on 1) developing genomic methods for species level identification of shrubs from lake sediments, and 2) using latitudinal gradients of sedimentary ancient DNA to study past effects of environmental changes on arctic greening. We have produced the genome skims of most arctic plant species through the project PhyloNorway, which will provide a basis for method development. Further, the centre has analyzed >50 sediment cores for plant and animal DNA, and these will be available for re-analyses using methods dedicated to distinguishing the shrubs. The available plant DNA data can be used

to reconstruct past temperature, moisture, disturbance, and a range of other environmental factors based on plant traits whereas the mammal DNA data can be used to estimate past grazing pressure. This allows disentangling long-term impact of different drivers of ecosystem changes.

Deadline 5th of June 2024 PhD application portal: <https://www.jobbnorge.no/en/available-jobs/job/-263171/phd-fellow-in-plant-ecology-and-evolution> Contact: Prof. Inger Greve Alsos The Arctic University Museum of Norway UiT - The Arctic University of Norway NO-9037 Tromsø $\frac{1}{2}$ Norway Telephone: +47 77 62 07 96 Email: inger.g.alsos@uit.no For the questions regarding “Changing Arctic” Research school Contact: Dr Galina Gusarova Email: galina.gusarova@uit.no

Galina Gusarova <galina.gusarova@uit.no>

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UHelsinki Virology

The Virus infections and Immunity research group, at the Department of Virology in the Faculty of Medicine of the University of Helsinki, is seeking a Doctoral Researcher to study the significance of persistent viruses on human health.

We provide an inspiring and collaborative environment, combining state-of-the-art tools for viral genetic analysis, at the interface between basic and clinical research. We are located at the Meilahti Campus, University of Helsinki.

The position will be filled from 1.8.2024 or as mutually agreed, beginning with a trial period of 6 months.

Job description: - Your task will be to investigate the genetic makeup of persistent viruses in various clinical contexts. - You will contribute to methods development, as well as perform wet-lab experiments and data analysis. - You will work closely with other members of our group to develop statistical models to estimate the impact of viruses on health and disease. - Aside of doctoral studies, you will be expected to teach, and participate in national and international conferences. - The salary will be in accordance with the University's Salary System.

Requirements: - Master's degree in genetics, microbiology, or alike (health or life sciences) - Fluency in English.

- Enthusiasm for data analysis, method development and experimental work. - Willingness to teach & supervise undergraduates and graduates. - Ability to work independently and in a group. - Desire to work in an international environment. - Experience with data analysis and statistics are considered an asset, yet not a must.

How to apply: Please submit your application to maria.perdomo@helsinki.fi and klaus.hedman@helsinki.fi by 9.6.24

The position will be filled once a suitable candidate has been selected. Please write your application and all accompanying documentations in English and attach them in a single PDF. Include the following documents: - CV (with internships, publications, conferences, awards, contributions, etc.) - A cover letter (maximum of 1000 words) briefly outlining your motivation to apply, background and skills, earliest starting date, and any other/miscellaneous remarks that you wish to make. - PDF copies of your Master's and Bachelor's degree certificates. - Summary of any research project you've been involved in. If the work took place in a team, please clarify your contribution. - Contact information of two referees.

For more information on our research activities: <https://www.helsinki.fi/en/researchgroups/virus-infections-and-immunity> Should you have any questions about the project, the working environment, or the application process, don't hesitate to contact directly:

Docent (MD, PhD) maria.perdomo@helsinki.fi

“Dickson, Zachery” <zachery.dickson@helsinki.fi>

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UIceland EvolutionMarineParasitology

Ph.D. STUDENT MARINE PARASITOLOGY

Applications are invited from suitably qualified students for one Ph.D. student position to work under the supervision of Dr Haseeb Randhawa and Dr Björn Schäffner at the Faculty of Life and Environmental Sciences, University of Iceland (HÍ). The position is funded by the IRF project grant (Conservation of ancient relationships: Assessment of skates (Rajiformes: Rajidae) and their parasite fauna in Iceland, IRF project no. 2410498-051).

The project aims to survey the status of parasitic organisms infecting skate hosts in marine ecoregions off Iceland to aid in the future implementation of conservation efforts of threatened host-parasite systems. Research goals will assess the entire diversity of parasites infecting this host group, assess the genetic diversity of skate species and parasite lineages, and evaluate the status of host-parasite systems based on IUCN Red List criteria to support their conservation through updated conservation agendas. This large-scale project benefits from the international cooperation between the Icelandic academic institution and the Natural History Museum, London, U.K. (NHM). It offers the research basis for one PhD project.

The PhD project contributes to the unknown faunal component of marine parasites infecting skate hosts with an active engagement in the Icelandic marine biodiversity assessment. Main tasks of the Ph.D. student will include (i) the assessment of parasite diversity using a combination of organismal-based and molecular-based studies; (ii) the evaluation of factors influencing the biogeographic distribution and dispersal of marine parasites in Icelandic ecoregions; (iii) the assessment of molecular data of both parasites and skate hosts via targeted sequencing (Sanger sequencing) and genome skimming via next generation sequencing (NGS); (iv) the application of 3D imaging of the neuromuscular system of exemplar parasite species using fluorescent in situ hybridisation (FISH) in combination with confocal microscopy; and (v) the assessment of IUCN Red List criteria of threatened host-parasite systems. The Ph.D. student will further be responsible for producing high quality data in the field and laboratory and will lead or be involved in the preparation of international publications and presentations of research outcomes at domestic and international conferences. Molecular research components, including phylogenetic analysis and barcoding, and FISH technologies will be performed at the NHM, London for at least 12 months of the project duration under the supervision of Dr. Peter Olson (NHM).

The selected Ph.D. student will be enrolled at HI and will conduct research both at HI and the NHM benefiting from world-class scientific infrastructure in Iceland and the United Kingdom with opportunities to spotlight the research and gain valuable experience in science communication. By conducting independent investigations in multidisciplinary research areas utilising facilities both in Iceland and the UK, the student will build a research profile, become experienced in publishing and project management, and gain experience in public engagement and student supervision. The doctoral student will be responsible for leading the main investigations under supervision to enhance and expand the professional career

perspectives, highlighting transferrable strengths with lasting implications on future career prospects. Ph.D. applicants must have been awarded the degree of B.Sc. (Honours) or M.Sc. in Parasitology, Ecology, Marine Biology or a related field, prior to the commencement of the Ph.D. project.

Applications should be made following the link for PhD Position in Marine Parasitology at <https://english.hi.is/vacancies>. Additionally, all materials should be sent electronically to Dr Haseeb Randhawa (email: hrendhawa@hi.is) or Dr Björn Schöffner (email: bjoern@hi.is). Applicants should send a cover letter stating their interest in this position, a recent curriculum vitae and contact information of 2 academic referees.

After initial review, confidential letters of recommendation will be requested from referees. Only complete applications will be reviewed at this time. The deadline for applications is May 31, 2024. Applications will continue to be accepted until this date, but those received after the review date will only be considered if the position has not yet been filled.

Further details regarding the University and how to apply for admission in postgraduate programs can be found at the following homepages: https://english.hi.is/school_of_engineering_and_natural_sciences/-doctoral_studies https://english.hi.is/university/-phd_programmes

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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>

ULausanne Drosophila Adaptation

PhD position in evolutionary genetics of adaptation to undernutrition in *Drosophila*

(deadline extended to 10 May)

A PhD position is available in Tadeusz Kawecki's lab at the Department of Ecology and Evolution, University of Lausanne, Switzerland (<https://www.unil.ch/-dee/kawecki-group>). We are looking for a qualified candidate motivated for research at the interface of experimental evolution, genetics and molecular biology. The student will work in the framework of a

larger project aiming to understand the mechanisms underlying improved tolerance to larval undernutrition generated through long-term experimental evolution in *Drosophila melanogaster*. At least initially, the project will focus on testing the role of a candidate gene involved in ecdysone metabolism in mediating growth responses to nutrition. It will involve a combination of organismal physiological and life history assays with molecular and genetic approaches (LC/MS, CRISPR/Cas9 gene editing, RNAi, enzyme activity rate etc.). For more background on the project see <https://doi.org/10.1093/evlett/qrad018>, <https://doi.org/10.7554/eLife.92465> and <https://doi.org/10.1371/journal.pgen.1011204>. The candidate must have a master's degree in biology, at least basis experience in molecular lab, solid understanding of statistics and experimental design, and aptitude for laboratory research. Some experience with experimental work with *Drosophila* or other insects would be a plus. No-preexisting knowledge of French is required (research-related discussions, seminars etc. and part of teaching are in English) but learning basic French would make living in Lausanne more enjoyable. The job involves some teaching assistantship, but 85% of work time is devoted to thesis work.

With 16 research groups and about 50 PhD students, and with members from over 30 nationalities, the Department of Ecology and Evolution is a diverse and dynamic academic environment. It shares the campus and multiple collaborations with several other departments, including Computational Biology, Fundamental Microbiology and Integrative Genomics. Lausanne is a medium-sized city on the shores of Lake Geneva, surrounded by a wine growing region recognized as a UNESCO World Heritage Site, and within one hour of the Alps. It offers a great variety of cultural, recreational and outdoor opportunities.

Expected starting date ideally between June and September 2024. The initial contract is for 1 year, renewable for a maximum of 4 years in total. $\frac{1}{2}$ Annual gross salary starting at CHF 47,699.- per year plus CHF 9,100 supplement for teaching assistantship.

With 16 research groups and about 50 PhD students, and with members from over 30 nationalities, the Department of Ecology and Evolution is a diverse and dynamic academic environment. It shares the campus and multiple collaborations with several other departments, including Computational Biology, Fundamental Microbiology and Integrative Genomics. Lausanne is a medium-sized city on the shores of Lake Geneva, surrounded by a wine growing region recognized as a UNESCO World Heritage Site, and within one hour of the Alps. It offers a great variety of cultural, recreational and outdoor opportunities.

For further information about the position please contact Tadeusz Kawecki <tadeusz.kawecki@unil.ch>.

Application documents must be submitted online through the University of Lausanne recruitment platform, which also contains the legally binding description of the job: <https://bit.ly/3VKhKCU> (sorry, the platform is a bit complicated).

Applications should include: - a cover letter detailing your research interests, experience and motivation for applying - CV - a summary of your master project (and other relevant research projects) - a copy of your Masters diploma/certificate (if you haven't yet finished your Masters indicate the expected date) - the names and contact details of 2-3 referees.

Deadline: May 10

UNIL is committed to equal opportunities and diversity. www.unil.ch/egalite UNIL supports early career researchers. www.unil.ch/graduatecampus Tadeusz Kawecki <tadeusz.kawecki@unil.ch>

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ULausanne ModellingBacterialEvolution

PhD in modelling bacterial evolution, ecology and epidemiology

- Four years - Flexible start-date from 1.8.2024 - Apply by 17.06.2024

Join the Evolutionary Epidemiology group as we move to the University of Lausanne!

The group works at the intersection of evolutionary theory, microbial ecology, and public health. We use mathematical and statistical modelling to address problems in public health and to answer fundamental questions about bacterial ecology and evolution.

We are looking for a PhD student to join our team! There are multiple projects available. Depending on the interests of the student, possibilities include: - Developing models to predict antibiotic resistance frequencies. - Modelling how interactions within the gut microbiome shape bacterial populations. - Uncovering the role of plasmid transmission and horizontal gene transfer in the spread of clinically concerning traits.

The Evolutionary Epidemiology group, led by Sonja

Lehtinen, is a friendly, growing team, soon to be based at University of Lausanne's Computational Biology Department. We are mostly focused on theory and computation, working with existing genomic and epidemiological datasets, as well as running our own sampling studies. We are affiliated with the NCCR Microbiomes, providing fantastic opportunities for collaborations with experimental, clinical and other modelling groups.

We're looking for curious, collaborative and thoughtful researchers. If you like our papers, we want to hear from you!

Your profile The position is ideal for someone combining an interest in theory, real-world data and public health. Curiosity and an aptitude for learning are more important than specific background. Essential requirements are: - Strong analytical and quantitative skills (MSc in a quantitative subject). - Fluency in at least one programming language (e.g. R, Python, C++, Matlab). - Excellent written and oral communication skills in English.

What we offer - An exciting opportunity to shape your research working in a supportive and stimulating environment. - Exceptional scope for collaboration through the NCCR Microbiomes network. - Access to top-notch resources and excellent support for further learning and professional development. - Plenty of opportunities to attend conferences and to build your scientific network. - Attractive salary, beautiful location and excellent quality of life in one of the best small cities in the world.

Apply here: https://career5.successfactors.eu/-career?company=universitdP&career_job_req_id=-21658&career_ns=job_listing&navBarLevel=-JOB_SEARCH We welcome informal enquiries (no applications) at: sonja.lehtinen@env.ethz.ch There will be a further position advertised later, so please get in touch even if the proposed timing isn't quite right for you!

Evolutionary Epidemiology group: <https://tb.ethz.ch/-research/lehtinen-group.html> NCCR Microbiomes: <https://nccr-microbiomes.ch/> Lehtinen Sonja <slehtinen@ethz.ch>

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ULille EvolPlantMatingSystem

PhD offer

We propose a fully funded 3-year PhD fellowship starting in October 2024, aiming at characterizing the evolution of the mating system of a protected plant species with high conservation value, the Dune Pansy (*Viola tricolor* ssp. *curtisii*). The student will be based at University of Lille.

Title of the thesis: Conservation and management of an endangered species, the dune pansy (*Viola tricolor* ssp. *curtisii*): mating system evolution and reproductive success along its geographic range.

Supervisors : Anne Duputié (MCF), Isabelle De Cauwer (MCF), Jean-François Arnaud (PR) Location : Unité Évolution, Écologie et Paléontologie UMR 8198 CNRS / Université de Lille - Faculté des Sciences et Technologies 59655 Villeneuve d'Ascq cedex, France.

How to apply: To apply, please send: — a CV — a short motivation letter (max 1 page) — university certificates with official grades in a single PDF — contact details from two referees and/or recommendation letters to Jean-François Arnaud (jean-francois.arnaud@univ-lille.fr), Anne Duputié (anne.duputie@univ-lille.fr) and Isabelle De Cauwer (isabelle.de-cauwer@univ-lille.fr).

Only complete applications received by 15 May 2024 will be considered. The selection criteria will be the excellence of the curriculum vitae and the adequacy between the professional project of the candidate and the thesis subject.

Requested skills: The candidate must hold a Master's degree in ecology or evolutionary biology, and have an interest in fieldwork, experiments in controlled environments, molecular biology and statistical analysis. Initial experience in one or more of these fields would be appreciated. Good oral and written communication skills are required.

Summary of PhD project:

Species specific patterns of genetic structure are influenced by spatial factors and by life-history traits, especially reproductive and dispersal related traits. These factors generate striking spatial genetic structure both at the scale of the species' distribution range but also at very fine scales of investigation. These spatial genetic patterns reflect both local adaptations and random variations that are not homogenized by gene flow. This thesis will explore the evolution of the mating system of a protected plant species with high conservation value, the Dune Pansy, and its impact on the levels of genetic diversity and on the reproductive success of individuals. The southern boundary of the geographic range of the Dune Pansy extends along the coastline of the "Hauts-de-France" region, where populations are exposed

to anthropogenic disturbances along the coastline and to potential reduction in pollinator density. A biogeographical break has been observed between core and marginal populations, with trailing-edge populations showing higher levels of genetic differentiation, reduced genetic diversity, and higher levels of selfing estimated through progeny arrays.

The objectives of this thesis are as follows: — Analysing the intra-population sources of variation in mating system (propensity for selfing) in relation to floral traits and pollinator abundance, while assessing pollen limitation in situ. — Evaluating the evolution of floral traits and the mating system at the center and the edge of the geographic distribution of the species over a few generations. — Assessing the feasibility of reinforcing wild populations located in the "Hauts-de-France" region using individuals coming from the Netherlands, evaluate their genetic disparity, and formulate operational recommendations for conservation management. — Determine if the Dune Pansy hybridizes with closely-related species in natural habitats, and if so, formulate management recommendations for these sites.

Jean-François ARNAUD Unité Evolution, Ecologie et Paléontologie UMR 8198 CNRS / Université de Lille - Faculté des Sciences et Technologies 59655 Villeneuve d'Ascq cedex, France Tel. : (+33) 03 20 33 62 96 ; Fax : (+33) 03 20 43 69 79 Mailto:jean-francois.arnaud@univ-lille.fr

Web Lab.: <http://eep.univ-lille.fr/> Perso. Page: <https://eep.univ-lille.fr/user/jean-francois.arnaud/> Master BEE : <https://master-bee.univ-lille.fr/> Jean-François Arnaud <jean-francois.arnaud@univ-lille.fr>

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UmeaU EvolMicrobeInteractions

Laura Carroll and Eric Libby are recruiting a PhD student as part of a national Data-Driven Life Sciences (DDLs) program in Sweden. The student will be based at the Integrated Science Lab (IceLab, <https://www.umu.se/en/research/infrastructure/integrated-science-lab-icelab/>) at Umeå University, a recently awarded 'Center of Research Excellence'. The PhD position is fully funded with a variety of career and scientific development opportunities from both DDLs and IceLab. The PhD will be in Computational Sci-

ences and thus interested applicants must have a masters degree in a computational science.

The PhD project addresses a fundamental topic in evolution concerning how and why microbes interact in the ways they do. We know that microbes have many possible options, or strategies, regarding what resources they consume to grow. Depending on these choices, pairs of microbes may either compete or cooperate. What actually happens depends on the ability of microbes to correctly assess the situation, i.e. solve a type of inference problem. Yet, little is known about the difficulty of this inference problem or what heuristics organisms might evolve. The PhD student will use machine learning techniques to infer the mechanisms by which microbes make decisions, bioinformatic techniques to compare these mechanisms to empirical data, and game theory and modeling approaches to improve our understanding. The project has many exciting directions and opportunities for different quantitative tools and approaches. The last day to apply is June 17, 2024 with an expected start date in Fall 2024.

Information about the DDLs program: This position is part of a national data-driven life science (DDLs) program recruitment. DDLs uses data, computational methods, and artificial intelligence to study biological systems and processes at all levels, from molecular structures and cellular processes to human health and global ecosystems. The SciLifeLab and Wallenberg National Program for DDLs aims to recruit and train the next generation of data-driven life scientists and to create globally leading computational and data science capabilities in Sweden. The program is funded with a total of 3.1 billion SEK (about 290 MUSD) over 12 years from the Knut and Alice Wallenberg (KAW) Foundation. In 2024, the DDLs Research School will be launched, and 20 academic and seven industrial PhD students will be recruited. During the course of the DDLs program, more than 260 PhD students and 200 postdocs will be part of the Research School. The DDLs program has four strategic areas: cell and molecular biology, evolution and biodiversity, precision medicine and diagnostics, epidemiology and biology of infection. For more information, please see <https://www.scilifelab.se/data-driven/ddls-research-school/> Apply here:

This is an open call. Please see the following link for more information and details on how to apply. <https://www.umu.se/en/work-with-us/open-positions/-phd-position-in-computational-sciences-within-the-national-data-driven-life-sciences-program-727379/> Questions? If you have any questions please contact Eric Libby (eric.libby@umu.se) or Laura Carroll (laura.carroll@umu.se).

Eric Libby <eric.libby@umu.se>

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UMissouri StLouis PlantEvoDevo

Are you fascinated by the diversity of plants and their reproductive structures? Is your goal a career in academia, biotechnology, agriculture, or government agencies in the most botanically focused city in the world? The Marchant Lab is opening at the University of Missouri - St. Louis and is recruiting PhD students. We are particularly interested in students with a background in plant biology, cellular biology, developmental biology, evolution, bioinformatics, or conservation; however, highly self-motivated students with a passion for botany and science are welcome to get in touch.

Who we are: The Marchant Lab (<https://www.marchantlab.com/>) is an innovative and collaborative research group at the forefront of both applied and basic plant sciences. We use single-cell RNA-sequencing (scRNA-seq), comparative genetics/genomics, and digitized herbarium specimens to investigate questions in plant reproductive biology, development, ecology, and evolution using both model and non-model plant systems. We are particularly interested in the biology and evolution of anthers. In the lab you will pursue a primary project plus there are ample opportunities for collaborative projects within the lab and with diverse cooperators. The lab atmosphere is supportive, inquisitive, and committed to providing each student with the most effective training cognizant with individual goals.

Where we are: We are based in the Biology Department at the University of Missouri - St. Louis (UMSL). With its world-class universities (UMSL, Washington University, St. Louis University), research institutions (Donald Danforth Plant Science Center, Missouri Botanical Garden), and agricultural companies (Bayer, Pivot Bio, Yield Lab), St. Louis has the highest concentration of plant science PhDs in the world and is an ideal setting for anyone interested in plant biology. St. Louis is one of the most livable cities in the US and was recently ranked the top city to start a career in.

If you are interested in joining the lab, email Dr. Marchant (dblainemarchant@umsl.edu) your CV and a brief statement on your background and research interests.

“dblainemarchant@umsl.edu”
<dblainemarchant@umsl.edu>

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golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

UppsalaU EvolutionaryGenomics

A PhD student position in evolutionary genomics, with focus on diversity and evolution on lichen-associated basidiomycetes, is available in my group at Uppsala University, Sweden.

Start date autumn 2024, deadline to apply 11 June 2024.

Please help me spread this to potential candidates!

Please find all the details and instructions on how to apply at: <https://uu.varbi.com/en/what:job/-jobID:728238/> Best regards, Veera Tuovinen Nogerius

Researcher Evolutionary biology Department of Ecology and Genetics Uppsala University Mobile: +46762513988

Page Title

Ni_{1/2}r du har kontakt med oss p_{1/2} Uppsala universitet med e-post si_{1/2} inneb_{1/2}r det att vi behandlar dina personuppgifter. Fi_{1/2}r att li_{1/2}sa mer om hur vi gi_{1/2}r det kan du li_{1/2}sa hi_{1/2}r: <http://www.uu.se/-om-uu/dataskydd-personuppgifter/> E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: <http://www.uu.se/en/about-uu/data-protection-policy> Veera Tuovinen Nogerius <veera.nogerius@ebc.uu.se>

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UppsalaU HostSymbiontEvolutionaryGenomics

A 4-year PhD position to work on evolutionary genomics of Host-Symbiont interactions is available in the lab of Lisa Klasson in the Molecular Evolution programme at Uppsala University.

Project description: The project aims to study how symbiotic interactions between bacteria and animal hosts

affect both partners' genetic material and evolution. Our model system is the endosymbiotic bacterium Wolbachia in different Drosophila species, primarily from the willistoni group. Using mostly large-scale sequencing of both Drosophila and Wolbachia genomes and performing comparative genomics, the goal is to determine the genetic factors in both Wolbachia and Drosophila that determine this variability in host-symbiont interaction and to elucidate the evolutionary events that took place to create it.

Duties: The work will mostly consist of bioinformatic analyses of sequence data from different species of the Drosophila willistoni group. To a lesser extent, the work might also include handling Drosophila and using standard molecular lab techniques such as DNA extractions and PCR. The Ph.D. student shall primarily focus on postgraduate studies, but other duties related to teaching and administrative work may be involved, up to a maximum of 20 % of the time.

Requirements: To meet the entry requirements for doctoral studies, you must hold a Master's (second-cycle) degree in bioinformatics, evolutionary biology, molecular biology, or another subject that the employer considers to be equivalent. The applicant must have a good ability to work independently as well as in a group. A prerequisite is good written and oral skills in English, as the work takes place in an international environment. To work creatively, goal-oriented and structured are central abilities during a doctoral education and will therefore be given special consideration. Previous experience of working with sequence data and bioinformatic analyses as well as familiarity with work in a Linux/Unix environment and a scripting language such as Python, R or Perl is highly desirable.

Read more and apply at: <https://www.jobb.uu.se/-details/?positionId=3D722807> Lisa Klasson <lisa.klasson@icm.uu.se>

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UppsalaU HumanPopulationGenetics

PhD position in human population genetics and ancient DNA analyses

Are you interested in working with human population genetics, with the support of competent and friendly

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

We're looking for a dedicated PhD student to join our team focused on the DNA research of African populations, both modern and ancient. The selected candidate will be responsible for laboratory work with ancient DNA and the bioinformatic analysis of population genetic data. The goal is to understand African population structure and their genetic responses to changes in lifestyle and environment over time. This position offers a chance to deepen our knowledge of Africa's human population history.

Research will be conducted within the Schlebusch group, Human Evolution Program, Department of Organismal Biology (Evolutionary Biology Center, Uppsala University). The group is funded by the Knut and Alice Wallenberg Foundation and the Swedish Research council. The Schlebusch group is specifically interested in studying human history on the African continent and uses genetic data from modern day populations and ancient remains as a tool for the inference of African history. The Human Evolution Program, in which the Schlebusch group is situated, has a broad interest in population genetics and human evolution. There are ample opportunities to work closely with post-docs and PhD students that focus on related projects. The research environment is international with English being the working language. See Prof. Schlebusch web-page for more information on the research and recent publications (<http://www.iob.uu.se/research/human-evolution/schlebusch/>) and Human Evolution Program web-page for more information on the Program (<http://www.iob.uu.se/research/human-evolution>).

Duties

The work consists of bioinformatic working in Uppsala University's computer cluster, implementing scripts and running population genetic software as well as programming and statistical analysis. Additionally, the position encompass work in an ancient DNA clean-lab environment.

Requirements

Completed university education of 240 university points (högskolepoäng, hp) out of which 60 hp on advanced level corresponding to master degree in relevant field. The ideal candidate is highly motivated with thorough education and strong interest in evolutionary genetics/genomics, population genetics and human evolution.

Good knowledge of English in speech and writing. Great emphasis is placed on personal qualities such as planning and organizational skills, accountability and accuracy.

Additional qualifications

Previous experience with large-scale genetic data analysis, bioinformatics, programming and implementation of aDNA bioinformatic pipelines is advantageous. Experience of work at molecular biology research lab or cleanroom. Experience of work with next generation sequencing methods, DNA extraction, PCR and DNA quantification. Experience and knowledge about human population genetics. Fieldwork experience (especially in Africa) and an interest/background in African history.

About the employment The employment is a temporary position according to the Higher Education Ordinance chapter 5 § 7. Scope of employment 100 %. Starting date 2024-08-01 or as agreed. Placement: Uppsala

For further information about the position, please contact: Carina Schlebusch carina.schlebusch@ebc.uu.se.

Please submit your application by 7th June 2024, UFV-PA 2024/1731.

Uppsala University is a broad research university with a strong international position. The ultimate goal is to conduct education and research of the highest quality and relevance to make a difference in society. Our most important asset is all of our 7,600 employees and 53,000 students who, with curiosity and commitment, make Uppsala University one of Sweden's most exciting workplaces.

Read more about our benefits and what it is like to work at Uppsala University <https://uu.se/om-uu/jobbarhos-oss/> Please do not send offers of recruitment or advertising services.

Submit your application through Uppsala University's recruitment system: <https://www.jobb.uu.se/details/?positionIdr8524> Placement: Department of Organismal Biology

Type of employment: Full time , Temporary position

Pay: Fixed salary

Number of positions: 1

Working hours: 100%

Town: Uppsala

County: Uppsala län

Country: Sweden

Last application date: 2024-06-07



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UQuebecARimouski CellAdaptation

Graduate position: Master degree project in evolutionary cellular biology

We are seeking a highly motivated and passionate graduate student in biology interested in studying the molecular bases of adaptation. The project aims to assess the impact of environmental conditions across an altitudinal gradient on adaptive potential using yeast as a model. Altitudinal gradients are characterized by significant environmental changes over a relatively short geographic distance. Thus, they constitute a relevant model system for studying the impact of environmental factors on biodiversity. The project details are open for discussion with the interested candidate.

Preferred candidates would have experience in molecular biology, microbiology, genomics and/or bioinformatics. The successful candidate will be supervised by Dr Souhir Marsit and will be based at Département de Biologie, Chimie et Géographie, Université du Québec À Rimouski (UQAR), Rimouski, Canada. <https://www.uqar.ca/etudes/etudier-a-l-uqar/programmes-d-etudes/3440> *Requirements:*

-BSc in biology.

-Experiences and skills in microbiology, molecular biology, genomics and/or bioinformatics would be appreciated.

Starting date: July - september 2024

Duration: 2 years.

Interested applicants should submit, in a single PDF file, a CV, a copy of their academic transcript, a cover letter outlining their research interests and the contact information of three people who can be contacted for reference to souhir.marsit@gmail.com.

Projet de Master en Biologie cellulaire et Évolutive

Nous recherchons une étudiante ou un étudiant très motivé(e) et intéressé(e) par l'étude des bases moléculaires

de l'adaptation. Le projet vise à évaluer l'impact des conditions environnementales à travers un gradient altitudinal sur le potentiel adaptatif en utilisant la levure comme modèle. Les gradients altitudinaux se caractérisent, en effet, par des changements environnementaux importants sur une distance géographique relativement courte. Ils constituent ainsi des systèmes modèles pertinents pour étudier l'impact des facteurs environnementaux sur la biodiversité. Les détails du projet sont à discuter avec le candidat intéressé.

Les candidats ayant une expérience en biologie moléculaire, en microbiologie, en génomique et/ou en bio-informatique seraient appréciés. Le candidat retenu sera supervisé par le Dr Souhir Marsit et sera basé au Département de Biologie, Chimie et Géographie, Université du Québec À Rimouski (UQAR), Rimouski, Canada. <https://www.uqar.ca/etudes/etudier-a-l-uqar/programmes-d-etudes/3440> *Exigences:*

-Baccalauréat (licence) en biologie.

-Expériences en microbiologie, biologie moléculaire, génomique et/ou bio-informatique seraient appréciées.

Date de début : juillet - septembre 2024

Durée : 2 ans.

Les candidats intéressés peuvent soumettre leur dossier (un seul fichier PDF) composé d'un CV, une copie de leurs relevés de notes, une lettre de motivation décrivant leurs intérêts de recherche et les contacts de 3 référents à souhir.marsit@gmail.com.

souhir.marsit@gmail.com

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UQueensland Australia PlasticityDynamics

PhD positions in Ecology and Evolutionary Biology University of Queensland, Brisbane, Australia.

Effects of Phenotypic Plasticity and/or Extreme Events on Ecological Dynamics

The HartLab at the University of Queensland focuses on understanding why population sizes of plants and animals rise and fall. This is one of the oldest and most fundamental problems in ecology, and underpins our ability to predict environmental impacts, and to manage threatened, harvested, and pest species. We are

currently recruiting PhD students to work on projects that address two important problems in this area of research:

1. The effects of phenotypic plasticity on ecological dynamics. Dominant explanations for the rise and fall of species have focused on environmental variation and species interactions but have typically excluded the ability of species to rapidly evolve or change plastically in response to changing conditions. This project will combine theory, lab and field experiments, molecular tools, and statistical analyses, to understand when and how phenotypic plasticity affects the dynamics of plants and animals in an era of global environmental change.
2. Dramatic ecology For the most part, ecological systems 'bubble along', changing slowly and/or in small ways but not really changing much at all. But ecological systems sometimes change dramatically, experiencing big changes over short periods of time. Examples include plagues and outbreaks, population collapses, as well as the 'turning over' of entire ecosystems. Sometimes these dramatic changes occur when systems reach a tipping point; other times these dramatic changes occur because of the effects of exogenous shocks such as extreme climatic events (e.g. heatwaves and floods). This project will explore these dramatic changes in ecological systems, primarily through theory development and/or analyses of time series data. There may also be opportunities for new empirical work. The ultimate goal of this work is to improve our ability to identify, understand, and predict these large, rapid, sometimes unprecedented, and often consequential changes, in population and community dynamics.

About us The HartLab is a group of biologists who use a suite of quantitative approaches (theory, smaller-scale [and clever] manipulative experiments, large-scale mensurative experiments, meta-analyses, analyses of large datasets [e.g. time series]) to solve big biological problems. We are motivated to increase our understanding of how our biological world works, particularly in the context of global environmental change.

We increasingly focus on the ecology of freshwater ecosystems. These systems provide wonderfully challenging opportunities for combining theory, observations, and experiments to discover how nature works. And importantly, freshwater ecosystems are, per unit area, the most biodiverse ecosystems on the planet, yet they remain underexplored, underappreciated, and under threat.

Our research is currently supported by grants from the Australian Research Council and private industry. Our group currently includes three PhD students and one senior research fellow, with additional PhD and Honours students due to begin in the second half of 2024.

We have extensive, active, research collaborations both within Australia and internationally.

The University of Queensland is a research-intensive University and the School of the Environment comprises more than 200 academic and postdoctoral research staff, and ~200 higher-degree research students. The students and projects will benefit from the School's formidable research expertise in ecology, evolutionary biology and genetics, physiology, and mathematical, statistical and computational biology. According to the Center for World University Rankings by Subject, the School is a global leader in biodiversity conservation (ranked #1), marine and freshwater biology (ranked #3), ecology (ranked #6), and environmental science (ranked #6). Just as importantly, life is good here, there are koalas, and the beach is pretty close.

About you We are looking for curious and creative students who can demonstrate a strong motivation to understand ecological and evolutionary dynamics, and who have a strong quantitative focus and a desire to work in a supportive and engaging team environment. We are particularly interested in candidates with one or more of the following attributes, each of which is desirable but not necessarily essential:

- a) a background in ecology and/or evolutionary biology,
- b) strong statistical, mathematical and/or computational skills,
- c) experience with laboratory and field experimental/sampling designs,
- d) some experience with molecular genetics,
- e) experience working in freshwater ecosystems,
- f) strong written and verbal communication skills.

PhD scholarship and application process

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UStrasbourg
TurtleComparativePhysiology

bonjour,

The Institut Pluridisciplinaire Hubert Curien(IPHC,

at the beginning of the contract

-Being self-motivated, organized, and highly team-oriented

-Proficiency in English (oral and written)

-Background in bioinformatics, especially genomics, transcriptomics and metagenomics.

-Familiarity with microscopy, molecular biology techniques, and microbiology techniques will be an advantage.

The requirements listed above need to be met before the employment starts, but not necessarily by the application deadline.

We offer a scholarship for up to 48 months. Starting date: 1 October, 2024

Application deadline: 3 June, 2024

More details about the application process at the website: <https://ibe.biol.uw.edu.pl/en/835-2/research-groups/eukaryotic-microorganisms/genomics-and-evolution-of-eukaryotic-microorganisms/positions>

Please feel free to reach out with any questions at the email address listed below.

Anna Karnkowska

Institute of Evolutionary Biology

Biological and Chemical Research Centre

University of Warsaw, Warsaw, Poland

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

Anna Karnkowska Associate Professor Institute of Evolutionary Biology Faculty of Biology & Biological and Chemical Research Centre University of Warsaw ul wirki i Wigury 101, 02-089 Warszawa

Anna Karnkowska <a.karnkowska@uw.edu.pl>

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UWesternAustralia BeetleEvolution

Doctoral (PhD) student position on the evolution, phylogenomics, and taxonomy of Australian carabid beetles (Coleoptera, Carabidae)

During this project you will collaborate to advance methods of monographic and revisionary systematic work in insects by combining comparative morphology with genomics. This project intends to discover, describe, and document insect species of the Pilbara Region of Western Australia and place them in their global and historical phylogenetic context. Selected groups of Abacetini and Harpalini (Coleoptera, Carabidae) will be the focus of the project. There is considerable scope for the successful applicant to develop projects investigating evolutionary questions of interest.

This is an open call for a fully-funded PhD student position as part of a University of Western Australia, Western Australian Museum, and University of California, Berkeley project and includes a full scholarship, tuition waiver, and funding for research costs/fieldwork. You will be enrolled at the University of Western Australia, a top-100 global university, also ranked number one in Australia for biological sciences.

Open to global international and Australian domestic students.

Applicants with experience in entomology and/or phylogenetics are encouraged to apply. Please send your updated curriculum vitae and a letter outlining your interests in this project to toniko-lai.tatarnic@museum.wa.gov.au

Renee Catullo <renee.catullo@gmail.com>

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VetMedU Vienna ComputationalEvolutionaryBiol

PhD position in computational evolutionary biology

Title: Unraveling the impact of gene flow during species divergence

We are seeking a highly motivated PhD student with skills in computational biology and/or biostatistics to embark on this cutting-edge research project. The goal is to develop more realistic models and computationally efficient methods that will enable the analysis of extensive phylogenomic datasets, which are now commonplace in evolutionary biology. The methods will be implemented into the widely-used software RevBayes.

Understanding how species diverge through the exchange of genetic material is a fascinating area of study. While evidence of gene flow exists across diverse biological groups, there is a critical need to assess its prevalence and impact at phylogenetic time scales. Current models fall short, particularly when evaluating gene flow along multiple speciation events, especially at deep time horizons.

This project will develop more complex phylogenetic models and draw insights from diverse organisms, including grasshoppers, fruit flies, persimmon trees, and fireflies. We aim to answer these three key questions:

* What is the evolutionary significance of gene flow during species divergence? * Are most regions of the genome affected by gene flow, or do some regions show an elevated impact of gene flow? * What is the interplay between natural selection and gene flow during species evolution?

The successful candidate will be stationed at the University of Veterinary Medicine Vienna and affiliated with the Vienna Graduate School of Population Genetics. For more information, visit <https://www.popgen-vienna.at/>. There is also a potential opportunity for a 6-month to one-year assignment abroad.

Requirements: The main requirement of this position is that the candidate is proficient in at least one coding language. A second skill would be either (1) understanding of evolution and handling of genomic data or (2) statistical inference.

Salary: 14 times a year, according to this table <https://www.fwf.ac.at/en/funding/steps-to-your-fwf-project/further-information/personnel-costs> How to Apply: Interested candidates are invited to submit their applications, including a brief CV and a one-page cover letter outlining their research experience and interest in the project, to ruiborges23@gmail.com. The application deadline is May 30th; however, applications will be evaluated on a rolling basis until a suitable candidate is selected.

Candidates interested in further information can contact me at ruiborges23@gmail.com.

Rui Borges

Group Leader Institute of Population Genetics
Vetmeduni Vienna Veterinaerplatz 1 A-1210 Vienna

Rui Borges <ruiborges23@gmail.com>

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WageningenU Insect Virome Analysis

PhD position in insect virome analysis

Are you looking for a PhD position focusing on the interplay between insects and their microbiomes? Are you a bioinformatician who wants to develop and apply computational methods for microbiome analysis and virus discovery using sequencing data sets? Then this PhD vacancy might be of interest to you.

Like all organisms, insects have a native microbiome, including bacteria, fungi, and insect viruses. Many insects also serve as vectors to transmit viruses among animals or plants and the insect microbiome potentially influences this virus transmission. Therefore, the focus of insect virus research expanded from individual virus-host systems to metagenomics, i.e., bulk sequencing the genetic content of environmental samples without the need for prior virus isolation.

In this project, we will study whiteflies, a diverse group of agriculturally important insects that feed on plants and can transmit a variety of plant viruses. Whiteflies pose a severe threat to many plant crops, both in greenhouses and open fields. The management of this pest currently relies on insecticides; however, most whitefly species have already developed insecticide resistance. Biological control based on microorganisms is a promising tool; however, this requires fundamental understanding of the microbiome of whiteflies and its impact on virus transmission.

In this PhD project, you will contribute to developing bioinformatics approaches for microbiome analyses in insects, with a focus on the virome. You will discover the microbiome players and reconstruct virus genomes from metagenomics sequencing data of individual whiteflies. You will then associate this information with additional meta-data (such as geographic location and host plant) and, additionally, zoom in on the co-occurrence of different microorganisms in individual whiteflies to reveal possible synergistic or antagonistic effects. This project will thus contribute to understanding the factors that shape the viromes of insects.

You will integrate data from public sources, from international collaborations and from individual insects to be sampled in the Netherlands. Beyond the scientific and potential application merits, you will build a network for your future career both within and outside Wageningen University.

The research is embedded in two chair groups at Wageningen University: the Bioinformatics Group led by prof. Dick de Ridder and the Laboratory of Virology led by prof. Monique van Oers. Your daily supervisors will be dr. ir. Astrid Bryon and dr. Anne Kupczok, with complementary expertise: insect virology, virome analysis, and agricultural entomology (Astrid Bryon) and bioinformatics, comparative genomics, and molecular evolution (Anne Kupczok). The position is for four years and you will join the graduate school PE&RC.

Your qualities * a successfully completed MSc degree in bioinformatics or a related field * demonstrable experience in high-throughput sequencing data analysis and comparative genomics; * proficiency in programming (e.g., python); * affinity with virology, ecology, and molecular evolution; * enthusiasm for working in close collaborations with experimental biologists; * a proactive attitude and teamwork skills and are committed to obtaining a PhD; * a very good level of oral and written English.

You can find more information and the application link here: <https://www.wur.nl/en/vacancy/phd-position-in-insect-virome-analysis.htm> “Kupczok, Anne” <anne.kupczok@wur.nl>

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AMNH NewYork ResAssist AncientDNA

Hello, all!

We have an exciting position opening here at the American Museum of Natural History in New York City. If you have experience or interest in working with ancient DNA, please consider applying! This job involves running the ancient biomolecules lab (AbLab) as well as the historical DNA lab. Come work with us and do

some cutting-edge science!

You can apply here:<https://careers.amnh.org/postings/-4102> Please share across your networks!

Best,

Lauren T. Clark American Museum of Natural History 200 Central Park West, New York, NY e: lclark@amnh.org

p: +1 212-313-7602

Lauren Clark <lclark@amnh.org>

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

BamfieldCenter BritishColumbia PartTimeLabTech FishEvol

Lab Research Technician: University of Connecticut & Bamfield Marine Sciences Centre

A part-time lab research technician position is available to assist with a fish biology project at Bamfield Marine Sciences Center (BMSC) on the west coast of Vancouver Island, British Columbia. The technician will be employed by the University of Connecticut and working for Dr. Dan Bolnick, who is based in the Department of Ecology and Evolution at the University of Connecticut. The position will be funded by a U.S. National Science Foundation (NSF) Ecology and Evolution of Infectious Disease (EEID) grant to study the biology of a tapeworm *Schistocephalus solidus*, as it infects copepods, stickleback fish, and piscivorous birds.

Tasks: The technician will assist in animal care, rearing stickleback fish at BMSC. They will be responsible for monitoring fish health, feeding, and cleaning. They will assist with record keeping. Towards the end of the project the technician will assist with experimental measures of behavior and immunity of the lab-raised fish. The successful applicant will be required to complete the UPEI Experimental Fish certification < <https://www.upei.ca/professional-development/-certificates/experimental-fish> >.

Minimum Qualifications: Applicants must be organized and reliable and have the ability to carry out laboratory research and fish care protocols. Previous educational experience and work records should demonstrate a good work ethic, organizational ability, and interest in scientific research. The successful applicant must have an undergraduate degree (e.g., BSc or BA) or a higher degree.

Preferred Qualifications: Experience with animal care is valuable, especially care of fish or other aquatic organisms. An undergraduate degree in biology or a related field is strongly preferred. A graduate degree (e.g., a Master's degree) would be valuable.

Duration: The appointment will be from late July 2024 through the end of February 2024. The position will assist a full time technician providing days off and emergency coverage, and will have an approximate work schedule of 15 hrs per week, with 4 days on, 10 days off.

Salary depends on experience but is expected to be

between 15 - 25 US\$ per hour.

Applicants should electronically submit a single pdf file containing the following in order:

1. Cover letter, including summary of research experience and career goals
2. CV
3. List of two (or three?) references, with contact information (email, telephone and mailing address) We will request letters directly from these references, after identifying top candidates.

The application pdf file should be emailed to Dr. Daniel Bolnick (daniel.bolnick@uconn.edu). Include the subject line "Field Technician Application: <YOUR NAME>". Applications must be received by June 15, 2024 for full consideration though late applications may be considered.

For questions about this position, please email Dr. Bolnick (daniel.bolnick@uconn.edu). For information about the Bolnick Lab, visit the lab website (<https://bolnicklab.wordpress.com>), and Dr. Bolnick's Google Scholar page < <https://scholar.google.ca/citations?user=Awxm0AAAAAJ&hl=en> >.

The University of Connecticut is an Equal Opportunity Employer. Applicants with questions about disability services can privately discuss their application with the University of Connecticut Disability Services Office.

"Bolnick, Daniel" <daniel.bolnick@uconn.edu>

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Eawag Switzerland Four ClimateChangeAdaptation

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is recruiting for 4 Tenure Track Group Leader Positions on Climate Change Adaptation.

At least one position will be in the general field of biodiversity, and evolutionary biologists are explicitly encouraged to apply.

Aquatic systems, renowned for their rich biodiversity, are vulnerable to the effects of climate change. They are experiencing rapid changes due to rising temperatures, shifting precipitation patterns, and - at higher altitudes - melting glaciers. At the same time, climate change can

lead to changes in water quality, exposing organisms to combinations of chemical or microbial pollution and physical stressors that contribute to biodiversity decline. Given its unique geographical and environmental characteristics, Switzerland offers opportunities for addressing challenges posed by climate change and biodiversity loss in mountainous regions, rivers and lakes.

The detailed announcement of this cluster hire and the application links can be found here: <https://apply.refline.ch/673277/1169/pub/1/index.html> "Vorbürger, Christoph" <Christoph.Vorbuerger@eawag.ch>

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FraunhoferIME Aachen TwoYr TechAssist

Dear EvolDir users, This job might be of interest if you are interested in experiments with plants and exciting novel technological advances for plant cultivation. The position is (initially) for two years. German language skills are a plus (first of all to read the ad linked below), but we will also consider non-German speakers.

Vertical Farming group at the Fraunhofer IME in Aachen Germany (start date 1-9-2024)

Technische*r Assistent*in (Laborant Biologie oder BTA) Stellendetails | Fraunhofer-Gesellschaft <<https://jobs.fraunhofer.de/job/Aachen-Technischer-Assistentin-%28Laborant-Biologie-oder-BTA%29-52074/1076238901/>>

Best regards Marc Stift Group leader - Vertical Farming
Marc Stift <marcstift@gmail.com>

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MichiganStateU KBS Tech SwitchgrassEvolution

The Lowry Lab at Michigan State University is seeking to hire a Research Technologist I to work on a large collaborative project studying adaptation to abiotic and

biotic stresses in the bioenergy feedstock switchgrass (*Panicum virgatum*), in the Lowry Lab. The successful candidate will participate in research focused on understanding the mechanisms of abiotic and biotic stress tolerance in switchgrass and how those stresses impact feedstock deconstruction and bioenergy conversion. The research will be primarily located at the Kellogg Biological Station in western Michigan until December 2024. At that point, the job will be relocated to the main Michigan State University Campus in East Lansing, MI. The work will be primarily field-based in warmer months and primarily laboratory-based in colder months. The technician will be expected to organize data collection efforts and coordinate these efforts with a larger team across MSU and at other research universities and USDA field stations. The position will begin as early as May 2024, but the start date is negotiable.

Apply for the position here: <https://careers.msu.edu/en-us/job/518321/research-technologist-i> For questions, please contact David Lowry at dlowry@msu.edu.

David B. Lowry Associate Professor Department of Plant Biology Associate Director Plant Resilience Institute Michigan State University, USA <http://davidbryantlowry.wordpress.com/> "Lowry, David" <dlowry@msu.edu>

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OklahomaStateU PlantEvolution

Job Title: Assistant Professor of Biology Department: Department of Biological and Biomedical Sciences Start Date: 1 January 2025 Applications received by 1 July 2024 will receive full consideration.

We are searching for a colleague who can contribute to upper-division plant biology courses. In the past we have taught Terrestrial Ecology, Plant Biology, Economically Important Plants, Plant Taxonomy and Plant Physiology. The successful candidate could also develop their own plant biology courses in their area of expertise.

Our department values undergraduate research and provides startup funds and lab space. We have several existing partnerships that provide access to field sites within a short drive of campus. Ecologists and evolutionary biologists would be awesome additions to our team. I've provided a link to the application. If you have any questions, do not hesitate to

reach out. <https://swosu.csod.com/ux/ats/careersite/-1/home/requisition/454?c=3Dswosu> Take care,

Rickey

Tenure-Track, Assistant Professor of Biology

swosu.csod.com

Rickey Cothran Associate Professor & Chair
 Depart. of Biological & Biomed. Sciences
 Southwestern Oklahoma State Univ. <https://rdcothran.wixsite.com/hyalella> “Cothran, Rickey”
 <rickey.cothran@swosu.edu>

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Pennsylvania State U ResTech Drosophila Symbiosis

Research Technologist (Advanced Professional) - Pennsylvania State University

Apply for the position: https://psu.wd1.myworkdayjobs.com/en-US/PSU_Staff/-details/Research-Technologist—Bordenstein-Lab_REQ_0000056596-1?q=Research+Technologist

The Bordenstein Laboratory in Penn State University's Departments of Biology and Entomology and One Health Microbiome Center seeks a Research Technologist Life Sciences - Advanced Professional to design, implement, and support fast-paced research in host-microbe symbioses and the microbiome sciences spanning insect endosymbionts, bacteriophages, evolution, epigenetics, and reproductive biology. This position will heavily focus on the use of transgenic expression, genetic editing techniques, fitness assays, reproductive tissue dissections, microscopy, and team management to understand the genetics and mechanisms of Wolbachia bacterial symbionts in *Drosophila melanogaster*.

The successful candidate will have priority tasks in the following areas: - Independent experimental design, implementation, analysis, time management, and reporting - Preparation and adherence to new scientific protocols, specimen evaluation, and biostatistics - Coauthorship of scientific papers, grants, presentations, and summary reports - Contribution to research methods, solutions, and technical approaches for problem solving - Data collection, data analysis, statistics, and visualizations - Management of trainees for molecular biology skills, biosafety

measures, lab policies, equipment, proper record keeping, organismal maintenance, and performance review - Various experimental tasks, including but not limited to tissue dissections, biological marker staining, fluorescent microscopy, microinjections, and genotyping and quantification of insect and symbiont cells using PCR and qPCR - Daily handling and maintenance of laboratory insect colonies at the scale of hundreds to thousands of insects per day - Troubleshooting of emergencies, day-to-day questions by lab members, and laboratory scheduling - Assistance of lab management and ongoing entomology, microbiology, molecular biology experiments, as assigned - Maintenance of a welcoming and professional environment adherent to lab expectations

Education and Experience: - Requires at least a Bachelor's degree or higher plus three or more years of work related experience, or an equivalent combination of education and experience. - Excellent problem-solving, interpersonal, organizational, communication, and documentation skills are essential. - The successful candidate must be able to work within a team environment and demonstrate a genuine appreciation in working, leading, and managing diverse audiences.

Additional Information: Application materials should include a single pdf with (i) a cover letter summarizing relevant experience and reasons for interest in the job, (ii) a CV that includes contact information for at least three references (name, position, telephone number, and e-mail address) and (iii) full length and first-authored works of research spanning papers, reports, posters, and presentations. This position is funded for 12 months from date of hire with excellent possibility of re-funding, pending review of performance. Please contact srb6251@psu.edu for additional information. Our lab is committed to advancing diversity and inclusivity, and we encourage individuals who identify as members of groups historically underrepresented in STEM to apply.

Community: Pennsylvania State University is a Land-Grant university located in central Pennsylvania. State College and the surrounding communities are home to approximately 100,000 people, including over 45,000 students. The area is known for its highly ranked livability, access to nature spanning beautiful mountains, streams, and parks, and superb recreational opportunities and sports. State College has an excellent school system and offers a multitude of cultural events.

The Pennsylvania State University is committed to and accountable for advancing diversity, equity, inclusion, and sustainability in all of its forms. We embrace individual uniqueness, foster a culture of inclusion that supports both broad and specific diversity initiatives,

leverage the educational and institutional benefits of diversity in society and nature, and engage all individuals to help them thrive. We value inclusion as a core strength and an essential element of our public service mission.

s.bordenstein@psu.edu

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PennsylvaniaStateU ResTech ForestConservationGenetics

Research Technologist - The Schatz Center for Tree Molecular Genetics

The Hamilton Lab at The Pennsylvania State University < <https://psu.edu/> > is seeking a candidate for a Research Technologist to develop and manage research projects, ensure quality and cost effectiveness, mentor staff, and author or coauthor published documents.

This position will manage laboratory, greenhouse, and field operations for the Hamilton Lab in research related to conservation and restoration for forest trees. Responsibilities include management and execution of workflow to complete research projects using genomics and greenhouse experiments in plants. The position will require leadership in the implementation of organization of field-collected material for plant genetics projects, the use of molecular methods; including an ability to troubleshoot DNA/RNA extraction for plants; preparation of data summaries and written reports; contributions to the development and maintenance of greenhouse, or growth chamber experiments, and include basic genetic and statistical analyses in a collaborative environment.

This position will manage laboratory operations, ensure compliance with safety requirements, contribute to financial management, and participate in broader impacts. The Hamilton Lab uses lab and field experiments, physiology, and genomics to study adaptation to climate change in forest trees, with goals of informing conservation and restoration under environmental change. This is a limited term position funded for one year from date of hire with excellent possibility of refunding.

Education and Experience:

This position will be filled as an Advanced of Senior Professional depending on the final applicant's education and experience. For the Advanced Professional level,

the minimum requirements are a Bachelor's degree and 3 or more years of relevant experience or an equivalent combination of education and experience. Additional experience and/or education and competencies are required for higher level jobs.

This position requires that you operate a motor vehicle as a part of your job duties. A valid driver's license and successful completion of a motor vehicle records check will be required in addition to standard background checks.

The Pennsylvania State University is committed to and accountable for advancing diversity, equity, and inclusion in all of its forms. We embrace individual uniqueness, foster a culture of inclusive excellence that supports both broad and specific diversity initiatives, leverage the educational and institutional benefits of diversity, and engage all individuals to help them thrive. We value inclusive excellence as a core strength and an essential element of our public service mission.

The salary range for this position, including all possible grades is:

\$42,100.00 - \$74,000.00

Interested applicants should submit a cover letter describing research interests and experience, a curriculum vitae, and contact information for three professional references to the WorkDay link below. This is a limited-term position funded for one year from date of hire with an excellent possibility of re-funding for multiple additional years. This position will be located at Pennsylvania State University in University Park in State College, Pennsylvania. Review of applications will begin immediately and continue until the position is filled. Applicants are required to have a Ph.D. or equivalent doctorate in an appropriate field and be able to provide evidence that all requirements have been met for completion of the Ph.D. prior to the effective date of hire. Informal inquiries are welcome - contact Jill Hamilton (jvh6349@psu.edu)

Research Technologist - The Schatz Center for Tree Molecular Genetics wd1.myworkdayjobs.com

Jill Hamilton Director, Schatz Center in Tree Molecular Genetics Ibberson Chair of Silviculture Research Department of Ecosystem Science and Management Pennsylvania State University University Park, PA, USA 16802 (she/her/hers)

jvh6349@psu.edu

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Senckenberg Frankfurt Comparative Genomics Bats

ERC-funded PhD and Postdoc Positions in Comparative Genomics

The Hiller Lab at the LOEWE Center for Translational Biodiversity Genomics (TBG) in Frankfurt, Germany has two openings for a PhD student and/or a Postdoc to work on the BATPROTECT project to investigate the genomic basis of long healthspans, disease resistance, and viral tolerance in bats.

BATPROTECT is a 6-year funded ERC synergy grant project that will use bats as natural models of healthy aging and disease tolerance to elucidate the molecular mechanisms behind bats' exceptional longevity and resistance to viral and age-related diseases. BATPROTECT brings together a team of global leaders in bat biology and ageing (Emma Teeling, Dublin), bat immunology and virology (Linfa Wang, Singapore), evolution and genomics (Michael Hiller, Frankfurt), and ageing model organisms (Bjoern Schumacher, Cologne) that will jointly investigate aging and immune responses in bats from the wild and captive colonies, discover genes with evolutionary importance for longevity and disease resistance, and functionally validate longevity and immune regulators in stem and differentiated cells of bats and model organisms, with the ultimate goal to uncover new directions to improve human healthspan and disease outcome.

The Project The overall goal is to uncover the genomic basis of exceptional healthspans and disease tolerance in bats, understand the evolution of these traits, and identify key molecular targets for functional validation. To this end, we will assemble ~150 new reference-quality bat genomes using HiFi and HiC sequencing to better cover the diversity of bats, generate comparative transcriptomic datasets, and analyze these data using our established methods repertoire (TOGA and others). Work includes phylogenomics, performing comparative screens to identify key adaptations in coding and non-coding (miRNA) genes as well as differences in gene expression patterns across the bat phylogeny, associating genomic changes with longevity and viral reservoir status traits, identifying novel bat genes, and investigating endogenized viral elements. The exact project will be defined based on the interests of the applicants.

The PhD student and postdoc will work closely with other members of the BATPROTECT team, the Hiller lab, and other Bat1K collaborators. We also offer exchanges with the other BATPROTECT labs as well as yearly retreats with all project members.

Your profile - Master or PhD degree in bioinformatics/computational biology, genomics or a related area - Solid programming skills in a Linux environment, experience with shell scripts and Unix tools - Strong interest in comparative genomics, experience in comparative genomics is an advantage - English in written and oral form

Our lab The mission of our lab is to understand how nature's fascinating phenotypic diversity has evolved and how it is encoded in the genome. Work in the lab includes sequencing and assembly of reference-quality genomes, genome alignment and gene annotation, development and application of comparative genomic methods to discover differences in genes and gene expression, and the use of statistical approaches to link phenotypic to genomic changes.

Our lab is part of TBG (<https://tbg.senckenberg.de/>) and the Senckenberg Research Society (<https://www.senckenberg.de/en/>), and is based near the city center of Frankfurt am Main, Germany. TBG provides access to cutting-edge computational (large HPC clusters, genome browser) and lab infrastructure to sequence and analyze genomes. English is the working language in our lab.

Senckenberg and TBG provide - Flexible working hours - opportunities for mobile working - leave of absence due to family reasons (certified by "auditberufundfamilie") - parent-child office - annual special payment - company pension scheme - Senckenberg badge for free entry in museums in Frankfurt. - leave of 30 days/year - Frankfurt is a vibrant and highly international city at the heart of Europe that combines a skyscraper skyline with ample parks and green areas. The Economist 2022 index ranked Frankfurt among the top 10 most livable cities worldwide.

Place of employment: Frankfurt am Main
Working hours: Full-time (40 hours/week) / part-time options are available
Type of contract: funding is available for 6 years
Postdoc: initially limited to 2 years
PhD: initially limited to 3 years
Start date: flexible, ideally summer of 2024
Salary and benefits: according to the collective agreement of the State of Hesse (TV-H), pay grade E13 (PostDoc 100%, PhD: 75%)

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

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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>

SenckenbergMuseum Frankfurt CuratorMarineInvertebrates

Dear all

We are recruiting a new permanent position at the Senckenberg Museum in Frankfurt, Germany. We are looking for someone who does collections-based research on marine invertebrates, in a group that fills a gap in our department (one of: sponges, corals, bryozoans, echinoderms, or possibly another clade... but the primary focus SHOULD NOT be molluscs, annelids, nor crustaceans).

We are part of a large and growing marine research team in Frankfurt and other sister institutes in Germany. Senckenberg is a bilingual research institute and the working language in many research groups is English, including the Senckenberg Ocean Species Alliance (sosa.senckenberg.de). The Senckenberg Research Institute and Museum Frankfurt has world renowned collections, outstanding lab facilities, and fun and friendly people, in a highly international city.

Please spread the word!

Job announcement Ref. #01-24011 <https://www.senckenberg.de/en/career/scientists/#content-0004.1> The Senckenberg Gesellschaft für Naturforschung (SGN) was founded in 1817 and is one of the most important research institutions in the field of biodiversity. At its eleven locations throughout Germany, scientists from almost 40 nations conduct cutting-edge research on an international scale. The Society's headquarter is in the Main metropolis of Frankfurt in the heart of Germany. This is also where one of the best-known Senckenberg facilities, the Senckenberg Natural History Museum, is located.

For our extensive collection of Marine Invertebrates at our location in Frankfurt, starting ideally on 1st of January 2025, we are looking for a

Collection Scientist and Curator of Marine Invertebrates (m/w/d) (tenure-track, full time / part time options

available)

We are looking for an internationally recognized invertebrate zoologist with an excellent research record in integrative taxonomy, systematics, evolutionary and/or ecological research on marine invertebrate organisms. The ideal candidate will apply modern approaches, using innovative methods to unlock scientific information from museum specimens, e.g. through imaging approaches and/or molecular analyses. The position will include responsibility and oversight for permanent scientific collections of the Senckenberg Research Institute and Natural History Museum Frankfurt. In particular, we are looking for candidates with an expertise in corals, or sponges, but applications are also welcome from candidates with expertise in other organismal groups that align with existing collection strengths, such as bryozoans or echinoderms. The proposed research program should be collections-based and complement the overall Senckenberg Marine Research portfolio and strategy.

Your tasks:

- Conduct innovative collection-based research on the taxonomy, systematics and biology of marine invertebrates
- Supporting the Senckenberg Collectomics concept: research using new approaches for low-invasive mass digitisation and/or the use of extended specimens for modelling
- Develop the collections and associated resources at the Senckenberg Research Institute and Natural History Museum Frankfurt
- Foster our collections as important international research tool through international networking, and development and growth of the specimen collections
- Secure external research funds
- Actively publish results of your research in international scientific journals
- Participate in collaborative marine research and expeditions
- Supervise students at undergraduate and postgraduate levels
- Promote collections-based research on marine invertebrates through national and international initiatives and partnerships (e.g. IUCN Red List, UN Decade of Ocean Science)

Your profile:

- Doctoral degree in organismal biology/zoology or a related field
- Expert knowledge of a relevant group of organisms and their systematics
- Experience in curating and using invertebrate research collections
- A research plan to leverage innovative research methods, such as genomic or imaging methods in a collections context
- Outstanding research record adequate to your career stage

What can you expect?

- A vibrant, international team of scientists with

collection- based research programs, focussed on curiosity-driven research and the preservation of Earths biodiversity - Excellent infrastructures and collaborations opportunities, e. g. in morphology, genomics, evolutionary biology, (paleo-)ecology - An attractive and challenging position in a research institution of international standing

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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>

Townsville Australia EvolutionaryModeller

Australian Institute of Marine Science, Townsville, Australia

Two job positions being advertised: 1) Evolutionary modeller 2) Geneticist

Some key details: -are permanent positions. -across as range of levels are invited to apply, from equivalents of senior postdoc (AOF 5) to Associate Professor (AOF 7) for the evolutionary modeller and to senior postdoc (AOF 5) to Assistant Professor (AOF 6) for the aquaculture geneticist.

-positions are based in Townsville, in tropical north Queensland.

-applications will be considered.

AIMS is Australia's tropical marine research agency - it is a government institute and research activities span applications to fundamental knowledge. The two positions in question would be contributing knowledge towards coral restoration and conservation planning, with the latitude to do a lot of fundamental science and collaborate with a diverse and interdisciplinary group of excellent scientists.

Deadline for applications: June 10, 2024 For full details and instructions: <https://www.aims.gov.au/about/careers-aims> Cynthia Riginos

Principal Research Scientist, Research Team Leader
Coral Reef Adaptation

Australian Institute of Marine Science

PMB3 | Townsville MC QLD 4810 | Australia

E: c.riginos@aims.gov.au | W: aims.gov.au

Follow AIMS < <https://www.aims.gov.au/docs/about/-contacts.html> >

c.riginos@aims.gov.au

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UExeter FieldAssistants InsectSociality

We seek multiple fieldwork assistants to help research how helping may have evolved using a wild digger wasp population (*Ammophila*) from early June until mid-end of August 2024.

The assistants will be working alongside a Postdoctoral researcher and several other field assistants at a nature reserve just outside of Guildford, Surrey, UK. *A. pubescens* is a non-social wasp which does not sting humans, and lays each egg in a separate burrow containing a paralysed caterpillar. The female wasp will provide further food items as her larvae grow, making the species an ideal system for testing how helping may have evolved. A couple of our previous papers on this system are: (1) Field & Brace (2004). Pre-social benefits of extended parental care. *Nature* 428: 650-652; (2) Field et al. (2023). Brood parasites that care: alternative nesting tactics in a subsocial wasp. *American Naturalist* 202(5): 655-666.

The fieldwork involves: observing and manipulating provisioning behaviour, handling and marking wasps, setting up video cameras, uploading video footage and data entry. In warm weather, this involves long days in the field! Because the work involves recording colour marks on individual animals, the job would not be suitable for someone who is colour-blind. See our research group website for more information about the kind of work we do (http://biosciences.exeter.ac.uk/-staff/index.php?web_id=Jeremy.Field).

Experience of conducting fieldwork (especially with insects) and a degree (or working towards a degree) in a Behaviour/Evolution/Ecology-related topic are desired. Flexibility around the start and end date of the assistant position is required. The successful applicants must have enthusiasm for fieldwork, and will obtain excellent experience of cutting-edge research.

Shared accommodation in Surrey is provided, but assis-

tants are required to pay for their own food/personal expenses. Assistants receive \hat{A} £125 per week to help cover personal costs.

Please contact Lucy Winder l.winder2@exeter.ac.uk to discuss these positions further, attaching a CV.

Dr Lucy Winder (she/her)

Postdoctoral Research Fellow University of Exeter
www.exeter.ac.uk Stella Turk Building, Treliiever Road,
Penryn, Cornwall TR10 9FE

“Winder, Lucy” <L.Winder2@exeter.ac.uk>

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UMontana BioinformaticsDataScience

Research Scientist, Bioinformatics and Data Science,
University of Montana, Montana INBRE Data Science
Core

The University of Montana (UM) invites applications for a Bioinformatics Data Scientist to support data science research and education activities of the UM Genomics Core (UMGC) and the Montana INBRE Data Science Core (DSC).

The primary responsibilities of the candidate will be to engage in collaborative research supporting the biological and biomedical research communities of the University of Montana and the Montana INBRE (MT-INBRE) network, which is a collaborative network of institutions invested in biomedical research in Montana. This is a full-time position that includes service, training, and independent research components. The successful candidate will collaborate with UMGc and MT-INBRE researchers on emerging bioinformatics and data science problems and work with UM Information Technology (IT) to facilitate use of local high-performance computing resources and cloud-computing environments. These activities will constitute the service component of the position. Training responsibilities will primarily consist of organizing and conducting activities (short courses, workshops, targeted sessions) to promote training in bioinformatics and data science. Pursuit of independent research in bioinformatics and data science will be strongly encouraged.

The University of Montana is home to a diverse and highly interactive collection of scientists with expertise

in biomedical sciences, genomics, evolution, ecology, and wildlife biology and a strong emphasis on the study of natural systems. Under the leadership of Director Jeffrey Good (www.thegoodlab.org), the UMGc and the DSC collaborate to support biological and biomedical research through the generation and analysis of diverse high-throughput sequencing applications, including whole genome sequencing, genotyping, viral surveillance, bulk and single-cell RNA sequencing, and related applications. Both facilities are part of recently constructed shared molecular and computational lab space (5,000 ft²) that includes five collaborative research groups dedicated to evolutionary genomics research. Candidates whose research interests and background complement and expand these existing strengths are encouraged to apply. UM is in Missoula, a charming city in the northern Rocky Mountains that offers an outstanding quality of life. The successful candidate will collaborate with the state-wide MT-INBRE research network composed of two R1 research intensive PhD-granting institutions, seven primarily undergraduate institutions, and seven tribal colleges supported by the National Institutes of Health (<https://inbre.montana.edu>). The mission of MT-INBRE to enhance biomedical research capacity, expand and strengthen the research capabilities of biomedical faculty and provide access to biomedical resources for promising undergraduate and graduate students throughout eligible states. Come join our supportive team of collaborative scientists in beautiful Missoula, Montana!

This is a s full-time non-tenure track appointment supported by a competitive salary and a comprehensive benefits package. Review of applications will begin on June 17 and the position will remain open until filled. Please apply at <https://bit.ly/UMJobs4437>. Candidates must apply online and will be asked to upload the following application materials: a cover letter describing your interests and qualifications, a CV, a combined statement of research/training experiences and interests (2 pages or less), and contact information for three references. All applicants are strongly encouraged to contact Dr. Good (jeffrey.good@umontana.edu) with any questions.

The University of Montana is an Affirmative Action/Equal Opportunity employer and has a strong institutional commitment to the principle of diversity in all areas. ADA/EOE/AA/Veteran’s Preference Employer

“Good, Jeffrey” <Jeffrey.Good@mso.umt.edu>

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UNorthCarolina Wilmington ResearchComputing

Research Computing and Data Professional job opportunity!

University of North Carolina Wilmington

The Center for Marine Science (CMS) at UNCW strives to support the computational requirements of researchers and instructors from coastal and marine-related efforts at UNCW. CMS has computing needs that include supporting researchers with software and coding needs, and aiding instructors with computation needs and instruction for students focused on the use of High-Performance Computing (HPC) and Research Storage. Emphasis for this position includes current projects including genomics and bioinformatics, oceanographic and coastal modeling, computational models of chemical structures, video and photo processing, and sensor development. Incorporation of artificial intelligence and machine learning into coastal and marine research is a priority. We do not expect any single individual to cover all areas. We are casting a broad net. There are approximately 25 research-active research laboratories utilizing research computation. A number of courses will take advantage of the service each semester to provide students with experience using HPC resources.

The minimum requirement is a Master of Science with a Ph.D. preferred. This person is expected to be involved in research activities. This individual will aid research and be an intermediary between scientists and The University's Office of Information Technology, especially with a new HPC running Rocky linux

A more complete list of qualifications and more information about the University are given on the web page listed below.

For official job posting please see: <https://jobs.uncw.edu/postings/31802> Closing date May 26, 2024.

Questions can be directed to "CMS_EA@uncw.edu"
halanychk@uncw.edu

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UPuertoRico Two PhylogeneticsNeuroscience

The jobs announced in the following link will continue accepting applications until filled. Dr. Tugrul Giray (tugrul.giray@upr.edu), Search Committee Chair <https://evol.mcmaster.ca/brian/evoldir/Jobs//UPuertoRico.Two.PhylogeneticsNeuroscience> —

“TENURE TRACK FACULTY POSITION ANNOUNCEMENT The Department of Biology of the College of Natural Sciences, Río Piedras Campus, University of Puerto, is inviting highly qualified candidates to apply for a tenure-track faculty position in Phylogenetics, effective August 1, 2024.

The position is open to candidates with research programs focused on Animal Phylogenetics, Animal Systematics, Biological Collections, and related areas.

Requirements: - Ph.D. or an equivalent degree in Phylogenetics, Systematics, or related field from an accredited university. - Post-doctoral research experience. - Strong publication record, in area of specialty. - Demonstrated ability to seek and obtain extramural funds. - Teaching experience using diverse technologies. - Availability to direct research projects, theses and dissertations.

Plus: - Bilingual (Spanish and English) skills are desirable. - Women and underrepresented minorities are encouraged to apply.

Responsibilities: The new faculty member is expected to develop a strong research program supported with external funds; strengthen the course offering of the Department at the undergraduate and graduate levels, including teaching at all available teaching hours and using diverse technologies; provide mentorship for undergraduate and graduate (M.Sc. and Ph.D.) students; supervise theses and dissertations; and participate in service activities at the level of the Department, University and beyond. Moreover. The faculty will be in charge of the maintenance and development of the Biology Department Zoological Collection.

We seek a colleague who has demonstrated a commitment to enhancing and promoting inclusion, equity, and diversity in research, mentoring, teaching, and outreach. The University of Puerto Rico is an equal opportunity employer and has a strong commitment to achieving diversity in faculty, staff, and students.

Documents required: - Intent letter briefly explaining the candidate's strengths - Updated Curriculum Vitae - Research statement (maximum 3 pages) describing research accomplishments, and short- and long-term research plans - Teaching statement (maximum 3 pages) describing overall teaching philosophy and approaches to teaching under diverse scenarios, prior teaching experience, and approaches to mentoring minority undergraduate and graduate students from groups that have been historically underrepresented in science - Official academic credentials and evidence of all degrees earned - Names and contact information of at least three reference writers

Deadline for applications: May 3, 2024

Applicants must submit documentation to: idelisa.rodriguez@upr.edu

Dr. Jose L. Agosto Rivera, Chair Department of Biology Univ of Puerto Rico PO Box 23360, San Juan, PR 00931

Sent via the Samsung Galaxy S23 5G, an AT&T 5G smartphone

tgiray2 <tgiray2@yahoo.com>

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Since evolutionary, basic, comparative neuroscience is relevant to Evolutionary biologists, again the announcement would be of interest to EvolDir clients. The announcement specify basic and also environmental neuroscience as desired research areas. Thanks.

“TENURE TRACK FACULTY POSITION ANNOUNCEMENT The Department of Biology of the College of Natural Sciences, R\355o Piedras Campus, University of Puerto, is inviting highly qualified candidates to apply for a tenure-track faculty position in Neuroscience, effective August 1, 2024. The position is open, to candidates with research programs focused on basic fundamental neuroscience, brain-related diseases such as neurodegenerative and mental disorders, and environmental neurosciences.

Requirements: - Ph.D. or an equivalent degree in Neuroscience or related field from an accredited university. -

Post-doctoral research experience. - Strong publication record, in area of specialty. - Demonstrated ability to seek and obtain extramural funds. - Teaching experience using diverse technologies. - Availability to direct research projects, theses and dissertations.

Plus: - Bilingual (Spanish and English) skills are desirable. - Women and underrepresented minorities are encouraged to apply.

Responsibilities: The new faculty member is expected to develop a strong research program supported with external funds; strengthen the course offering of the Department at the undergraduate and graduate levels, including teaching at all available teaching hours and using diverse technologies; provide mentorship for undergraduate

— / —

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>

UVValencia ProgrammingTech

Dear colleagues,

Within the ERAHUMED project we are looking for a *technician with programming experience* to develop a Shiny App or similar that is able to incorporate results of environmental models applied to the Natural Park of l'Albufera de Valencia.

The offer can be found here: <https://www.uv.es/-uvweb/servicio-recursos-humanos-pas/es/personal-investigacion/convocatorias/convocatorias/cpi-24-144-1285931577510/ConvPASInves.html?id=-1286379137136> For more information, please contact: andreu.rico@uv.es

Pablo <pamadorc@gmail.com>

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DecodingGenomes

Dear EvolDir community

We are proud to announce our book “DECODING GENOMES - from sequences to phylodynamics” diving into how to analyse genomic sequences with an evolutionary perspective. See <http://decodinggenomes.org> for a free pdf, Amazon links for print orders, and further information.

Happy reading! Tanja Stadler in the name of all co-authors

Carsten Magnus, Tim Vaughan, Joëlle Barido-Sottani, Veronika Bořková, Jana S. Huisman, JÅ«lija PeÄerska; JÅ«lija PeÄerska (editor), Cecilia Valenzuela Agüí (illustrations).

Stadler Tanja <tanja.stadler@bsse.ethz.ch>

EvolEcology CallForPapers DispersalInSmallOrganisms

Dear all,

We are pleased to announce a call for papers in Evolutionary Ecology, “Dispersal in Small Organisms.” This Special Issue will appear on the 50th Anniversary of the publication of D. O. Wolfenbarger’s “Factors Affecting Dispersal Distances of Small Organisms” and will cover dispersal in viruses, bacteria, plants, fungus, and insects. This solicitation calls for papers on behavior, ecology, genetics, and evolution that deal with

factors promoting and restricting dispersal. The effects on dispersal for landscape connectivity, distributions, invasions, host diversity, and speciation are of particular interest. The submission deadline is November 1, 2024. Publication is expected in mid-2025, but accepted articles will be made available Online First on an ongoing basis. Pre-submission enquiries are welcome.

Find more information here: <https://link.springer.com/journal/10682/updates/26984662> Best, Frank and Aur?lie

Frank W. Stearns Department of Biological Sciences Stevenson University Owings Mills, MD USA fstearns@stevenson.edu

Aur?lie Coulon Mus?um National d’Histoire Naturelle Centre d’Ecologie et des Sciences de la Conservation (CESCO), Paris, France and Centre d’Ecologie Fonctionnelle et Evolutive (CEFE), Montpellier, France aurilie.coulon@mnhn.fr

fstearns@stevenson.edu

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EvolutionMeetings AssistantMeetingOrganizer

Assistant Meeting Officer

The Society for the Study of Evolution (SSE), on behalf of the Joint ASN/SSB/SSE council, seeks a member of one or more of our societies to help plan and run our annual scientific conference - the Evolution meetings. The meetings are coordinated by one or more Chief Meeting Officers (CMOs), academics who oversee all aspects of

the meeting and who are responsible for final decisions about schedules, activities and venues, in consultation with a tri-society Joint Meeting Committee (JMC) and the larger ASN/SSB/SSE Joint Council. The CMOs also act as the principal liaisons with a Professional Conference Organizer (PCO), whose responsibilities include executing the logistics of conference management, interactions with vendors and service providers, and helping identify and negotiate contracts with future meeting venues.

We are currently seeking an Assistant Meeting Officer who will help the CMO(s) with organization, including interfacing with society councils and other stakeholders, producing the scientific program, and providing academic insight to help guide the work of the PCO. The Assistant Meeting Officer's primary responsibilities will be for the in-person meeting, although some engagement with the virtual meeting may also be requested. Specific duties will be determined by the CMO and the JMC, in consultation with the AMO. Assistants normally serve a 3-year term and, if interested, may transition into the lead CMO role at some point, with approval of the JMC. Helping run our meetings is an important and valuable service to our societies and our field which is largely a volunteer effort, but the AMO will be given a stipend of \$5000/year in appreciation. All meeting attendance costs will also be covered, as well as any other costs associated with carrying out meeting responsibilities.

The time commitment is variable but is expected to average a few hours per week, ramping up at certain times depending on particular tasks and in the month preceding the meeting. Much of the time is spent in electronic communication and virtual meetings, but there are also some duties at the conference.

This position is best suited to someone who has attended several of our recent meetings, has academic organizational and leadership experience, enjoys teamwork, and would find it rewarding to serve the societies by fostering dynamic and high-quality meetings. We welcome expressions of interest; please email these to evolution.meetings@gmail.com with 'AMO position' in the subject and include any relevant experience and a CV. These will be reviewed starting on July 1, 2024, so that the new AMO can work on the 2025 meeting (to be held in Athens, GA from June 20-24). There are no geographic restrictions, nor citizenship or residency requirements, but attendance at the 2025 and subsequent meetings is expected and in-person attendance at the 2024 meeting would be an asset.

About the annual conference The Evolution meeting is the joint conference of the American Society of Naturalists, the Society for the Study of Evolution, and

the Society of Systematic Biologists. Since 2022, the Evolution meeting has had options for both virtual and in-person participation, and we anticipate this continuing in future years. The in-person conference is held in a different location every year, primarily in the United States but occasionally in other countries. Recent locations include Portland OR, Providence RI, Cleveland OH, and Albuquerque NM. The in-person conference runs for about 5 days and attracts between 1000-2000 attendees, with oral presentations, posters, a diverse array of social events, and a variety of workshops. The virtual conference is typically 2-3 days, and includes presentations, special symposia, and workshops. Evolution has an enforced meeting Code of Conduct and a strong commitment to promoting equity and inclusion. More information is available on the conference web site: <http://www.evolutionmeetings.org>, including complete programs from recent meetings. Conferences are run on a break-even basis with careful attention given to minimizing registration costs for attendees.

Alex Wong <AlexWong@cunet.carleton.ca>

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Inclusive Evolution Education Working Group

Dear Colleagues,

The Resources for Inclusive Evolution Education (RIE2) collective is organizing a virtual working group to develop inclusive teaching modules for undergraduate courses that improve and deepen understanding of evolutionary concepts and examine their historical and social contexts. One of the first places students engage with evolutionary biology in-depth is in undergraduate courses, and evolutionary concepts can be confusing and difficult to grasp at this early stage. Furthermore, to facilitate a deeper understanding of evolutionary concepts within our classrooms and research community, it is important to address how exclusionary systems influenced foundational work in our disciplines, and how it continues to shape the way we study the natural world.

We are seeking scientists, historians, sociologists, and Science and Technology Studies scholars of all career stages who want to collaborate in small interdisciplinary teams to develop accessible undergraduate teaching modules that help educators combat misuse of evolutionary

concepts as well as examine and dismantle the eugenic and settler-colonial underpinnings of the field. Potential concepts include: fitness, heritability, sexual selection, and more. Through this experience, participants will connect with others interested in evolution education, develop important pedagogical skills, and create a citable teaching resource shared on QUBES < <https://qubeshub.org> >. Participants will also receive a small honorarium, thanks to funding from the American Genetics Association and the Society for Molecular Biology and Evolution.

We are providing two options for participation: a shorter, “hack-a-thon” style model over this summer or a longer timeline that extends into the fall. If you are interested in participating, please fill out a short Google application form by 5 p.m. PT on May 28, 2024. Accepted participants will be notified by the beginning of June: <https://forms.gle/SU4gujeGKC4nT4P49> . You can find more information about this working group at <https://qubeshub.org/community/groups/rie2>. Please contact inclusive.evoedu@gmail.com with any questions, suggestions, or if you’d like to contribute further to this effort.

Please forward this message to your networks.

Thank you!

Alejandra Camargo, Dr. Nancy Chen, Dr. Angela Google, Dr. Kiyoko Gotanda, Dr. Suegene Noh, Amanda Puitiza, Lucia Ramirez, Dr. Banu Subramanian, Juleyska Vazquez, Dr. Yaamini Venkataraman

Nancy Chen, Ph.D. Assistant Professor Department of Biology University of Rochester [popgenchen-lab.github.io/](mailto:popgenchen-lab.github.io)

Pronouns: she/her/hers

“Chen, Nancy” <nchen11@UR.Rochester.edu>

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NewCaledonia FieldAssistants AvianBehaviour

Field assistants ??? Avian behavioural ecology New Caledonia

We are looking for 2-3 field assistants to work on avian behavioural ecology in New Caledonia. The research is part of a long-term study on the co-evolutionary arms race between the Fan-tailed Gerygone and the Shining Bronze-cuckoo conducted by the Behavioural Ecology Group at the Museum and Institute of Zoology of the Polish Academy of Sciences (see Attisano et al, 2018 SciRep 8:10359; Attisano et al., 2021, CurrZool, 67:653-663; Attisano et al., 2023, JAnimEcol, 92:30-43). Postgraduate students are particularly encouraged to apply as there are possibilities to develop research projects on co-evolutionary interactions, avian breeding ecology and vocal repertoire and communication.

When: October - December 2024, exact dates and duration to be agreed.

Where: main island of Grande Terre, in managed nature reserve with tropical savannah and dry forest habitats.

Duties: nest searching and monitoring, mist-netting and banding, data collection and analysis, maintenance of field equipment. The full scope of tasks for prospective M.Sc. students might vary depending on the specific research project.

Requisites: experience of behavioural research with wild birds in particular nest searching, nest monitoring (including video monitoring), mist-netting, bird banding. Additional training will be provided. Fieldwork is physically demanding (UV exposure, heat, humidity, rain) therefore physical fitness, enthusiasm and self-motivation are essential. Ability to work independently or as part of a team and to share living spaces is also essential. Previous experience of working in the tropics, driving license and knowledge of French are desirable.

Working conditions: 8-10 hours daily for 6 days a week on average, up to 10-12 hours during the peak of the breeding season with an early morning start (5-6am). The project will provide accommodation and a weekly allowance to cover personal food costs and living expenses. Selected applicants will need to arrange their own travel to and from New Caledonia.

How to apply: send a single PDF named

???NC2024_Assistant_NameSurname.pdf??? with CV, cover letter (max 1 A4 page) describing relevant experience and contact details of 2 referees to aattisano@miiz.waw.pl. The initial deadline is 20/06/2024, but positions are open until filled. Prospective postgraduate candidates should include a short preliminary research proposal (max 1 A4 page). Only selected applicants will be contacted and invited for an online interview.

For informal enquiries please contact: dr Alfredo Attisano (aattisano@miiz.waw.pl).

Alfredo Attisano <aattisano@miiz.waw.pl>

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Sweden FieldVol SiberianJays

Field volunteer positions for a project investigating climate change adaptations of Siberian jays in Northern Sweden, 5 August to 20 October 2024

We are looking for 2 highly motivated, expenses-paid field volunteers to assist with our field project (lead by principal investigators Dr. Michael Griesser, University of Konstanz & Dr. Miya Warrington, Oxford Brookes University). Our project aims to understand how animals are adapting to changing environments, and how social interactions facilitate this.

The study site is located near Arvidsjaur in Northern Sweden. An overview over our past work can be found here: <https://www.youtube.com/watch?v=-JaH6wjAYAiE> Our current projects investigates the effect of social interactions on group coordination and social learning, using GPS tagging and experimental foraging tasks. The latter will be recorded with multiple video cameras to reconstructed body postures and gaze during the foraging tasks.

The work of the field volunteers will be to help with catching (mist netting), and colour-ringing birds, sampling blood, conducting behavioural observations, assist PhD students with experiments and managing data. This work will provide insights into a long-term study system and will be carried out in managed and pristine boreal forests. These positions are suitable for persons considering further studies (e.g., postgraduate degrees) in wildlife conservation, ornithology or ecology, or looking to expand their field skills.

Please note that daytime temperatures at the end of the season can be as low as -10C. Fieldwork at times involves walking up to 10km per day.

Qualifications:

- 1) Field work experience, involving behavioural observations and experiments
- 2) Bird ringing and preferably mist-netting experience
- 3) Ability to work in small team and sociable personality
- 4) Driver's license (manual transmission)
- 5) Working knowledge of English

Further information can be found here: <https://sites.google.com/view/c-wild-griesser/home> We will cover accommodation, food, and travel expenses to and from the study site (up to 400 euros return).

Applications, including a CV, letter of motivation (1 page), and the name of two referees, should be sent to Michael Griesser michael.griesser@uni-konstanz.de, preferably in a single PDF.

Review of applications will start 15 June 2024, position will remain open until filled.

Michael Griesser Department of Biology University of Konstanz

<https://scholar.google.com/citations?user=-IEIH0xkAAAAJ> <https://sites.google.com/view/c-wild-griesser> Michael Griesser <michael.griesser@uni-konstanz.de>

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UMass Amherst PostdocProfessionalDevelopmentProgram

Dear Colleagues, A reminder that our application deadline for the UNVEIL program is coming up May 3rd, 2024. Please see details below and pass on to any interested potential applicants and your networks! Many thanks for your help getting the word out!

Best, Lisa

Lisa M. Komoroske, Ph.D. (pronouns she/her) Assistant Professor, Dept. of Environmental Conservation University of Massachusetts Amherst phone: (413) 545-2491 | <http://lmmkomoroske.com/> Dear Colleagues,

We are excited to invite applicants for our second co-

hort of a professional development program at UMass Amherst: UNVEIL: Revealing the hidden curriculum of faculty job application, interviewing and negotiation to contribute to diversifying scientific leadership. This program is sponsored and hosted at UMass Amherst, but open to participants across North America.

The main goal of this program is to increase diversity among faculty and scientific leadership in the Natural Sciences, with a specific focus on groups under-represented in their fields. The program provides training to early career researchers to help them excel during the application and faculty interview process by exposing admitted fellows to the same components that they will experience during the faculty job process. The program is open to postdoctoral fellows and finishing graduate students residing in North America, with priority given to applicants planning to pursue jobs in the 2024-2025 academic year (see more details on eligibility at the link below). For this year's cohort, participating departments are Environmental Conservation, Biology, and Earth, Geographic and Climate Sciences.

More details on programmatic activities, eligibility, focal sub-fields, and the application can be accessed here: <https://forms.gle/SaGv3PyHhGpFL8ep8>. The deadline for applications is May 3rd, 2024.

This program is sponsored by the National Science Foundation Divisions of Biological Sciences and Geosciences, the Howard Hughes Medical Institute Gilliam Program, the UMass Amherst Office of Equity & Inclusion and Graduate School Office of Professional Development, and the departments of Environmental Conservation, Biology, and Earth, Geographic and Climate Sciences.

We appreciate your assistance in distributing this to your networks as appropriate. Any questions can be directed to Dr. Lisa Komoroske, program director at lkomoroske@umass.edu.

Respectfully,

Lisa Komoroske

Lisa M. Komoroske, Ph.D. Assistant Professor of Conservation Genomics & Ecophysiology Dept. of Environmental Conservation UMass Amherst <https://lmkomoroske.com/> <https://www.umass.edu/gloucester-marine-station/> Lisa Komoroske <lkomoroske@umass.edu>

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WildAnimalMicrobiomeEvolution ResearchExchangeFunding

Dear all,

The ESEB Wild Animal Microbiome and Evolution (WAME) special topic network are pleased to announce the next round of funding for early career research exchanges.

We invite applications from early career researchers working in the field of microbiome science who wish to visit a lab/group with complementary research interests.

WHO: Early career researchers - postgrad research students, postdocs and junior research fellows. Anyone not currently in a permanent faculty position or on a senior fellowship. ESEB membership is not a requirement but is encouraged.

WHAT CAN BE FUNDED: Applicants can request up to euro 1400 each towards travel to a host lab and accommodation during their exchange. ESEB policy is that we should strive to keep environmental impact as low as possible. As part of this, airfares are only eligible expenses if the distance travelled is more than 500 km or the travel time with alternative transport options is more than 6 hours. Research costs, stipend, or wage are not fundable.

HOW TO APPLY: Applicants should fill out the WAME ECR Research Visit form available on the [wame stn website \(https://www.wamestn.com/research-exchanges\)](https://www.wamestn.com/research-exchanges) and submit this in a single PDF file to stn.wame@gmail.com along with two short letters of support (one from current supervisor / line manager) and one from host research group.

KEY DATES: Deadline for applications 26th May 2024

Awards announced first week of June 2024

All costs must be claimed before June 2025

Best regards, WAME organising committee

“Sarah Worsley (BIO - Staff)” <S.Worsley@uea.ac.uk>

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ArizonaStateU PrimateGenomics

Postdoctoral position in primate genomics at Arizona State University

The Pfeifer Lab at Arizona State University is looking for a postdoctoral researcher to study non-human primates from a biomedical and/or evolutionary perspective, supported by NIH MIRA and NSF CAREER awards. Research in the lab focuses on (i) gaining a better understanding of the molecular and genetic differences that underlie species-specific traits and heritable disease, (ii) the evolutionary processes that explain the accrual, and fate, of these differences, and (iii) the impact of these processes on genome evolution. Our work combines the development of novel genomics datasets with computational methods for evolutionary inference, and is performed in partnership with external collaborators at the primate research centers and colleagues working at the forefront of computational methods development.

Research topics are open to discussion and mutual interest though should align with the overall interests of the lab and focus on the analysis of cutting-edge genomic data, theoretical and computational population genetic method development, as well as the implementation

of population genetic simulations. The ideal applicant will have a strong computational, mathematical, and/or statistical background along with a genuine interest in comparative genomics and primate evolution. Prior experience with large-scale genomic data and strong analysis skills - including proficiency in a programming language/shell, theoretical and computational population genetics, and/or statistical modeling experience - are beneficial. Applicants should have good organizational skills and enjoy working in a collaborative and interdisciplinary team.

The Pfeifer Lab offers a supportive and stimulating work environment with excellent opportunities for training and collaboration. The Lab is based in the School of Life Sciences and is associated with both the Center for Evolution and Medicine (<https://evmed.asu.edu/>) and the Center for Mechanisms of Evolution (<https://biodesign.asu.edu/mechanisms-of-evolution/>). The lab has strong intellectual ties - including lab meetings, seminars, and journal clubs - with the local evolutionary/population genetics, primate genomics, and computational biology research communities (<http://asupopgen.org/>).

Appointments will initially be offered for one year, with extension contingent on performance. The start date is flexible.

Interested? Contact Susanne Pfeifer
<susanne@spfeiferlab.org> for informal inquires,

and/or to send an application (including a CV, names of 3 references, and a cover letter describing your interests and fit for the position). The evaluation of applications will begin June 15, and will continue until a suitable candidate has been found.

Susanne P. Pfeifer Associate Professor School of Life Sciences Arizona State University spfeiferlab.org

susanne@spfeiferlab.org

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BangorU

EvolutionAntimicrobialResistance

I wonder if you can please post this on the jobs section.

A position has become available for a 2-year full-time Postdoctoral Research Officer to work with Prof Davey Jones (Bangor University) and Prof Rachel McKendry (University College London) on the EPSRC-funded Digital Health Hub for Antimicrobial Resistance (AMR).

The position will specifically look at ways to link clinical and environmental AMR data and to investigate effective ways to communicate this information to the wider stakeholder community. It will also seek to integrate this information with other core data streams (e.g., intelligence, prescribing information) to form part of an integrated One Health AMR surveillance and active management system. The environmental AMR data is being collected as part of the national wastewater-based public health programme but also includes information on the diversity and abundance of antimicrobial resistance genes (ARGs) and associated pathogens in rivers, marine waters, sediments, shellfish, wild birds and veterinary reservoirs. The position will also be involved in the design and validation of in-situ devices for on-site ARG testing within different environmental settings.

<https://www.jobs.ac.uk/job/DHT263/postdoctoral-research-officer-in-antimicrobial-resistance> Dr Helen Howard-Jones FCMI Swyddog Cefnogi Prosiect Ymchwil Ysgol Gwyddorau Amgylchedd & Naturiol Canolfan yr Amgylchedd Cymru

E-bost:aos602@bangor.ac.uk

Rydw i'n siarad Cymraeg

Dr Helen Howard-Jones FCMI Research Project Support Officer School of Environmental & Natural Sciences

Environment Centre for Wales

Email:aos602@bangor.ac.uk

I speak Welsh

Mae croeso i chi gysylltu gyda'r Brifysgol yn Gymraeg neu Saesneg. Ni fydd gohebu yn Gymraeg yn arwain at oedi.

You are welcome to contact the University in Welsh or English. Corresponding in Welsh will not lead to delay.

Rhif Elusen Gofrestredig 1141565 - Registered Charity No. 1141565

Gall y neges e-bost hon, ac unrhyw atodiadau a anfonwyd gyda hi, gynnwysdeunydd cyfrinachol ac wedi eu bwriadu i'w defnyddio'n unig gan y sawl y cawsant eu cyfeirio ato (atynt). Os ydych wedi derbyn y neges e-bost hon trwy gamgymeriad, rhwch wybod i'r anfonwr ar unwaith a dilewch y neges. Os na fwriadwyd anfon y neges atoch chi, rhaid i chi beidio a defnyddio, cadw neu ddatgelu unrhyw wybodaeth a gynhwysir ynddi. Mae unrhyw farn neu safbwynt yn eiddo i'r sawl a'i hanfonodd yn unig ac nid yw o anghenraid yn cynrychioli barn Prifysgol Bangor. Nid yw Prifysgol Bangor yn gwarantu bod y neges e-bost hon neu unrhyw atodiadau yn rhydd rhag firsau neu 100% yn ddiogel. Oni bai fod hyn wedi ei ddatgan yn uniongyrchol yn nhestun yr e-bost, nid bwriad y neges e-bost hon yw ffurfio contract rhwymol - mae rhestr o lofnodwyr awdurdodedig ar gael o Swyddfa Cyllid Prifysgol Bangor.

"Helen Howard Jones (Staff)" aos602@bangor.ac.uk

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CER Hungary

EvolBiologicalInvasions

CER_Buadapest.EvolutionaryEcology

Postdoctoral Position in evolutionary ecology of biological invasions

HUN-REN Centre for Ecological Research (CER) is looking to hire a Postdoctoral Researcher for 18 months (with a possibility of continuation) to work on the evolutionary ecological aspects of invasion biology as a part of the Invasion Biology Division (IBD) of the National Laboratory for Health Security.

BACKGROUND:

The establishment and expansion of non-native species is one of the great challenges of our time. Invasive alien species are one of the major drivers of biodiversity loss, which generally negatively affect the economy and human health. The Invasion Biology Division (one of the four pillars of the National Laboratory of Health Security, <https://www.eglab.hu/en/>) aims to understand the ecological and evolutionary causes and consequences of the establishment and spread of invasive species through a unified approach. Our goals are also to explore the social and economic consequences of invasions, and develop methods of prediction and control based on scientific evidence.

OUR WORK:

Invasion Biology Division (<https://invaziobiologia.hu/en/mission/>) covers all aspects of invasion biology research with a focus on a broad spectrum of animal and plant taxa. We aim to document and continuously monitor invasion and spread of various target species that play a key role in conservation, economic or social terms by applying various methods, e.g. citizen science mapping, field sampling, taxonomic identification, genetic screening, meta-analysis and phylogenetic comparative methods. We intend to reveal the causes behind the success of invasive species by studying the morphological, physiological and life-history traits and invasion pathways, as well as to uncover the evolutionary dynamics of invasion.

JOB DESCRIPTIONS:

We are looking for an applicant with a solid background in ecology and/or evolution who demonstrates interest in the research fields of Invasion Biology Division and is keen to work on any of the studied model organisms (see the research topics of different working groups at <https://invaziobiologia.hu/en/research-groups/>)

Ideally, we expect the candidate to work on her/his own (but with the ability to communicate effectively as a member of a team), and could bring novel concepts/expertise within the research project. As a formal qualification, the candidate must hold a PhD degree (or equivalent), and a considerable publication record.

The postdoc will be based at the CER (<https://ecolres.hun-ren.hu/en/>), Hungary's largest ecology and evolution institute, with more than 200 researchers and a diverse array of research topics. The research program is incorporated into a larger National Laboratory platform that establishes strong collaborations with sixteen research institutes along the One Health concept. The postdoc will work in Budapest or in Vácrátót (a beautiful botanical garden) and will interact with members of the other research groups and institutes,

but we offer high flexibility with regard to the working routine. Salary range will be subject to further negotiations and will depend on professional experience of the candidate as well as on the requirements of the National Laboratory program in Hungary.

To apply, please just send an email to kiss.orsolya@ecolres.hu with the following pdf documents as attachments: CV (max 2 pages), cover letter specifying the applicant's motivations (max 1 page), one or max two recommendations suggested. All applications, irrespective of age, gender, disability, race, religion or ethnic background, are welcome. The deadline for applications is 15/06/2024.

László Zsolt Garamszegi Project leader (IBD) Director general (CER)

László Zsolt Garamszegi
<garamszegi.laszlo@ecolres.hu>

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CPG StockholmU Sedimentary Palaeogenomics

The Department of Geological Sciences (IGV) at Stockholm University invites applications for a two-year postdoctoral position based at the Centre for Palaeogenetics (CPG) on the Stockholm University campus.

The position forms a part of the Fluxes from Land to Ocean: How Coastal Habitats in the Arctic Respond (FLO-CHAR) project, which is funded through the BNP Paribas Foundation and co-ordinated by the Alfred Wegener Institute (AWI) in Potsdam, Germany. The overall goal of the project is to resolve our understanding of changing Arctic land-ocean matter fluxes, permafrost thaw and associated impacts in one of the most rapidly changing ecosystems on Earth, the Arctic coastal environment. You can learn about the project at <https://www.awi.de/en/science/geosciences/permafrost-research/projects/flo-char.html> and https://asset.mediahub.bnpparibas/is/content/bnpparibas/FLO%20CHAR_film%20Fondation%20BNPP_vEN-0x720-1200k. The postdoctoral project aims to provide baseline data of past coastal biodiversity and identify responses of Arctic coastal ecosystems to environmental change over the past ~1000 years by applying ancient DNA approaches to shallow marine sediments in the Beaufort Sea. These data will be used to investigate

the consequences of (1) sea ice reductions on the population connectivity and range expansion of key vertebrate resources, and (2) increased organic matter input on benthic microbial and planktonic communities. Sediment cores for these analyses were recently collected by the FLO-CHAR team in Spring 2024.

The postdoc will join the CPG/IGV research group led by Peter Heintzman, which focuses on developing and using (sedimentary) ancient DNA methodologies to address a broad variety of questions in ecology and evolution, and will work in close collaboration with Matt O'Regan at IGV.

The main tasks for the candidate are directed towards recovering and analysing sedimentary ancient DNA data, using a combination of state-of-the-art metabarcoding, shotgun metagenomics, and target enrichment approaches, and testing methodologies where necessary, to address the research questions. The candidate will also have the opportunity to be involved in geochemical and palaeoenvironmental data generation and analysis. The selected candidate will be expected to collaborate with project partners at AWI and the University of Basel, publish their results in peer-reviewed scientific journals, and present their findings at national and international conferences. It is also expected that the successful applicant will participate in the vibrant daily activities at CPG, and attend relevant meetings and seminars at IGV.

Assessment criteria The PhD degree must have been completed at the latest before the employment decision is made, but no more than three years before the application closing date. An older degree may be acceptable under special circumstances. Special reasons refer to sick leave, parental leave, elected positions in trade unions, service in the total defence, or other similar circumstances as well as clinical attachment or service/assignments relevant to the subject area.

The candidate should have a strong set of research skills within the subject area, including a demonstrated track-record of (1) applying one or more of the three key state-of-the-art methods listed above for generating (sedimentary) ancient DNA data, (2) handling high-throughput DNA sequencing data using scripts and bioinformatics analysis pipelines in High Performance Computing environments, and (3) analysing and converting pipeline outputs into publishable products. The candidate should also have a good working knowledge of ancient DNA methodology, especially in sedimentary contexts. Knowledge of evolutionary biology and/or palaeoecology, especially from northern North America, is considered a merit.

Selection We are looking for a creative, responsible, and

highly motivated person who can work both independently and in collaboration with others. Selection among eligible candidates is based on both their expected capacity to complete the project tasks and their suitability for working at both CPG and IGV. The appointment process will consider the applicant's documented knowledge and skills, quality of English language communication, capacity for analytical thinking, ability to take initiative, publication record (articles in peer-reviewed international journals of good quality), experience in organising or leading work tasks, research activity (networks, funding applications/awards), and communication skills (conference presentations, outreach). The evaluation is based on previous education and experience, quality of previous published research, ambition expressed in the motivation

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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>

INRAE France WildTroutEcoEvolFeedbackLoops

Postdoc position: Eco-evolutionary feedback loops in wild brown trout

- Laboratories:

DECOD, Rennes, France. EGCE, Saclay, France. CEES, University of Oslo, Norway. BioSP, Avignon, France.

- Project description: We are looking for candidates who are willing to apply on the ECODIV-INRAE call for postdoctoral fellowships. This call targets early-career scientists (from PhD students to < 3 years postdocs) to help them transition towards permanent research positions at INRAE. If successful, candidates will be granted a 12 to 24-month full-time postdoc position at INRAE.

Application is in the form of a 5-page postdoc project co-constructed with the postdoc candidate. Our group proposes a project coupling mark-recapture and quantitative-genetic animal models to explore eco-evolutionary feedback loops acting on body size in fish. The project uses data collected on stream-resident brown trout native to a small natural stream (Bellbekken)

in Norway. This fish population was the object of a long-term mark-recapture monitoring programme that included individual phenotyping and parentage assignment. Specifically, mark-recapture data are available for > 12000 fish from 1997 to 2009, including tag id, body size, sex if possible, and age (not complete), and genotyping data are available for > 3300 offspring genotypes and > 560 parent genotypes from 2002 to 2007.

Previous studies have shown that heritability for length at age ranges from 0.16 to 0.31 in Bellbekken trout, that somatic growth and survival are negatively density- and size-dependent, and that sexual selection favours larger-bodied individuals. These previous studies suggest that trout body size, and possibly other traits such as dispersal propensity, might be subject to eco-evolutionary feedback loops involving natural and sexual selection.

- Information and contact: If you are interested in this project and proficient in programming and statistical modelling, please send an E-mail with your CV to: Eric Edeline: eric.edeline@inrae.fr Arnaud Le—Rouzic: arnaud.le-rouzic@universite-paris-saclay.fr Leif Asbjørn Vøllestad: l.a.vollestad@ibv.uio.no Julien Papaix: julien.papaix@inrae.fr.

- Timeline: Application deadline is in July 2024. We will organize interviews until mid June, so as to let us enough time to co-write the application with the successful candidate.

Eric Edeline UMR DECOD 65 rue de Saint Briec 35042 Rennes cedex <https://www.umr-decod.fr/en/people/278> <https://youtu.be/zzHcQO8NvT4> <https://sites.google.com/site/ericedeline/> Eric Edeline <eric.edeline@inrae.fr>

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LeidenU AmphibianSpeciesInvasions

Postdoctoral position in Modelling Amphibian Species Invasions

<https://www.universiteitleiden.nl/vacatures/2024/q2/-14891-postdoctoral-position-in-modelling-amphibian-species-invasions> of Science and Institute of Environmental Sciences are looking for:

1 Postdoctoral researcher related to applying landscape models to the evolutionary ecology and invasion trajectory of amphibians

Vacancy number: 14891

Key responsibilities Are you a curious scientist, wanting to bridge evolutionary ecology questions to environmental science applications? Does combining landscape models with real-world data, and interfacing with policy decision-makers for conservation applications pique your interest? Do you have experience with using environmental DNA (eDNA) or have a desire to learn and apply this approach in aquatic systems to help stem biodiversity loss? If so, the Institute of Environmental Sciences (CML) at Leiden University is looking for a postdoctoral researcher who has experience and an affinity with applying landscape modelling methods to study questions relating to invasive species (mainly Triturus spp. amphibians but possibly also Salmonid fish), conservation, and evolutionary dynamics. We are particularly interested in candidates familiar with Species Distribution Models (SDMs), evolutionary ecology theory (e.g., speciation, hybridization) and if possible (but not required) environmental DNA (or eDNA).

Specifically, the postdoctoral researcher will look at applying modelling methods to (already collected) genetic data to track and predict hybridization and invasion dynamics. Specifically, we are looking for someone to integrate eDNA data into landscape genetic frameworks to understand genetic connectivity of populations across the composition of the landscape, and how this influences hybridization and invasion potential. The Postdoc will investigate whether landscape features, such as water body fragmentation or elevation (e.g. with LiDAR and GIS) promote or hinder invasive species spread and potentially hybridization. For SDMs, the postdoc will be expected to overlay biotic and abiotic covariate data for different species for forecasting distributional trajectories. With these projects, we aim to deliver critical information needed for meaningful conservation recovery strategies.

The postdoctoral research will work closely with PhD candidates collecting genetic data through field work, and will be expected to work in a large research group comprised of 3-4 PhD students and numerous masters students. These projects are a part of a Nationally funded research program that links many collaborators across two continents (Europe and N. America) and numerous academic institutions, private enterprises, and NGOs, ultimately offering a unique, large, and dynamic research network. Within the network, the candidate will be expected to liaise with others and potentially travel to various countries across Europe and North America.

The postdoctoral research will become a member in the laboratory of Dr. Stewart whose research has been

fully funded through the Dutch VIDI program. As such you will work closely alongside a similarly funded PhD candidate and be expected to offer some degree of mentorship. This collaboration may also see the postdoc doing some fieldwork if wished. Funding for this position also offers the postdoctoral researcher the ability to attend multiple national and international conferences. Dr. Stewart is dedicated to an inclusive and open research environment to promote passion, independence, and transferable skills for whatever future career goals the candidate may have. In our research group, we strongly value a collaborative approach. Researchers will enter an environment of weekly informal meetings to promote progress and cohesion within the larger research group, while also engaging with the larger e3DNA working group (e3DNA.com; the Dutch eDNA research hub hosted by Dr. Stewart and Dr. Trimbos at Leiden University) that meets twice a month.

If you are an interdisciplinary thinker with a PhD degree in Evolutionary or Molecular Ecology, Biology, Sustainability, Environmental Science (or a related field), this postdoctoral position might be a great fit for you.

You are expected to:

Be a collegial person but have a proactive attitude towards balancing your research endeavors
Contribute to a dynamic research group involved in genetic, ecological and evolutionary analysis both within our institute but also with project collaborators in other countries
Be comfortable and confident working independently when required
Be comfortable supervising BSc or MSc students for thesis projects
Contribute to a mentorship role for PhD candidates
Attend national and international conferences
Work with supervisors outlining research methodologies and proposals
Stimulate

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New York U Plant Evolutionary Genomics

Postdoctoral Positions in Plant Evolutionary Genomics

The Purugganan laboratory at New York University is looking for postdoctoral research scientists in evolutionary functional genomics and population genomics

of crop domestication, with a focus on rice. The work will largely involve computational analysis of large-scale DNA and RNA sequencing data and environmental analysis to study the evolution of crops and its adaptation to local environments. The position is based in the NYU Center for Genomics and Systems Biology, in downtown Manhattan and will be part of a thriving research community that includes colleagues working on a broad range of topics.

The annual salary range for this position starts at \$70,000 and includes benefits. The ideal candidate will hold a PhD, have a very strong interest in questions in plant evolutionary biology, and have prior research experience using computational approaches, and a track record of peer-reviewed publications. Candidates should have a strong record of research productivity, able to work semi-independently, and are interested in working across large-scale genome data sets and computational analyses. It may also be possible that the postdoc will be involved in acquiring data in wet lab work as needed. If you are interested, please email Michael Purugganan at mp132@nyu.edu and apply at <https://-apply.interfolio.com/145610> Michael Purugganan

Academic Director, 19 Washington Square North New York University Abu Dhabi in New York Tel. (212) 992 7231

Silver Professor of Biology Center for Genomics and Systems Biology/New York and Abu Dhabi 12 Waverly Place New York University New York, NY 10003 Tel. (212) 992 9628

Michael Purugganan <mp132@nyu.edu>

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North Carolina State U EvolGenetics

The Heil Lab at North Carolina State University seeks a postdoctoral fellow to join our evolutionary genetics group. Current projects in the lab are focused on hybridization, recombination rate variation, and domestication using genetics, genomics, and experimental evolution in *Saccharomyces* yeast.

The position could be tailored to the applicant's interests and skill set within the realm of these topics. This position could be a split between empirical and computational work, or could be computational only. Experience with genomic data and a strong interest

in evolutionary processes are required. Start date is flexible, but preferred start in summer/early fall 2024. Funding is for 2 years and follows the NIH postdoctoral fellow payscale.

Please see www.heillab.com for more information about the Heil lab. Contact Caiti Smukowski Heil at cheil@ncsu.edu with any questions. Interested candidates should email Caiti and include a CV and a brief statement of interest.

Caiti Smukowski Heil, PhD Assistant Professor | Biological Sciences North Carolina State University

Office: 919-515-2709 3556 Thomas Hall Raleigh, NC 27695 www.heillab.com she/her/hers

Caiti Heil <cheil@ncsu.edu>

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North Carolina State University Weed Genomics

The VanWallendael Lab at North Carolina State University seeks a postdoctoral researcher to study the genomic changes underlying rapid evolution in agricultural weeds. Our new lab has the twin goals of better understanding evolution by studying weeds and improving weed control using evolutionary knowledge. The postdoc will have the opportunity to focus on the evolution of weedy traits in crop-related weeds, as well as monitoring genomic changes in wild weed and invasive species populations. Candidates should have interests related to these topics, but will have flexibility to investigate lines of inquiry specific to their research goals.

The successful candidate will have a PhD in: evolutionary biology, genetics/genomics, weed science, or bioinformatics. Specific skills in plant genomics, quantitative genetics, and molecular biology in non-model plant systems are preferred. The candidate should be comfortable working in a team or independently, and should have excellent organizational and writing skills. We specifically request applications from candidates whose backgrounds are traditionally underrepresented in biology.

The VanWallendael Lab is newly formed, so this postdoc will have the opportunity to work closely with the PI on projects and receive tailored mentoring. Though the lab is small, we are part of a large community of re-

searchers in an excellent location for plant genetics, the Research Triangle. Our lab is affiliated with the Weed Science Program, the Plant Breeding Consortium, the Genetics Program, and is split between two departments: Horticulture and Crop and Soil Sciences.

You may find more information about the VanWallendael lab here: <https://avanwallendael.github.io/>. Please contact Dr. Acer VanWallendael (avanwal@ncsu.edu) with further questions. Informal inquiries are welcome.

This position will be paid at minimum the NIH postdoc rate, with the potential for higher salary depending on experience level. Funding is available for at least two years, further extensions are contingent on grant funding availability.

To apply, please submit a personal statement/cover letter describing your interest in and fit for the lab, a CV including all publications at or beyond the preprint stage, and contact information for three references. We will accept applications for this position until May 21.

You can apply at the NCSU job site: <https://jobs.ncsu.edu/postings/200949> Acer VanWallendael

Assistant Professor Horticulture/Crop and Soil Sciences Departments

North Carolina State University avanwallendael.github.io

Acer VanWallendael <avanwal@ncsu.edu>

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Paris Bacterial Genomic Evolution

In the context of an ERC-funded project, we developed a longitudinal cohort to study the evolution of commensal *Escherichia coli*. We are looking for a postdoctoral researcher to analyze 500+ genomes isolated at several timepoints from 50 healthy volunteers to unravel the bacterial genetic determinants of colonization dynamics. *E. coli* is a major pathogen but little is known of its commensal lifestyle; this project represents a unique opportunity to make progress on these questions.

For more info, and to apply:

<https://emploi.cnrs.fr/Offres/CDD/UMR7241-FRABLA-002/Default.aspx?lang=EN> Also feel free to email me at francois.blanquart@college-de-france.fr for more info.

Francois Blanquart <francois.blanquart@college-de-france.fr>

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Paris EvolutionArchaea

A 2-year postdoc position is open at the Diversity Ecology and Evolution of Microbes DEEM team. Our laboratory is located in the new Saclay Campus of the University Paris-Saclay, ~30 km south of Paris. A suburban train connects the Campus to the city.

We look for candidates to engage in a project with the following objectives:

- Resolve the phylogenetic position of several unstable lineages in the tree of Archaea.
- Study the evolution of gene content in the main archaeal groups.
- Identify horizontal gene transfer events that may have contributed to the adaptation of archaeal lineages to their environments.

The genome sequences needed to address these questions are already available. The postdoc will be involved in their analysis using and developing different bioinformatics tools.

Candidate profile: The candidates should be familiar with broad aspects of the diversity and evolution of archaea and have expertise in bioinformatics, in particular in molecular phylogeny and comparative genomics. Scripting abilities (e.g., Python, Perl, R) are necessary. Additional requirements: English proficiency (written and spoken); Good presentation and communication skills; Autonomy and organization; Synthetic mind and critical thinking.

Application : Send your application (CV, cover letter and the name and contact information of at least two referees) to david.moreira@universite-paris-saclay.fr, puri.lopez@universite-paris-saclay.fr, and laura.eme@universite-paris-saclay.fr

David Moreira <david.moreira@universite-paris-saclay.fr>

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PennsylvaniaStateU AdaptiveIntrogression

The Hamilton Lab (<http://jillahamilton.com/-index.html>) at Pennsylvania State University is seeking to hire a postdoctoral scholar to contribute to an NSF Plant Genome funded research program aimed at studying the role of hybridization to climate adaptation and the evolution of species barriers using *Populus* as a model system. The researcher will analyze full-genome resequencing data from Poplar clones of mixed ancestry (*P. trichocarpa* x *P. balsamifera*) alongside phenotypic data (phenology and other), and climatic data from Poplar planted in replicated common gardens established in arboreta across the United States as part of the PopUpPoplar Network (<http://popuppoplars.com/index.html>). The post-doctoral position is highly interdisciplinary, with the potential to combine phenotypic data across a broad range of environments and genome resequencing to identify regions of the genome that contribute disproportionately to phenotypic differences across varying ancestral backgrounds and environments. The aims of the position will be tailored to the expertise of the successful applicant and complement the Hamilton Lab's broad interests in understanding the genomic basis of adaptation, the role of hybridization to adaptation, and the evolution of species barriers in forest tree systems.

This is a term position funded for one year from date of hire with an excellent possibility of re-funding for multiple additional years. This position will be located at The Pennsylvania State University in University Park in State College, Pennsylvania.

Education and Experience The position requires a Ph.D. in forestry, evolutionary biology, population genomics, speciation, quantitative genetics, bioinformatics, or a related field, and the applicant must be able to provide evidence that all requirements have been met for the completion of the PhD. The postdoc will work closely with the PI, collaborators, and lab personnel to lead research in the lab and field on the role of hybridization to climate adaptation. Familiarity with analyzing whole-genome resequencing data and expertise using and trouble-shooting bioinformatic tools, as well as experience using Unix or Linux environments is required. The postdoctoral scholar will be expected to analyze genomic, phenotypic and climatic datasets, lead preparation and

publication of peer-reviewed manuscripts, contribute to the preparation of grant proposals, present findings from the research project, and contribute to outreach associated with the project. In addition, there will be ample opportunity to pursue research questions besides those of the particular study. The ideal candidate will demonstrate the ability to integrate across biological disciplines, identify and troubleshoot promising new methodologies independently, and use the appointment to develop and pursue novel, exciting questions.

Preferred qualifications:

- Demonstrated expertise in evolutionary and ecological genomics
- Expertise in analysis of genomic or transcriptomic datasets
- Programming for bioinformatics, biostatistics, and simulations
- Quantitative genetics, GWAS, or gene expression studies
- Excellent writing and communication skills

Interested applicants should submit a cover letter describing research interests and experience, a curriculum vitae, and contact information for three professional references to the WorkDay link below. This is a limited-term position funded for one year from date of hire with an excellent possibility of re-funding for multiple additional years. This position will be located at Pennsylvania State University in University Park in State College, Pennsylvania. Review of applications will begin immediately and continue until the position is filled. Applicants are required to have a Ph.D. or equivalent doctorate in an appropriate field and be able to provide evidence that all requirements have been met for completion of the Ph.D. prior to the effective date of hire. Informal inquiries are welcome - contact Jill Hamilton (jvh6349@psu.edu)

Postdoctoral Scholar - Adaptive Introgression in Populus wd1.myworkdayjobs.com

Jill Hamilton Director, Schatz Center in Tree Molecular Genetics Ibberson Chair of Silviculture Research Department of Ecosystem Science and Management Pennsylvania State University University Park, PA, USA 16802 (she/her/hers)

jvh6349@psu.edu

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PennsylvaniaStateU ForestAdaptation

Post doctoral opportunity in Forest Ecology: Adaptation to Climate in Forest Tree Species and Climate-smart Seed Sourcing Strategies.

Applications are invited for a postdoctoral scholar to join the Leites lab and a highly dynamic team of scientists from Penn State University, Purdue University, University of Kentucky, and the US Forest Service, who are working on the multidisciplinary project “Future-proofing forests through a genetically informed reforestation/restoration decision network”.

The postdoctoral scholar will join the team to work on ecological genetics (a.k.a. genecology) of forest tree species, modeling population responses to climate in tree species native to the eastern US, and delineating climate-smart seed sourcing strategies for resilient forests. Duties include assembling and managing a large number of datasets from provenance and common garden trials for multiple species, statistical modeling and data science work, preparation and submission of manuscripts for peer reviewed journals, writing reports, oversight and coordination of activities with collaborators, serving as a role model and providing support to graduate students in the project, and performing other tasks as they arise.

The postdoctoral scholar will have the opportunity to mentor undergraduate and graduate students, participate in extension and outreach activities, and participate in professional development activities as well as attend relevant and agreed-upon scientific conferences.

This is a limited-term position funded for one year from date of hire with an excellent possibility of re-funding for a second year pending performance and funding availability. A minimum of one submission or publication in a peer-reviewed journal during the first year is required to be considered for contract renewal. This position will be located at Penn State in University Park, Pennsylvania (State College, PA).

Required Qualifications:

- * PhD in a relevant field such as forest ecology, forestry, or ecology,
- * Strong proficiency in statistical modeling and familiarity in data science,
- * Proficiency in R,

- * Record of publications in peer-reviewed journals,
- * Field experience in forest settings,
- * Excellent organizational skills,
- * Excellent teamwork, mentoring, and communication skills,
- * Committed to an ethical, inclusive, and nurturing work environment.

Preferred Qualifications:

- * Knowledge or background on ecological genetics (a.k.a. genecology),
- * Field experience working with common gardens and provenance trials,
- * Familiarity with forest tree species native to the eastern US,
- * Proficiency in geospatial analysis in R.

Start Date: Fall 2024

The Leites lab provides an intellectually rigorous and stimulating environment where we strive to be inclusive and welcoming so that all members can achieve their academic and professional goals. Visit our lab page for more information (<https://ecosystems.psu.edu/-research/labs/leites-lab>).

Applicants are required to have a Ph.D. or equivalent doctorate in an appropriate field and be able to provide evidence that all requirements have been met for completion of the Ph.D. prior to the effective date of hire. To apply, visit Penn State University Careers (<https://hr.psu.edu/careers>) and search for position REQ_0000054453. For inquiries, please contact Dr. Laura Leites at lpl3@psu.edu.

Kevin Potter <kpotter@ncsu.edu>

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QueenMaryU London BatGenomics

London. BatImmunity.EvolGenomics 3-year Postdoc position in bat Comparative Genomics

School of Biological and Behavioural Sciences Queen Mary University of London (QMUL)

Salary: ??37,182 to ??44,722 per annum plus benefits

Deadline: 01 July 2024 (later start date can be negoti-

ated)

We seek a motivated and experienced Postdoc to conduct comparative genomics analyses as part of a BBSRC-funded project entitled 'The molecular basis of viral tolerance in bats' awarded to Prof Stephen Rossiter (QMUL) and Prof Clare Bryant (Cambridge). Several bat species have been shown to possess diverse immune adaptations, yet only a small fraction of bat diversity has been examined to date. To expand this diversity for our analyses, the Postdoc will combine raw sequence data with published assemblies. They will then combine methods in comparative genomics and phylogenetics to identify suitable candidate loci for functional testing by our collaborators. The successful candidate will have the opportunity to develop this research to explore new discoveries in line with the project's overall aims.

Applicants must have a PhD in a relevant field (e.g. bioinformatics/comparative genomics/evolutionary genetics). Experience of coding and handling big data-sets are essential. In addition, we are looking for candidates with excellent written and oral communication skills, time management skills, and the ability to complete large tasks on a schedule. The project is highly collaborative, and the Postdoc will also be expected to work both independently as well as part of a wider team.

How to apply: Qualified applicants are encouraged to submit an informal application (CV and covering letter outlining your suitability for the position) to Stephen Rossiter (s.j.rossiter@qmul.ac.uk) before the formal deadline.

For the upcoming official link, see: <https://www.qmul.ac.uk/jobs/vacancies/> Other keywords: mammals, genomics, selection, adaptation, immunity

SJ Rossiter <s.j.rossiter@qmul.ac.uk>

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RIKEN-iTHEMS Japan TheoreticalEvolution

TheoreticalAndMathematicalEcologyEvolution RIKEN-iTHEMS, Japan

Seeking a few Postdoctoral Researchers (W24022)

https://www.riken.jp/en/careers/researchers/-20240424_2/index.html Laboratory: RIKEN Interdisciplinary Theoretical and Mathematical Sciences

Program (Program Director: Tetsuo Hatsuda)

Research Field: The RIKEN Interdisciplinary Theoretical and Mathematical Sciences Program (iTHEMS) promotes interdisciplinary collaborations and the creation of new interdisciplinary fields through interactions among researchers in mathematics, theoretical sciences, and computational sciences. iTHEMS aims to nurture and support young scientists eager to cross disciplinary boundaries.

For more information, please refer to the following website: RIKEN Interdisciplinary Theoretical and Mathematical Sciences Program (iTHEMS)The webpage will open in a new tab.

Job title and Job description: Job title, available positions Postdoctoral Researcher, a few positions

Job description: iTHEMS is seeking postdoctoral researcher(s) in ecology, evolutionary biology, and biodiversity. The successful applicants are expected to work with Dr. Ryosuke Iritani (Senior Research Scientist, iTHEMS) on theoretical studies on biodiversity changes under environmental variability. Also, such applicants are expected to engage in interdisciplinary interactions and collaborations among different fields such as mathematics, physics, chemistry, biology, information sciences, computational sciences, and social sciences, under the concept of iTHEMS. For more details, send an email to the contact address below.

The job description may be changed during the contract period or upon contract renewal to the extent described above.

Qualification: The candidate should possess or is expected to obtain a doctoral degree by the starting date.

Work location: RIKEN Wako (2-1 Hirosawa, Wako, Saitama 351-0198)

RIKEN has implemented a work-from-home system. Employees can work from home in accordance with the prescribed procedures. RIKEN may order the employee to change work locations, if necessary.

Salary and benefits: 1.A one-year fixed-term employment contract, renewable based on evaluation, to a maximum 3 years of employment. 2.RIKEN may adjust the above maximum period of renewability based on a) the employees abilities, work load at the time of contract completion, performance and work attitude and b) the continuation of the employees center, laboratory or project and RIKENs management situation and budget at the time. In principle, employment contracts will not be renewed for individuals older than 70 years. In principle, the first two months of employment is considered a trial period. Salary will be an annual salary based on

experience, ability, and performance, and will consist of a base salary and a variable salary. The variable salary will be determined each fiscal year based on experience, ability, and performance. The monthly base salary and variable salary are subject to change due to amendments to RIKEN regulations.

Discretionary work, commuting and housing allowances will be provided. Social insurance will be applied.

The approximate amount of annual salary at the time of employment: The monthly salary including discretionary work allowance at the time of employment will be 400,000JPY or more for postdoctoral researcher.

Mandatory membership in the RIKEN Mutual Benefit Society (RIKEN Kyosaikai).

This position falls under the specialized duties discretionary work system; one working day will be calculated as 7 hours and 30 minutes. Days off include public holidays, New Year's holidays (Dec. 29 - Jan 3), and RIKEN Foundation Day. Paid leave includes annual paid leave (up to 20 days depending on the month of employment), special paid leave (childcare, family nursing care, etc.), and work life balance holidays (up to 7 days depending on the month of employment). There are also additional leave systems such as maternity leave, childcare leave, and family nursing care leave. Smoking will be entirely prohibited on site from April 2024. These and other provisions are in accordance with RIKEN regulations.

RIKEN is actively undertaking initiatives to promote gender equality and diversity, and moving forward with the establishment of a diverse and vibrant research environment. If multiple candidates are found to have the same aptitude following a fair assessment, active efforts will be made to recruit female candidates.

Also, eligible for an exemption from repayment for category 1 scholarship loans provided by the Japan Student Services Organization before fiscal year 2003, and eligible applying for the MEXT Grants-in-Aid for Scientific Research (Kakenhi).

The Wako Campus has an on-site daycare, RIKEN Kids Wako. For details, please send an email to the HR at kids [at] riken.jp.

Application and required documents Required documents

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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>

Sweden DairyCattleQuantGenomics

Do you want to work on large dairy cattle datasets, heat tolerance breeding, and the future of genomic prediction?

Postdoc position at the Swedish University of Agricultural Sciences, department of Animal Biosciences.

We're looking for a postdoctoral researcher in dairy cattle quantitative genetics and genomics. You'll work on genetic evaluation for heat tolerance in Swedish dairy cattle, evaluating new methods for genomic prediction, and modelling deleterious variants in cattle breeding programs. This research will mix data analysis, computational modelling and theoretical work. The research will be performed in collaboration with breeding organizations and in interaction with several ongoing projects in cattle genetics and genomics. There will be considerable room for the successful candidate to shape the contents of the research and be creative.

This is a 24-month position with the possibility of extension, based at Ultuna campus, Uppsala, for a postdoctoral researcher whose doctorate was awarded no more than 3 years ago.

<https://www.slu.se/en/about-slu/work-at-slu/jobs-vacancies/?rmpage=3Djob&rmjob=10291&rmlang=-UK> If you are interested and have questions, please send me an email at martin.johnsson@slu.se.

I'd be much obliged if you'd spread the message to suitable candidates.

Best wishes,

Martin

Martin Johnsson <sorill@gmail.com>

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

UCentralFlorida CoralReefPopulationGenomics

Postdoctoral position in marine population genomics.

Applications are invited for a three-year postdoctoral researcher position in population genomics in the lab of Associate Prof. Michelle R. Gaither at the University of Central Florida Genomics and Bioinformatics Cluster (Department of Biology). Our NSF funded project seeks to integrate mean dispersal distances estimated from isolation-by-distance theory with biophysical models of larval dispersal. Based at UCF, the postdoc will work in close collaboration with project PIs at Penn State (Dr. Eric Crandall) and the University of Leeds (Dr. Maria Beger) and will be responsible for leading extensive field collections in the South Pacific archipelagos of Fiji, New Caledonia, and Vanuatu. The candidate must be able to take an independent leadership role, supervising a team of up to 6 researchers and graduate students through intensive marine field work. The postdoc will lead molecular lab efforts to generate RADSeq data, mentor and train students, generate publications, analyze data, contribute to grants; and collaborate as part of a team to help with day-to-day operations of the lab.

The project involves the collection of reef fishes and conducting reef fish surveys at 10 sites across each of the three archipelagos. RADSeq data will be generated and used for population genomic analyses as well as the estimation of dispersal kernels. Depending upon personal interest, the candidate will have the opportunity to learn approaches in biophysical modeling and conservation planning.

Qualifications

1. Ph.D. in the fields of population genomics, evolutionary genomics, phylogenetics
2. Must have experience working/living in developing countries and be able to organize and lead field expeditions lasting 6-10 weeks.
3. Must have logged at least 40 research dives and be able to provide an AAUS letter of reciprocity upon hiring.
4. Have an established record of productivity and publications

New graduates and applicants from groups that are traditionally underrepresented in the sciences are strongly encouraged to apply. Further information on the Genomics and Bioinformatics Cluster at UCF can be found at <https://www.ucf.edu/faculty/-cluster/genomics-bioinformatics/>. Inquiries about the position can be made to Michelle R. Gaither at michelle.gaither@ucf.edu with the subject line Disker_Postdoc_Position.

To apply, please send your CV, a list of three references, and a letter of interest briefly describing your field experience as well as your experience in genomics/bioinformatics (not more than 2 pages) to michelle.gaither@ucf.edu with the subject line

Diskr_Postdoc_Position. We will begin reviewing applications May 28th with an expected start date in early July/August.

Michelle R. Gaither Associate Professor University of Central Florida Genomics and Bioinformatics Cluster Department of Biology

Michelle Gaither <Michelle.Gaither@ucf.edu>

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ing your field experience as well as your experience in HABs/genomics/bioinformatics (not more than 2 pages) to michelle.gaither@ucf.edu with the subject line HAB_Postdoc_Position. Application review will begin May 17th and continue until a suitable candidate is identified. Expected start date in early July/August.

Michelle R. Gaither Associate Professor University of Central Florida Genomics and Bioinformatics Cluster Department of Biology

Michelle Gaither <Michelle.Gaither@ucf.edu>

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UCentralFlorida HarmfulAlgalBloom Metagenomics

Postdoctoral position in metabarcoding/metagenomics of harmful algal blooms. Applications are invited for a postdoctoral researcher position in metabarcoding/metagenomics of HABs in the lab of Associate Prof. Michelle R. Gaither at the University of Central Florida Genomics and Bioinformatics Cluster (Department of Biology). Working with state agencies, my lab is developing new protocols for the monitoring of harmful algal bloom species in the waters and sediments around Florida using qPCR, ddPCR, and metabarcoding. I am looking for a postdoc interested in HAB tracking and mitigation who can take an independent leadership role in ongoing projects while developing new ideas. The postdoc must be able to supervise graduate and undergraduate students, generate publications, analyze data, contribute to grants; and collaborate as part of a team to help with day-to-day operations of the lab. Qualifications

1. Ph.D. in the fields of population genomics, evolutionary genomics, phylogenetics, metabarcoding, metagenomics
2. Have an established record of productivity and publications

New graduates and applicants from groups that are traditionally underrepresented in the sciences are strongly encouraged to apply.

Further information on the Genomics and Bioinformatics Cluster at UCF can be found at <https://www.ucf.edu/faculty/cluster/genomics-bioinformatics/>. Inquiries about the position can be made to Michelle R. Gaither at michelle.gaither@ucf.edu with the subject line HAB_Postdoc_Position.

To apply, please send your CV, a list of three references, and a letter of interest briefly describ-

UCentralFlorida Two MarinePopGenomics Barcoding

Postdoctoral position in marine population genomics.

Applications are invited for a three-year postdoctoral researcher position in population genomics in the lab of Associate Prof. Michelle R. Gaither at the University of Central Florida Genomics and Bioinformatics Cluster (Department of Biology). Our NSF funded project seeks to integrate mean dispersal distances estimated from isolation-by-distance theory with biophysical models of larval dispersal. Based at UCF, the postdoc will work in close collaboration with project PIs at Penn State (Dr. Eric Crandall) and the University of Leeds (Dr. Maria Beger) and will be responsible for leading extensive field collections in Year 1 in the South Pacific archipelagos of Fiji, New Caledonia, and Vanuatu. The candidate must be able to take an independent leadership role, supervising a team of up to 6 researchers and graduate students through intensive marine field work. In Years 2 and 3 the postdoc will lead molecular lab efforts to generate RADSeq data, mentor and train students, generate publications, analyze data, contribute to grants; and collaborate as part of a team to help with day-to-day operations of the lab.

The project involves the collection of reef fishes and conducting reef fish surveys at 10 sites across each of the three archipelagos. RADSeq data will be generated and used for population genomic analyses as well as the estimation of dispersal kernels. Depending upon personal interest, the candidate will have the opportunity to learn approaches in biophysical modeling and conservation planning.

Qualifications

1. Ph.D. in the fields of population genomics, evolutionary genomics, phylogenetics 2. Must have experience working/living in developing countries and be able to organize and lead field expeditions lasting 6-10 weeks. 3. Must have logged at least 40 research dives and be able to provide an AAUS letter of reciprocity upon hiring. 4. Have an established record of productivity and publications

New graduates and applicants from groups that are traditionally underrepresented in the sciences are strongly encouraged to apply. Further information on the Genomics and Bioinformatics Cluster at UCF can be found at <https://www.ucf.edu/faculty/-cluster/genomics-bioinformatics/> . Inquiries about the position can be made to Michelle R. Gaither at michelle.gaither@ucf.edu with the subject line Disker_Postdoc_Position.

To apply, please send your CV, a list of three references, and a letter of interest briefly describing your field experience as well as your experience in genomics/bioinformatics (not more than 2 pages) to michelle.gaither@ucf.edu with the subject line Disker_Postdoc_Position. We will begin reviewing applications June 10th with an expected start date in July/August.

Michelle R. Gaither Associate Professor University of Central Florida Genomics and Bioinformatics Cluster Department of Biology

Postdoctoral position in metabarcoding/metagenomics of harmful algal blooms.

Applications are invited for a postdoctoral researcher position in metabarcoding/metagenomics of HABs in the lab of Associate Prof. Michelle R. Gaither at the University of Central Florida Genomics and Bioinformatics Cluster (Department of Biology). Working with state agencies, my lab is developing new protocols for the monitoring of harmful algal bloom species in the waters and sediments around Florida using qPCR, ddPCR, and metabarcoding. I am looking for a postdoc interested in HAB tracking and mitigation who can take an independent leadership role in ongoing projects while developing new ideas. The postdoc must be able to supervise graduate and undergraduate students, generate publications, analyze data, contribute to grants; and collaborate as part of a team to help with day-to-day operations of the lab.

Qualifications

1. Ph.D. in the fields of population genomics, evolution-

ary genomics, metabarcoding, metagenomics 2. Have an established record of productivity and publications

New graduates and applicants from groups that are traditionally underrepresented in the sciences are strongly encouraged to apply. Further information on the Genomics and Bioinformatics Cluster at UCF can be found at <https://www.ucf.edu/faculty/-cluster/genomics-bioinformatics/> . Inquiries about the position can be made to Michelle R. Gaither at michelle.gaither@ucf.edu with the subject line HAB_Postdoc_Position.

To apply, please send your CV, a list of three references, and a letter of interest briefly describing your field experience as well as your experience in HABs/genomics/bioinformatics (not more than 2 pages) to michelle.gaither@ucf.edu with the subject line HAB_Postdoc_Position. Application review will begin June 10th and continue until a suitable candidate is identified. Expected start date

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UGeorgia SticklebackSexDetermination

Postdoc position in the White lab at the University of Georgia

Our lab combines molecular genetics, evolutionary genetics, and genomics to investigate how genetic sex determination evolves. We work with stickleback fish as a model system, which have multiple independently evolved sex chromosomes to address these fundamental questions. The threespine stickleback fish is a leading genetic model organism, with a well-assembled genome, including a fully assembled Y chromosome, and tools for efficient functional genetics.

The postdoctoral researcher will have the opportunity to lead projects investigating the genetic and developmental mechanisms underlying male sex determination in the threespine stickleback fish and the brook stickleback fish. Both species have independently evolved duplications of the anti-Mullerian hormone gene, which has gained function in male sex determination. These species offer

a unique opportunity to explore the genetic basis of convergent evolution among closely related species. The postdoctoral researcher will have considerable flexibility in their direction of research under this topic.

Successful candidates must have a doctoral degree or equivalent in the life sciences and will have a strong record of research productivity.

The White lab is in the Genetics Department that houses over 30 faculty with diverse molecular and evolutionary genetics research programs (<https://www.genetics.uga.edu>). The White lab also frequently interacts with a broader community of evolutionary biologists across multiple life sciences departments. The University of Georgia is located in Athens, GA, a vibrant and affordable college town that is consistently ranked one of the top places to live.

To apply please email Mike White (whitem@uga.edu) a single PDF that contains: (1) a short statement (~1 page) that describes your research accomplishments and motivation for applying, (2) a CV, and (3) contact information for two references.

Informal inquiries are also welcome.

For more information about research in our lab, please visit: <https://mikewhitelab.org> Mike White Associate Professor Department of Genetics University of Georgia whitem@uga.edu mikewhitelab.org

whitem@uga.edu

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UKansas EvolutionaryGenomics

The Mack lab (ww.katyamack.com) at the University of Kansas is recruiting a Postdoctoral Researcher. We are an evolutionary genomics lab focused on understanding the role of gene regulatory variation in phenotypic evolution. Our research involves diverse systems but focuses on house mice and other rodents.

The postdoctoral researcher will contribute to work in the lab aimed at understanding the genomic basis of complex traits using a combination of wet-lab and bioinformatic approaches (transcriptomics, population genomics, phenotyping, and genome-editing). The aims of the position will be tailored to the expertise of the successful applicant to complement the lab's broad interest in the genetic basis of adaptation and specia-

tion, gene expression evolution, and the role of gene-by-environment interactions in phenotypic evolution. This position offers a unique opportunity to utilize diverse phenotypic and genomic datasets to understand the role of gene expression evolution in shaping phenotypic evolution within and between species in the premier mammalian model system.

Applicants may contact katya.mack@ku.edu in advance of applying with any questions. The start date for this position is negotiable (Target start-date: 7/1/2024).

Full details and application available here: <http://employment.ku.edu/staff/27747BR> <<https://t.co/pUh7kDEN1g>>

“Mack, Katya Luise” <katya.mack@ku.edu>

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UKentucky Macroevolution

The Zenil-Ferguson Lab (roszenil.github.io) of the Department of Biology, in the College of Arts & Sciences at the University of Kentucky is seeking a full-time postdoctoral researcher to participate in an NSF funded project that uses phylogenomic trees to investigate trait evolution, biogeography, and diversification of Andean flora (NSF-DEB2323170). The ultimate goal of the project is to develop models of diversification and trait evolution that include Andean Mountain uplift. This project is part of a broader collaboration with the Lagomarsino Lab (LSU) and the Schwartz lab (URI).

The successful candidate is independent, organized, motivated, and has a keen interest in using phylogenetic comparative methods to address fundamental questions in macroevolution. We encourage candidates with experience implementing comparative methods software (R or RevBayes) to apply. We are looking for someone who is personable and enthusiastic about working in a collaborative environment. Candidates should have a Ph.D. in evolutionary biology, statistics, plant biology, or a related field.

Applicants must include the following: 1) cover letter describing research interests/experience and 2) CV. In addition, please email the names and contact information for two references to roszenil@uky.edu.

Questions about this position should be address to Dr. Rosana Zenil-Ferguson, Professor, Department of Biol-

ogy (roszenil@uky.edu).

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

Apply using this link <https://ukjobs.uky.edu/postings/-529948> “Zenil-Ferguson, Rosana” <roszenil@uky.edu>

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

ULausanne ModellingBacterialEvolEco

Postdoc in modelling bacterial evolution, ecology and epidemiology

- Two years - Flexible start-date from 1.8.2024 - Apply by 17.06.2024

Join the Evolutionary Epidemiology group as we move to the University of Lausanne!

The group works at the intersection of evolutionary theory, microbial ecology, and public health. We use mathematical and statistical modelling to address problems in public health and to answer fundamental questions about bacterial ecology and evolution.

We are looking for two postdoctoral researchers with experience in mathematical and/or statistical modelling and/or bacterial genomics to work on bacterial population and community dynamics. There are multiple projects available, with freedom to collaboratively shape the direction. Possibilities include: - Developing models to predict antibiotic resistance frequencies. - Modelling how interactions within the gut microbiome shape bacterial populations. - Uncovering the role of plasmid transmission and horizontal gene transfer in the spread of clinically concerning traits.

The Evolutionary Epidemiology group, led by Sonja Lehtinen, is a friendly, growing team, soon to be based at University of Lausanne’s Computational Biology Department. We are mostly focused on theory and computation, working with existing genomic and epidemiological datasets, as well as running our own sampling studies. We are affiliated with the NCCR Microbiomes, providing fantastic opportunities for collaborations with experimental, clinical and other modelling groups.

We’re looking for curious, collaborative and thoughtful researchers. If you like our papers, we want to hear from you!

Your profile - A PhD in a relevant topic, such as evolutionary theory, computational biology, or bacterial genomics. - Expertise in mathematical/statistical modelling and/or genomics. - Excellent written and oral communication skills in English.

What we offer - An exciting opportunity to shape your research in a supportive and stimulating environment. - Exceptional scope for collaboration through the NCCR Microbiomes network. - Access to top-notch resources and possibilities for independent funding and fellowships. - Excellent support for further learning and professional development. - Plenty of opportunities to attend conferences and to build your scientific network. - Attractive salary, beautiful location and excellent quality of life in one of the best small cities in the world.

Apply here: https://career5.successfactors.eu/-career?company=universitdP&career_job_req_id=-21637&career_ns=job_listing&navBarLevel=-JOB.SEARCH We welcome informal enquiries (no applications) at: sonja.lehtinen@env.ethz.ch There will be a further position advertised later, so please get in touch even if the proposed timing isn’t quite right for you!

Evolutionary Epidemiology group: <https://tb.ethz.ch/-research/lehtinen-group.html> NCCR Microbiomes: <https://nccr-microbiomes.ch/> Lehtinen Sonja <slehtinen@ethz.ch>

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ULeicester OriginOfVision

A funded postdoctoral position is immediately available to join Dr Roberto Feuda’s lab within the Department of Genetics and Genome Biology at the University of Leicester. You will work on a project funded by the Leverhulme Trust to understand the origin of vision.

You will generate new single-cell RNA-seq data for non-bilaterian metazoans to identify photoreceptor cells. The work will be done in collaboration with Davide Pisani (University of Bristol) and $G_{\frac{1}{2}}spi_{\frac{1}{2}}r_{\frac{1}{2}}Ji_{\frac{1}{2}}kely$ (University of Heidelberg).

The Feuda lab, composed of 6 members (and two cats as mascots), combines experimental and computational biology in different model systems to investigate various aspects of nervous system evolution, from genes to developmental gene regulatory networks and cell types.

Furthermore, you will be part of the Neurogenetics Group at the University of Leicester, composed of 8 PIs, 10 PDRAs, and 20 PhD students. The group conducts research in evolutionary genomics (Feuda, Hammond, and Mallon labs), neurogenetics (Kyriacou, Rosato, and Chen labs), auditory physiology (Warren lab), and neurodegeneration (Giorgini lab). You will actively participate in group meetings and social activities to facilitate networking and independent collaborations. Other opportunities in science career development, including leadership, teaching opportunities, and grant and manuscript preparation, will also be part of the role.

The initial contract is for one year, with the possibility of extending it for a total of three years, contingent upon satisfactory performance.

About You The ideal candidate will have a PhD (or be about to submit) in molecular or developmental biology, strong expertise in the bioinformatic analysis of single-cell data, and a strong track record of research excellence. You will be highly motivated, creative, and have a passion for interdisciplinary research. Additionally, the ideal candidate should be interested in developing the project further through independent fellowship applications (e.g., EMBO and Marie Curie).

Interested candidates should apply by June 10th with a CV and a brief cover letter using this <https://jobs.le.ac.uk/vacancies/10068/research-associate.html>. For informal inquiries, please contact Dr. Roberto Feuda at rf190@leicester.ac.uk.

“Feuda, Roberto (Dr.)” <rf190@leicester.ac.uk>

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UNaples Two PlantEvolution

UniNaples.interorchids

Postdoctoral Position at the University of Naples Federico II, Naples, Italy

We are accepting applications for a one-year post doctorate fellow position in the field of orchid biotic interactions metabarcoding.

Review of applications begins on early-July 2024

OVERVIEW:

We are looking for an enthusiastic candidate with a

strong expertise in Bioinformatics alongside a strong background in plant evolutionary ecology. The candidate must have completed a Ph.D. degree in the last three years, preferably in the areas of plant-pollination, plant-fungal interaction, pollen or soil metabarcoding and must show a clear experience of application of bioinformatic tools to these fields. The work will focus on analysing NGS metabarcoding data already generated for identification of fungal partners and pollinator network of orchid communities.

HOW TO APPLY:

To apply, please submit in one PDF file: (i) one page cover letter including motivation and research interests, (ii) a CV, and (iii) contact information for two references electronically, to cozzolin@unina.it Review of applications will continue until the position is filled. Job can start as early as September 2024.

*The selected candidate will be required to present official credentials from all his/her academic degrees.

If you have questions about the position and the project, please email me.

Kind regards,

Prof. Salvatore Cozzolino Ph.D Dept. of Biology University of Naples Federico II Complesso Universitario di Monte S. Angelo Via Cinthia, 80126, Napoli, Italia Building 7, room 0D-27 Email: cozzolin@unina.it Phone: +39-081679186 (room); +39-081679185 (lab) <https://www.docenti.unina.it/salvatore.cozzolino> —

UniNaples.genorchids

Postdoctoral Position at the University of Naples Federico II, Naples, Italy

We are accepting applications for a 1,5 year post doctorate fellow position in the field of genomics of orchid biotic interactions.

Review of applications begins on mid-July 2024

OVERVIEW:

We are looking for an enthusiastic candidate with an interest in Bioinformatic and a strong background in plant population genomics/genetics. The candidate must have completed a Ph.D. degree in the last three years, preferably in the areas of genomics and bioinformatics. The work will focus on the assembly and comparative analyses of already sequenced plant genomes. We aim to identify region of genomic divergence among orchid species with a special emphasis on structural variants associated to plant-pollinator and plant-herbivore interactions.

HOW TO APPLY:

To apply, please submit in one PDF file: (i) one page

cover letter including motivation and research interests, (ii) a CV, and (iii) contact information for two references electronically, to cozzolin@unina.it Review of applications will continue until the position is filled. Job can start as early as September 2024.

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If you have questions about the position and the project, please email me.

Kind regards,

Prof. Salvatore Cozzolino Ph.D Dept. of Biology University of Naples Federico II Complesso Universitario di Monte S. Angelo Via Cinthia, 80126, Napoli, Italia Building 7, room 0D-27 Email: cozzolin@unina.it Phone: +39-081679186 (room); +39-081679185 (lab) <https://www.docenti.unina.it/salvatore.cozzolino> salvatore cozzolino <cozzolin@unina.it>

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analyses, SNP calling, genome assembly and annotation. Knowledge of molecular techniques is desirable.

Our research group values diversity and encourages the application of individuals from different social, cultural, and ethnic backgrounds, especially mothers and Black women.

Send an email to cpalma@unicamp.br attaching: a letter of intent (maximum of 2 pages); detailed CV; contact information for 2 academic references. List of your 5 main publications in the vacancy area.

Thank you very much, $i_{\frac{1}{2}}$ Best regards, $i_{\frac{1}{2}}$

Clarisse Palma da Silva Departamento de Biologia Vegetal Instituto de Biologia Universidade Estadual de Campinas - Unicamp Cidade Universitária Zeferino Vaz Rua Monteiro Lobato, 255 - Campinas - SP - Brasil - CEP 13083-862 $i_{\frac{1}{2}}$

clarisse silva <clarissepalma@yahoo.com.br>

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UNICAMP Brasil Climate Adaptation

Postdoctoral position in $i_{\frac{1}{2}}$ Molecular Ecology and Climate Changes

A postdoctoral position in Plant Molecular Ecology is available at the Institute of Biology (IB) at UNICAMP, for the study of Ecological Genomics and Evolution of Neotropical Plants in the face of climate and environmental changes. The opportunity is offered by the Research Center on Biodiversity Dynamics and Climate Change (CBioClima) and will be developed at the IB of the State University of Campinas. The project aims to analyze the mechanisms of genomic regulation in Neotropical plants, aiming to understand their adaptation and evolution in the face of future climate and environmental changes. $i_{\frac{1}{2}}$

Candidates should have a PhD in related fields such as genetics, evolution, and molecular biology, as well as a strong interest in plant ecological genetics, evolutionary biology, and field ecology. $i_{\frac{1}{2}}$

Experience with the Linux operating system and programming languages (such as R, bash, Python, Java, Perl, etc.) are required. The candidate must also have knowledge in statistical data analysis and bioinformatics, applied to: NGS data, population genetics, phylogenetic

UZurich Population Genomics Humans And Plants

The NCCR Evolving Language (www.evolvinglanguage.ch) invites applications for a Postdoctoral Researcher in population genomics and bioinformatics to study human language diversification from the viewpoints of the spread of humans and domesticated crop species at the Department of Evolutionary Biology and Environmental Studies, University of Zurich.

Please apply from this link, which has more information and web links <https://jobs.uzh.ch/-offene-stellen/postdoc-in-population-genomics-and-bioinformatics-on-language-evolution/08d2f305-50fc-4bf0-8c4f-a93840c64feb> The NCCR is a Swiss National Center of Competence in Research with the goal of creating a new discipline, Evolutionary Language Science, that targets the past and future of language. The center consists of leading scientists from traditionally separated academic domains, which allows us to harvest the diverse expertise from the humanities, social sciences, computational sciences, natural sciences and medicine towards a broadscale interdisciplinary collaboration. Your responsibilities

The similarity of the genetic and linguistic evolution

was pointed out by Charles Darwin. In the first phase of the NCCR, we found that both match and mismatch are common world-wide using the database of genomic and linguistic data GeLaTo (GENes and LAnguage TOgether) (Barbieri et al. PNAS 2023) as well as local case studies (Matsumae et al. Science Advance 2021, Arango-Isaza et al. Curr Biol 2023). In the second phase, we plan to strengthen population genetic analysis including demographic analysis and genome-wide association studies to study the evolution of languages. This project is a part of the "Population History" Task in the Work Package Stationarity of the NCCR which includes Prof. Kentaro Shimizu (Main PI of this position, group website), Prof. Balthasar Bickel (Department of Comparative Language Science), Prof. Andrea Migliano (Department of Evolutionary Anthropology), Prof. Chiara Barbieri (Univ. Cagliari) and a planned new professor in genetics of language. We expect further collaboration within and beyond the NCCR. Furthermore, we plan to analyze genomes of crop plants to examine the farming/language dispersal hypothesis stating that many language families dispersed along with farmers and crop species.

Employment is at 70-80% FTE, and the position is mainly funded by the NCCR Evolving Language (50%) and supplemented by additional sources (20-30%).

Your profile PhD degree in biology using genome-wide polymorphism analysis to infer demography, selection or genome-wide association studies. Experience in linguistic data or machine learning will be an asset. Experience either in human or plant data is not essential but the motivation to study them is important.

What we offer The University of Zurich offers a highly international, mostly English speaking and an interdisciplinary collaborative environment. In addition to NCCR, the opportunity to interact with colleagues in computational and experimental biology is available at the Department of Evolutionary Biology and Environmental Studies (Prof. Shimizu as the Director) as well as through the University Research Priority Program in Evolution in Action (as a Co-Director). Zurich offers a great quality of life, consistently ranking in the top three cities worldwide.

UZH offers excellent opportunities and strong support for career development. Salaries are internationally competitive. Link: Salary ranges, guidelines for employees in SNSF-funded projects The initial contract is for 1 year and renewable up to 4 years of the project time-frame. We take gender balance and diversity seriously in our hiring decisions.

Place of Work Pending budgetary approval, the positions are primarily located at the Department of Evolutionary

Biology and Environmental Studies at the University of Zurich (UZH) but the NCCR supports exchange with other departments in its network.

Start of employment We will begin reviewing applications end April and seek to fill positions by June. Earlier or later start points may be negotiated.

Application procedure Please submit your application including your past research achievements, a letter of motivation that highlights your interests, your CV and two or more contacts for reference (or reference letters) and one or two samples of your work in a single PDF via Jobs UZH. Please direct all inquiries to our administrative assistant Ms. Judith Baumgartner, judith.baumgartner@uzh.ch.

Prof. Dr. Kentaro K. Shimizu, Director and Professor of the Department of Evolutionary Biology and Environmental Studies Co-Director of University Research Priority Program (URPP) of Evolution in Action University of Zurich

Winterthurerstrasse 190, CH-8057 Zurich, Switzerland
E-mail: kentaro.shimizu@uzh.ch

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WageningenU Experimental Evolution

Postdoc position: Experimental evolution of antibiotic resistance in spatially structured environments

Laboratory of Genetics, Wageningen University, the Netherlands

â€Job description â€

A fully funded postdoc position (three years when full-time employed) is available in our group for an experimental evolutionary biologist/microbiologist to work as part of an interdisciplinary project studying how spatial environmental structure affects the evolution of antibiotic resistance (supervised by prof. Arjan de Visser and dr. Hilje Doekes; full project proposal available upon request). You will construct bacterial strains with common beta-lactam resistance mechanisms and use these in fitness assays and evolution experiments, to help

develop spatially explicit models of bacterial growth, competition and evolution under beta-lactam pressure. Throughout the project, you will collaborate closely with a PhD student who will develop these analytic and computational models.

Your duties and responsibilities will include: * Construct bacterial strains with common resistance mechanisms; * Perform experiments with these strains to measure fitness and estimate relevant parameters (e.g. kill rate, antibiotic degradation rate); * Perform and analyse evolution experiments with constructed strains; * Engage in frequent model-experiment feedback; * Communicate your results by delivering talks at (inter)national conferences and prepare scientific publications; * Participate in supervising BSc and MSc thesis students.

â€Qualifications â€

You are a highly motivated researcher with a PhD in molecular evolutionary biology, microbial genetics, or a related field. You have solid experience in microbiological and molecular genetics and expertise in genome analyses and are familiar with evolutionary theory and quantitative models. Further, you have good communication skills to operate in a multidisciplinary team and interact closely with the theoretical PhD student.

â€Offer â€

Wageningen University & Research offers excellent terms of employment (<https://www.wur.nl/en/Jobs/Tailor-made-conditions-of-employment.htm>). Your salary will be between €3.226 and €5.090 gross per month for a full-time working week of 38 hours, depending on work experience. A contract for 0.8 FTE can be discussed. Initially, we offer you a one-year contract, which will then be extended to the full period if there is mutual enthusiasm.

â€More info â€

If you have questions about this position, please contact Arjan de Visser: arjan.devisser@wur.nl.

Applications are welcome until 27 May. For more info or to apply: <https://www.wur.nl/nl/vacature/postdoc-in-experimental-evolution-of-beta-lactam-resistance-in-structured-environments.htm> “Visser, Arjan de” <arjan.devisser@wur.nl>

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ZhejiangU EvolVertSetDetermination

Postdoctoral Position in Evolution of Vertebrate Sex Determination Mechanisms

We are looking for a postdoctoral researcher who has interest and expertise in genome and sex chromosome evolution, gonad development and single-cell RNA-seq analyses. The aim of the project is to address how the hierarchy of sex determining cascades evolve across vertebrates, with a single-cell resolution. We have been collecting developing gonads of both sexes of various vertebrates in order to address this fundamental question, and look forward to your participation. The candidate is expected to lead the project, including data collection and analyses, and interacting with the PI and other members of the lab to coordinate the project. The initial contract is for 2 years, and can be renewed for another 3 years. The yearly salary is between 300,000 to 400,000 RMB (41k to 55k USD) depending on the candidate’s qualifications. The candidate receives benefits of campus housing/dining compensation and can apply for research grants from National Natural Science Foundation of China. The lab (qizhoulab.org) has been studying evolution of sex chromosomes and sex determination since it was established in 2015. It is affiliated with the newly established Center for Evolutionary & Organismal Biology at Zhejiang University (<https://evolution.zju.edu.cn/en/index.html>), which provides a vibrant research environment. The university is 3 hours’ drive away from Shanghai International Airport, and is located at Hangzhou, one of the most developed cities in China, that still enjoys the UNESCO World Heritage site, the West Lake (<https://whc.unesco.org/en/list/1334/>) in the city center dated to the 9th century. Interested candidates please send their CVs and at least two reference letters, or any questions to tozhouqi1982@zju.edu.cn

Prof. Dr. Qi Zhou Center for Evolutionary & Organismal Biology Zhejiang University 866 Yuhangtang Road Hangzhou 310058, China Lab: <http://qizhoulab.org/> Twitter: @zhouqi1982

Zhou Qi <zhouqi1982@zju.edu.cn>

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Berlin FloralSystematics Jun3-14

Dear colleagues,

This is a last call for an intensive two-week workshop in Berlin, providing a critical basis for diverse areas of research in botany. We have still a few places available.

Best wishes,

Louis Ronse De Craene and Julien Bachelier

Berlin Summer Course in Flower Morphology and Systematics 3-14 June 2024

This is the second version of a highly successful two-week workshop held in 2023. The course is based at the Biological Institute of the Freie Universität Berlin and the Berlin Botanical Garden, which offer extensive facilities, including functional microscopy laboratories and a huge plant collection of more than 20,000 species. The course is set up as lecture-based, laboratory taught, and interactive visits of the living collections.

FORMAT: 2-week workshop, lectures and hands-on practical sessions.

INTENDED AUDIENCE: Final year undergraduate students, PhD students, post-doctoral and advanced researchers, professionals (but no formal restriction). A basic knowledge of botany is preferred but not essential. The course will run with a minimum of 8 and a maximum of 20 participants.

REGISTRATION FEE: euro 800 (euro 600 for Undergraduate and Master students) (Registration includes coffee breaks, daily lunches with snacks, and visits, but does not include travel and accommodation).

HOW TO APPLY AND SECURE A PLACE: Please contact Dr. Louis Ronse De Craene (l.ronsedecraene@gmail.com) to request an application form and information about fee payment.

COURSE INSTRUCTORS AND CONTACT: Dr. Louis Ronse De Craene, Research Associate Royal Botanic Garden Edinburgh (l.ronsedecraene@gmail.com) Prof. Julien Bachelier, Freie Universität Berlin (julien.bachelier@fu-berlin.de)

PROGRAMME:

Course Description and outline: This short course will introduce students to the structure and development of flowers, with a focus on floral diversity and evolution and the significance of flowers for systematics. Major plant families will be identified within the framework of the main lineages of seed plants to understand their evolution and diversification. Additionally, students will learn to analyse, describe, and study the structure of inflorescences, flowers, and fruits, and based on their observations, to identify the main evolutionary patterns underlying their tremendous morphological diversity, as well as their potential pollination and dispersal mechanisms.

Course objectives and learning outcomes: Through this course students will acquire the following skills: - a guide to identifying plants using morphological characters in the context of the molecular classification system. - a

better understanding of the origin and evolution of floral structures, including their importance for classification, and of the main developmental patterns and evolutionary trends which underlie the tremendous diversity of reproductive structures. - an ability to observe and recognise key characters through the study of live floral material and the building up of floral diagrams.

Course outline: Daily activities will be in the following format: 9-12 Lecture, seminar and discussion of paper. 12-13 Lunch break 13-18 Plant collecting and observation.

Monday 3 June: Student presentations - introduction to morphology of vegetative structures and flowers, inflorescence and flower structure (floral diagrams and formulas).

Tuesday 4 June: Overview of major groups of flowering plants; major characteristics of Flowers and special attributes (phyllotaxis, aestivation, merism, symmetry, floral tubes and hypanthia).

Wednesday 5 June: Floral evolution from the ANITA grade to Mesangiosperms I

Thursday 6 June: Floral evolution from the ANITA grade to Mesangiosperms II

Friday 7 June: Monocot evolution: variations on a theme

Saturday 8 June: Basal eudicots and rise of the core eudicots

Sunday 9 June: Visit of the paleontological collections of the Museum of Natural Sciences

Monday 10 June: Rosid diversification I

Tuesday 11 June: Rosid diversification II

Wednesday 12 June Rosid-Asterid transition

Thursday 13 June: Asterid diversification I

Friday 14 June: Asterid diversification II - Conclusions and wrap-up

Recommended Textbooks and Reading: Please note that this list is not exhaustive, and that these books will be available in class:

* Endress, P.K. 1996. Diversity and evolutionary biology of tropical flowers. Cambridge University Press, Cambridge. * Leins, P. & Erbar, C. 2010. Flower and fruit: morphology, ontogeny, phylogeny, function and ecology. Schweizerbart Science Publishers, Stuttgart. * Ronse DeCraene LP. 2022. Floral Diagrams: An Aid to Understanding Flower Morphology and Evolution. 2nd Edition. Cambridge University Press. * Simpson MG. 2019. Plant systematics. 3th Edition. Elsevier. * Soltis DE, PS Soltis, PK Endress, MW Chase, S Manchester,

W Judd, L Majure, E Mavrodiev. 2018. Phylogeny and evolution of

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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>

Como Italy BayesianPhylogenetics Aug26-30

We are glad to inform you that the next Applied Bayesian Statistics school - ABS24 will be held in the city of Como, along the Lake Como shoreline, on August 26-30, 2024.

The school is organised by CNR IMATI (Institute of Applied Mathematics and Information Technologies at the National Research Council of Italy in Milano), in cooperation with Fondazione Alessandro Volta.

The topic will be BAYESIAN PHYLOGENETICS AND INFECTIOUS DISEASES.

The lecturer will be Prof. MARC SUCHARD (Department of Biostatistics, UCLA Fielding School of Public Health, USA), with the support of Filippo Monti (PhD student in Biostatistics, UCLA, USA).

If interested, you can register on the school website:

<https://abs24.imati.cnr.it/> This course aims to explore the core challenges of Bayesian phylogenetics, phylogeography and phylodynamics and is geared towards early-career researchers across both evolutionary biology and statistics.

Marc Suchard <msuchard@ucla.edu>

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EPFLLausanne LandscapeGenomics Jun17-21 LastCall

Dear all,

Registrations for the Landscape Genomics course close on May 21st. Don't miss the opportunity to delve into Landscape Genomics with (https://www.linkedin.com/in/-ACoAAAB4TMIBp1xEkMtZvCjo4_A5z5HcyquXNdc) Dr. Stéphane Joost, one of the pioneers of the field, and his team.

Dates: June 17th-21st

Where: EPFL, Lausanne, Switzerland

Course website: (<https://www.physalia-courses.org/-courses-workshops/course17/>)

Join us for a 5-day course in the beautiful Lausanne, where you'll explore how genetic diversity is distributed across space and how environmental features can modify this structure through local adaptation.

Attendees will also have the exclusive chance to learn directly from the developers of the software SamÅ£ada: (<https://lnkd.in/d56wWfpj>)

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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golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

Online 2024 SIGNAL GradProfDevelopment May16-17

We're hosting the virtual SIGNAL graduate student professional development program on May 16-17 at 10am-2:30pm ET. We have two keynote speakers Drs. Ambika Kamath (Liminal) and Charissa Owens, Ph. D. (Yale University). We have career panelists from industry, government and academia - Mikel Delgado, PhD (Feline Minds), Amrita Bhattacharya, PhD (Rancho Bio-Sciences), Mingzi Xu (UMN), Sebastian Echeverri (BBC Earth), Ebenezer Nyadjro (NOAA), Matthew LeFauve (EPA). Graduate students at all levels including those starting Fall 2024 and those that have recently graduated and looking towards next steps are invited to

attend. The SIGNAL program is a professional development workshop to promote inclusivity and belonging for graduate students in evolution, animal behavior, ecology, toxicology, and other related fields. Further, students can learn about career opportunities in government, industry, and academia from evolutionary biologists and animal behaviorists PhDs that transitioned to the next career stage. Students from minoritized groups in STEM are encouraged to apply.

Apply by May 14, 2024. Costs: Free <https://lnkd.in/en4TZz9Y> Organizers: Delia Shelton, Elizabeth Hobson, Paula Alex Trillo, Jen Hamel, Beth Reinke, Andrew Fulmer, Grace Smith Vidaurre, PhD, Sponsors: Animal Behavior Society, National Science Foundation (NSF) For questions contact: SIGNAL.popnetwork@gmail.com

Delia Shelton <shelton.delia@gmail.com>

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Online AdvancedPythonForLifeSciences Sep9-11

Dear all, We are excited to announce our upcoming online course: Advanced Python for Life Sciences, which will be held from 9-11 September 2024.

Course Website: <https://www.physalia-courses.org/-courses-workshops/advanced-python/> This three-day course aims to provide the foundations and typical workflow of data science, with a particular focus on biology and life sciences, using the Python programming language. Participants will delve into intermediate to advanced Python concepts through engaging, hands-on coding exercises.

This course is intended for biologists and life scientists at all levels who have some prior programming experience and basic knowledge of Python (including general syntax, variables, lists, dictionaries, conditionals, loops, and functions).

By the end of the course, participants will be able to: - Understand the different steps of a data science workflow in biology. - Write Python code for data wrangling and interaction with common bioinformatics formats. - Grasp the basics of machine learning using Python. - Understand the principles of data visualization with practical applications in Python.

Monday - Classes from 2-6 PM Berlin time Introduction to data science and its applications in biology Python refresher Intermediate Python: functions, classes, modules, tips & tricks Data preprocessing and wrangling

Tuesday - Classes from 2-6 PM Berlin time Machine learning: Introduction and theoretical foundations Supervised, unsupervised, and reinforcement learning Commonly used algorithms Feature engineering and selection Train-test split and cross-validation Hands-on with scikit-learn

Wednesday - Classes from 2-6 PM Berlin time Data visualization: Introduction and theoretical concepts Principles and common errors Hands-on with Python plotting libraries such as matplotlib and seaborn

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 AdvancedR Sep16-19

Dear all,

registrations are now open for the online Physalia course “BEYOND BEGINNER R: ADVANCING YOUR CODING SKILLS”.

Dates: September, 16th-19th

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

This course is designed for anyone with basic knowledge of R who is looking to enhance their skills and take their programming abilities to the next level. Each session in the course will be hands-on, providing you with practical examples to work through and apply the concepts you’ve learned, and lots of support to answer questions and overcome any challenges.

By the end of the course, you’ll have the skills and confidence to tackle complex programming problems in R and create high-quality reports, figures, and dashboards.

For the full list of our courses and workshops, please visit:

(<https://www.physalia-courses.org/courses-workshops/course47/>) Best regards, Carlo

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Online BioinformaticsTransElements Jun3-7

Dear all,

There are only 4 seats left for the upcoming online course “BIOINFORMATIC ANALYSIS OF TRANSPOSABLE ELEMENTS ”.

Dates: June, 3th-7th

Course website: (<https://www.physalia-courses.org/courses-workshops/course24/>)

In this course, participants will learn about Trasposable Elements (TE) biology, computational analyses of TEs in genome assemblies and raw read data (building de-novo TE library, TE quantification, Insertion polymorphism) as well as transcriptomics (differential expression of TE families), and the manual analyses of TEs (consensus curation, classification).

The participants will also have the opportunity to discuss their own projects and receive guidance regarding TE analysis. To achieve this, each day will be composed of lectures on TE biology and practical sessions covering diverse bioinformatic analyses.

For the full list of our courses and Workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/course24/>)

Best regards, Carlo

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Online DeepLearning Sep30-Oct4

Dear all,

We're thrilled to announce our upcoming online course, "Introduction to Deep Learning for Biologists," taking place from September 30th to October 4th, 2024.

Course website: (<https://www.physalia-courses.org/courses-workshops/course67/>)

Our course dives deep into the world of deep learning predictive algorithms for regression and classification, specifically tailored for biological data applications.

At the end of the course, the student will have an understanding of:

- the basic theoretical background of deep learning, both in terms of basic building blocks and of commonly used, state-of-the-art architectures
- differences between classification, regression, segmentation, and how to frame a real-world problem in terms of these classes
- the main steps involved in building a deep learning model for prediction problems in biology, comprising how to evaluate prediction accuracy and how to compare and choose different models
- how to use real-world data for statistical learning, comprising data preparation and data augmentation

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/course67/>)

Best regards, Carlo

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Online GeneralisedAdditiveMixedModels May27-31

Dear colleagues,

Nowadays many analyses in Evolutionary Biology are

developed using R. If you want to improve your understanding of the functions you use, write your own and apply them, this course can interest you: "Functional programming with R".

Dates and schedule: Online live sessions on 27th and 31st of May; 15:00 to 19:00 (Madrid time zone).

More information and registration: <https://www.transmittingscience.com/courses/statistics-and-bioinformatics/functional-programming-with-r>
Course Overview:

The growing availability of data and the versatility of analysis programs have led to an increase in the quantity and complexity of analyses conducted in ecology. This makes efficiency in data management and analysis increasingly necessary. One possible way to optimise these processes and reduce working times for R users is functional programming. Functions allow the automation of common tasks (such as reading different databases) in a more powerful and general way, simplifying the code.

The objective of this course is to learn how to write functions and employ them in iterative programming, using both base R and the {purrr} package from {tidyverse}. Additionally, participants will learn a coding style that facilitates understanding for their future selves and their collaborators while minimising errors. Learning to write good functions and applying them to our data is a dynamic process, and new techniques and better ways to address old problems can always be learned.

Programme:

- * Introduction
- * Theory of functions in R
- * How to write functions. Arguments and return values.
- * Bases of imperative programming
- * Iterations over one argument
- * Iterations over multiple arguments
- * Iterations without output
- * Function operators
- * Other functionals

Best regards,

Sole

Soledad De Esteban-Trivigno, PhD Transmitting Science www.transmittingscience.com Twitter @SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated

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Online GeneralisedLinearMixedModelsInR Oct21-24

Dear all,

registrations are open for the 3rd edition of the Physalia course on “Generalised Linear Mixed Models in R”.

Dates: online, October 21st-24th

Course website: (<https://www.physalia-courses.org/courses-workshops/glmms-in-r/>)

This course is aimed at graduate students and researchers who have experience with generalized linear regression models in R and want to extend their knowledge by learning how to add random effects, correlation structures, and variance models to these models. The basics of LM, GLM, and ANOVA are reviewed at the

beginning of the course.

After attending this course, you will be able to:

1. Deepen your understanding of fundamental regression concepts, including centering, scaling, interactions, contrasts, and ANOVA.
2. Understand the components of the GLMM framework (choice of distributions, random effects, variance structures, correlation structures)
3. Choose the appropriate model structure in an applied analysis of experimental or observational data (focusing on the R packages lme4 and glmmTMB)
4. Interpret the fitted models and calculate the expected effect of predictors on the response.
5. Know how to visualize fitted GLMMs (R package effects) and to check the assumptions of the model (R package DHARMa)

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

Best regards, Carlo

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Online GeneticDataAnalysis Aug26-Sep4

Genetic Data Analysis Course and Workshop: “ConGen-2024” Online

Theme: Applications of SNP and Next Gen Sequencing Data in Population Genomics, Molecular Ecology, and Conservation Genetics.

Instructors include Eric Anderson, Ellie Armstrong, Chris Funk, Matthew Desaix, Marty Kardos, Brenna Forester, Will Hemstrom, Gordon Luikart, Angel Rivera-Colon, Rena Schweizer, Stephen Spear, Robin Waples, and 3-4 more TBA.

When: August 26 - Sept 4, 2024 (with August 19th pre-course lecture on using command line & R)

Where: Online via Zoom For details on ConGen-2024: see <https://www.umt.edu/ces/conferences/-congen/default.php> 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, targeted capture) and interpretation of output from recent novel statistical approaches, pipelines, and software programs. The course includes discussions among early career researchers (student participants) and >12 leaders in population genomics (instructors) to help develop our next generation of molecular ecologists, conservation geneticists, and evolutionary geneticists. Course lecture topics include taking raw reads to genotypes (de novo and with reference), genome assembly, N_e , GWAS, RoH, landscape genomics, assignment tests with low-coverage-WGseq data, and more (see past course contents). New lectures in 2024 (with hands-on exercises) will include eDNA metabarcoding analysis, phylogenomics, and genome assembly. Past course lecture videos will be available (e.g., RNAseq, epigenetics, Genome-QC, landscape genetics, etc.).

Who should apply: Advanced Undergrads, M.S. & Ph.D. students, post-docs, faculty, agency researchers, and population biologists who have taken at least a one-semester university-level course in population genetics and a course in population ecology. Participation will be limited to ~30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own NGS data to analyze.

Past courses: see

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

ConGen participants-2024. A course/meeting review, contents to be determined but might include democratization of genomics and “doing genomics to not do genomics in the future”

Registration & Cost: Early Bird (before June 15th): \$US 840 - which includes all lectures (real-time and recorded) by at least 15 expert instructors, online question and answer sessions during hands-on exercises with worksheets and dummy datasets, copies of lecture PowerPoint slides, along with ConGen-2022 Swag (T-shirt, mug). Course materials are also available after the end

of the course to all students in a box repository including all recorded lectures and class materials. \$US 890 if payment is after June 15th.

Sponsors: American Genetic Association (AGA), Journal of Heredity, National Aeronautics and Space Administration (NASA), National Science Foundation (NSF-USA), Dovetail Genomics, PacBio, NanoPore. Journal of Heredity

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Online ModernStatThinking Sep19-Dec19

Dear evoldir community,

I am happy to announce another edition of Modern Statistical Thinking for Biologists, set to run as weekly online sessions from the 19th of September till the 19th of December 2024. The course uses an approach that differs drastically from most introductory statistics courses. The goal is both to make learning more intuitive and to address some of the criticisms that have been raised against the way statistical analyses are often performed in the biological sciences (notably an over-reliance on dodgy P-values).

Unlike most introductory courses, we will put heavy focus on Bayesian modelling. This may sound very advanced but most beginners actually find this approach easier than classical methods, such as P-values and confidence intervals. Bayesian methods have become particularly common in ecology and evolutionary biology, so training in Bayesian methods is becoming more and more relevant to researchers in these fields. Don't worry - at the end of the course, we will also talk about the more classical techniques but they should be easier to learn at that point as you'll already have your Bayesian baggage.

The course will be highly interactive, with lots of group work in break-out rooms and weekly individual assignments, to which you will always receive written feedback. There are no pre-requisites in terms of maths or stats skills. Usually, there are both participants that have very little background in any kind of statistics, as well as participants that already have a fair amount of experience with classical statistics and want to learn more

about Bayesian approaches. So both of these profiles are very much welcome!

For more information and for registration, see here: <https://www.mondegoscience.com/courses/modern-stat-think-online-19-sep-19-dec-2024> Kind regards,

Rosina Savisaar, Mondego Science.

Rosina Savisaar <rosinasavisaar@gmail.com>

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Online NanoporeDirectRNAseq Oct7-10

Dear all,

We're thrilled to announce our upcoming online course: An Introduction to Nanopore Direct RNA Sequencing.

Dates: (online) 7-10 October 2024

Course website: (<https://www.physalia-courses.org/courses-workshops/course59c/>)

Our comprehensive 4-day course is designed to equip researchers with the theoretical knowledge and practical expertise necessary to navigate the intricacies of direct RNA-Seq analysis. From fundamental concepts to advanced techniques, participants will explore everything from data QC and gene expression quantification to transcriptome assembly and RNA modification detection.

This course is tailored for researchers with a foundational understanding of RNA sequencing concepts. While prior bioinformatics training is not mandatory, familiarity with command-line tools and *nix environments (e.g., Linux or MacOS) is highly beneficial.

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 NGS Data Jun5-14

Dear colleagues,

There are two slots available for the course “Manipulation of NGS Data for Genomic and Population Genetics Analyses” - 5th edition

Schedule: Online live sessions 5th, 7th, 12th, 13th, and 14th of June, 2024; from 13:00 to 17:00 (Madrid time zone).

Instructors: Dr. François Sab [1]ot [1] (Institute of Research for Development, France) and Julie [2] Orjuela (Institute of Research for Development, France)

More information and registration: <https://www.transmittingscience.com/courses/genetics-and-genomics/manipulation-ngs-data-genomic-population-genetics-analyses/> Course programme:

- * Introduction to NGS sequencing platforms.
- * Introduction to basic command lines.
- * Basic raw data manipulations (counting sequences, listing files).
- * Raw data QC & Cleaning.
- * Introduction to TOGGLE, a NGS pipeline framework.
- * Mapping: principle, tools, execution.
- * Mapping: cleaning, data control, realigning, duplicates marking.
- * SNP calling: raw calling, cleaning calling, filtering.
- * VCF manipulations: filtering on MAF, heterozygosity
- * Impact of SNPs on genes.
- * Population genomics using sNMF.
- * Context-based analyses.
- * Piping large scale analyses for multiple samples using TOGGLE.
- * Testing new tools and different conditions to answer different biological questions.
- * Questions.

With best wishes

Sole

Soledad De Esteban-Trivigno, PhD Transmitting Science www.transmittingscience.com Twitter @SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual

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Links:

[1] <https://www.transmittingscience.com/-instructors/francois-sabot/> [2] <https://www.transmittingscience.com/instructors/christine-tranchant-dubreuil/> Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

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Online PopGenLowCoverageWGS Oct21-24

Dear all, We are excited to announce that registrations are now open for our upcoming online course (5th edition) “Population Genomic Inference from Low-Coverage Whole-Genome Sequencing Data” taking place from October 21-24.

Course website: (<https://www.physalia-courses.org/-courses-workshops/course64/>) Course Overview: This course offers a cost-effective approach to survey genome-

wide variation at a population scale using low-coverage sequencing. Participants will learn how to navigate the challenges of high genotyping uncertainty through probabilistic frameworks, essential for accurate population genomic inference. Key topics include: Workflows centered around genotype likelihoods for whole-genome and reduced representation studies.

Methods and algorithms in the ANGSD software package and related programs.

Best-practice guidelines for processing and analyzing low-coverage sequencing data.

Target Audience: This course is ideal for researchers with experience in next-generation sequencing (NGS) (e.g., exome, RAD, pooled sequencing) who are interested in low-coverage whole-genome sequencing. It is also suitable for those seeking an introduction to the ANGSD software and its probabilistic framework.

Prerequisites: Participants should have a basic background in population genomics and familiarity with NGS data. Knowledge of UNIX-based command line and R is advantageous. Participants without prior experience in Unix and R should complete suggested tutorials beforehand, as the course will not cover these environments in detail.

Course Outcomes: By the end of the course, participants will: Understand the use of whole-genome sequencing for population genomics.

Recognize the challenges and statistical frameworks of low-coverage sequencing data.

Be able to build bioinformatic pipelines for various population genomic analyses using ANGSD/ngsTools/Atlas.

Teaching Format: The course includes interactive lectures, small exercises, and longer independent practical sessions each day. Data for exercises will be provided.

Best regards, Carlo

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Online RFunctionalProg May27-31

Dear colleagues,

Nowadays most evolutionary analyses are developed using R, however, biologists are not trained in proficiently using this language.

If you are R users struggling to get the most of it to help you understand how evolution works, you can learn how to write and apply functions with the course “Functional programming with R”.

Dates and schedule: Online live sessions on the 27th and 31st of May; 15:00 to 19:00 (Madrid time zone).

More information and registration: <https://www.transmittingscience.com/courses/statistics-and-bioinformatics/functional-programming-with-r>
Course Overview:

The growing availability of data and the versatility of analysis programs have led to an increase in the quantity and complexity of analyses conducted in ecology. This makes efficiency in data management and analysis increasingly necessary. One possible way to optimise these processes and reduce working times for R users is functional programming. Functions allow the automation of common tasks (such as reading different databases) in a more powerful and general way, simplifying the code.

The objective of this course is to learn how to write functions and employ them in iterative programming, using both base R and the {purrr} package from {tidyverse}. Additionally, participants will learn a coding style that facilitates understanding for their future selves and their collaborators while minimising errors. Learning to write good functions and applying them to our data is a dynamic process, and new techniques and better ways to address old problems can always be learned.

Programme:

* Introduction * Theory of functions in R * How to write functions. Arguments and return values. * Bases of imperative programming * Iterations over one argument * Iterations over multiple arguments * Iterations without output * Function operators * Other functionals

Best regards,

Sole

Soledad De Esteban-Trivigno, PhD Transmitting Science www.transmittingscience.com Twitter

@SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or <http://transmittingscience.com/additional-terms>. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www.aepd.es. Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

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Online TransposableElements Jun3-7

Dear all, Only 3 seats remain for our upcoming online course, “Bioinformatic Analysis of Transposable Elements,” scheduled for 3rd-7th June. This course is a unique opportunity to delve into the fascinating world of transposable elements (TEs) and their bioinformatic analysis.

Course website: (<https://www.physalia-courses.org/-courses-workshops/course24/>)

Course Overview: Explore the evolution of TEs, their impact on genomes, and learn cutting-edge techniques for their bioinformatic analysis. Gain practical skills in TE discovery, annotation, classification, and expression analysis, guided by expert instructors.

Key Topics: TE diversity and mechanisms TE discovery and annotation TE classification and manual curation Insertion polymorphism and TE expression analysis Practical sessions and project-specific guidance Requirements: Basic command line and sequence alignment program knowledge is beneficial but not required. There will be time to discuss about your own data and projects.

Why Attend? By the end of this course, you will be equipped to conduct comprehensive TE analyses, interpret your results within the context of TE biology, and enhance TE annotations through manual curation. This is a rare chance to deepen your expertise and advance your research in genomics and evolutionary biology.

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

Best regards,

Carlo

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Online Two MetabarcodingPipelines TimeSeries

Metabarcoding Pipelines for Eukarriotic Communities (MPEC01)

<https://www.prstats.org/course/metabarcoding-pipelines-for-eukarriotic-communities-mpec01/>

Instructor-Dr. Adrià Antich

21st 25th June 2024

Please feel free to share!

COURSE OVERVIEW - Metabarcoding has emerged as a pivotal technique, rapidly expanding and revolutionizing the way we study biodiversity. From soil samples to aquatic environments, metabarcoding provides insights into the diverse array of organisms present, offering crucial information for conservation efforts and ecological research. However, metabarcoding encounters intrinsic biases inherent in its methodology. Metabarcoding pipelines are designed to mitigate these biases, and this course will offer insights into optimizing these pipelines for accurate and reliable results. With new techniques continuously evolving, we'll explore methodologies geared towards unraveling both inter and intra-species diversity while addressing the common challenges encountered in a methodology. Additionally, we'll navigate the landscape of methods enabling comprehensive biodiversity assessments, alongside showcasing new machine learning approaches for inferring ecological quality status. This course will focus on the MJOLNIR3 pipeline and its theoretical framework. This R package is based on eight simple functions divided into four different blocks. For each function, a comprehensive description of the process will be provided, including alternatives from other pipelines and their basic command line usage.

By the end of the course, participants will:

Gain a comprehensive understanding of the theoretical foundations underpinning metabarcoding pipelines. Develop the ability to identify potential biases and effectively apply specialized software to mitigate them. Acquire proficiency in working across three distinct levels of coding requirements, encompassing command-line operations and graphical user interface packages. Demonstrate a thorough comprehension of basic biodiversity analysis techniques, spanning inter and intra-species

levels. Please email oliverhooker@prstatistics.com with any questions.

Oliver Hooker PhD. PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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ONLINE COURSE - Time Series Analysis and Forecasting using R and Rstudio (TSAF01)

<https://www.prstats.org/course/time-series-analysis-and-forecasting-using-r-and-rstudio-tsaf01/> Instructor - Dr. Rafael De Andrade Moral

17th - 26th October

Please feel free to share!

In this six-day course (Approx. 35 hours), we provide a comprehensive practical and theoretical introduction to time series analysis and forecasting methods using R. Forecasting tools are useful in many areas, such as finance, meteorology, ecology, public policy, and health. We start by introducing the concepts of time series and stationarity, which will help us when studying ARIMA-type models. We will also cover autocorrelation functions and series decomposition methods. Then, we will introduce benchmark forecasting methods, namely the naïve (or random walk) method, mean, drift, and seasonal naïve methods. After that, we will present different exponential smoothing methods (simple, Holt's linear method, and Holt-Winters seasonal method). We will then cover autoregressive integrated moving-average (or ARIMA) models, with and without seasonality. We will also cover Generalized Additive Models (GAMs) and how they can be used to incorporate seasonality effects in the analysis of time series data. Finally, we will cover Bayesian implementations of time series models and introduce extended models, such as ARCH, GARCH and stochastic volatility models, as well as Brownian motion and Ornstein-Uhlenbeck processes.

Please email oliverhooker@prstatistics.com with any questions.

Oliver Hooker PhD. PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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Otjiwarongo Namibia ConservationGenetics Jan5-15

The early application deadline (June 6th, 2024) is approaching for CONGEN2025 (the "2025 Recent Advances in Conservation Genetics" course), to be held at the Cheetah Conservation Fund Research Center in Otjiwarongo, NAMIBIA, from January 5th to 15th, 2025.

Applications submitted by June 6th, 2024, incur no fee.

Applications received post-June 6th will incur a late fee of US\$250.

Complete the application form here to be considered for participation using the CONGEN2025 Application Form: (<https://conservationgenetics.org/congen2025/-congen2025-application/>).

The application process is complimentary, with no registration fee required upfront, but upon acceptance by our selection committee, early application candidates may qualify for various sponsored scholarships that cover tuition, living expenses, or both. Thanks to our sponsors, ConGen2025 will have several scholarships available to cover these expenses, and these will be offered to successful candidates after they are chosen by the committee based on merit. However, you must first submit your regular application to be eligible for these funds. To receive full consideration for the scholarships, the applications must be submitted before June 6th, 2024.

CONGEN2025 is an immersive course that will accommodate 25-30 students, prioritizing participants from African nations, and will feature 15-20 distinguished faculty members from across the globe. It aims to delve into the latest methodologies, interpretations, and practical applications of genetic and genomic analyses in the conservation of endangered species. Our faculty will impart their knowledge on cutting-edge technologies, research methodologies, and the practical application of population-based studies in conservation efforts.

Application to ConGen2025 is competitive. The committee will review submissions and notify successful applicants via mail. Early applications, submitted by June 6th, 2024, incur no fee. Early applicants will have until September 15th, 2024, to secure their spot with a registration deposit or risk losing their place to the next candidate on the waiting list. Applications received post-June 6th will incur a late fee of US\$250.

The comprehensive registration fee of \$2,500 includes tuition, accommodation, meals, and course-related transportation. Participants are responsible for their travel arrangements to Namibia.

Successful early applicants will be informed of the committee's decision by July 1, 2024. Those accepted post-early submission must confirm their participation by July 15, 2024, and secure their spot with a US\$1,250 deposit by September 15, 2024.

Accommodations will be provided at the CCF Educational Lightfoot Camp, near Otjiwarongo, NAMIBIA, offering an authentic African experience. The camp features basic but comfortable huts with essential amenities. Shared facilities include wash stations with open-air showers and a communal kitchenette. A picnic and fire area is available for relaxation and socializing. Additional accommodations may include dormitories or rondavels.

The course is organized by esteemed professionals, including local hosts Dr. Laurie Marker and Dr. Anne Schmidt-Küntzel of the Cheetah Conservation Fund, Namibia, and members of the ConGen Organization Committee from various prestigious institutions worldwide. The ConGen Organization Committee are Stephen J. O'Brien (NOVA Southeastern University, FL, USA, chair), Taras K Oleksyk (Oakland University, MI, USA), Emma Teeling, (University College Dublin, Ireland), Eduardo Eizirik (PUCRS, Brazil), Laurie Marker (CEO Cheetah Conservation Fund, Namibia), Cindy Harper (University of Pretoria Veterinary College, South Africa), Laurie Goodman (Executive Editor, GigaScience), Klaus-Peter Koepfli (Smithsonian-Mason School of Conservation, George Mason University, USA)

The CONGEN2025 course, now in its 29th year, continues to evolve, highlighting the latest advancements in conservation genetics and genomics. The curriculum includes plenary lectures, hands-on tutorials, and practical applications, addressing a wide range of topics from study design to the integration of AI in conservation genomic data analysis. For more information and examples of past course schedules, please visit our website: www.conservationgenetics.org/congen2025 Tarás K. Oléksyk, Ph.D.

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SapeloIsland US eDNA SciComm Aug4-10

“Telling Stories Through Data” Workshop August 4-10, 2024 UGA Marine Institute on Sapelo Island

Workshop Website: <https://bit.ly/TSTD2024> Apply to participate (form closes on Friday June 14, 2024): <https://forms.gle/Jza1rAVy6Aubu7wc8> The TSTD workshop series is designed to foster practical skills in both bioinformatics and science communication, training participants in how to “tell stories through data.” Each weeklong workshop will be centered around two overarching questions: How do you find the story? and What do you do with the story? Morning sessions (led by Holly Bik, Associate Professor at the University of Georgia) will focus on how these questions are applied to bioinformatics data analyses, guiding participants in how to visualize data, conduct appropriate statistical analyses, and build narratives for scientific manuscripts. Afternoon sessions (led by Virginia Schutte, freelance science communicator) will provide complementary training on storytelling for public audiences, teaching participants how to identify compelling public narratives and prepare science outreach products using a variety of digital media tools. This workshop is targeted towards graduate students and postdoctoral researchers, and participants are expected to have some basic familiarity with command line tools and scientific programming (e.g. Unix, R, and/or Python). The 2024 TSTD workshop will be focused on analysis of eDNA Metabarcoding data (e.g. 16S/18S rRNA environmental amplicons). Please refer to workshop website for a full description and preliminary schedule.

This workshop is targeted towards graduate students and postdoctoral researchers, although we will consider applications from other early-career scientists who would especially benefit from participating. All participants are expected to have some basic familiarity with command line tools and scientific programming (e.g. Unix, R, and/or Python) in order to fully benefit from the workshop trainings. This is NOT an introductory programming course; we will be focusing on -Omics workflows and downstream data visualizations of target datasets. The 2024 TSTD workshop will be focused on eDNA Metabarcoding data (e.g. 16S/18S rRNA environmental amplicons).

Holly Bik Associate Professor Department of Marine

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The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

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