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# E v o l D i r

April 1, 2024

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

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## 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](mailto: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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**Campinas Brazil  
EvolutionPlantFungalInvasions  
Jun26-29**

Dear all,

Please note the following approaching deadline and share it with friends and colleagues.

45th New Phytologist Symposium: Ecological and evolutionary consequences of plant-fungal invasions

26-29 June 2024 UNICAMP, Brazil

Register to present a poster at the symposium by 1 April: <https://npf-events.evessiocloud.com/45NPS/en/-page/home> Best wishes, Mike

Dr Mike Whitfield (he / him), Development Coordinator The New Phytologist Foundation < <https://www.newphytologist.org/> > Registered charity number 1154867 Twitter & Instagram: @newphyt | Facebook: fb.com/NewPhytologist

Dedicated to the promotion of plant science

“Whitfield, Mike (whitfield)”  
<m.whitfield@lancaster.ac.uk>

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**Italy EvolutionOfNonVerbalCommunication  
Oct19-23**

The workshop is dedicated to the exploration of the intricacies of non-verbal communication across species. The meeting, scheduled to take place on October 2024 at Ettore Majorana Foundation and Centre for Scientific Culture, International School of Ethology, Erice, Italy aims to bring together a diverse array of researchers, scholars, and practitioners who share a common interest in unraveling the complexities of communication beyond

linguistic boundaries. In particular, the aim is to unveil the nuances of non-verbal communication within and between human dyads, as well as across different species. As evolutionary biologists, you are keenly aware of the pivotal role that communication plays in shaping social dynamics, facilitating cooperation, and driving evolutionary processes. From the subtle gestures and facial expressions exchanged between individuals within a species to the intricate signaling mechanisms employed in interspecies interactions, non-verbal communication serves as a rich tapestry through which behaviors, emotions, and intentions are conveyed and interpreted. The purpose of the present workshop is to give an overview of the “state of the art” of the importance of the ethological approach for the understanding of nonverbal communication between human interactions specifically in clinical therapeutic setting. Given our evolutionary history nonverbal behaviour will be explored in nonhuman primates and in animal-human interactions. This aim will be achieved by interdisciplinary discussion between ethologists, primatologists, child psychologists, psychiatrists and psychotherapists.

Chiara Scopa, PhD student Dipartimento di Medicina e Chirurgia, Unità di Neuroscienze Università di Parma Viale delle Scienze 11/A, 43124, Parma

Chiara SCOPA <chiara.scopa@unipr.it>

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## London MathMolBiol Aug29-30

Registration and abstract submission for the next MASAMB (Mathematical and Statistical Aspects of Molecular Biology) meeting at Queen Mary University of London 29th-30th August 2024 are now open.

With typically around 100 participants from mathematics, statistics, computer science, bioinformatics, biology and related fields, the MASAMB meetings provide an intimate setting for exchanging ideas in methodological and applied research. Research students and scientists newly entering the field of genomic research are particularly welcome and encouraged to submit abstracts.

Please visit our website for more information on the venue and the registration process: <https://-masamb2024.wixsite.com/masamb2024> We offer grants for caring duties and are able to accommodate for other needs to offer an inclusive in-person meeting.

Looking forward to seeing many of you in East London this Summer.

Matteo Fumagalli

Matteo Fumagalli <m.fumagalli@qmul.ac.uk>

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## Marseille EvolutionaryBiology 2025

We are very happy to announce that the evolutionary biology meeting 'in' Marseille will be back in 2025 after an interruption due to the COVID-19 pandemic.

More information can be found on the meeting's website: [aeeb.fr](http://aeeb.fr)

Pierre Pontarotti DR CNRS new email [pierre.pontarotti@cnrs.fr](mailto:pierre.pontarotti@cnrs.fr) UMR MEPHI D-258, CNRS SNC5039 IHU Mi<sub>1/2</sub>diterrani<sub>1/2</sub>e Infection

19-21 Boulevard Jean Moulin 13005 Marseille

Bureau 408

tel 0413732425 / 0695177328 <https://sites.google.com/view/pontarotti/> The evolutionary biology meeting will be back in 2025 ([aeeb.fr](http://aeeb.fr))

< <https://twitter.com/pontarotti> >

PONTAROTTI Pierre <[pierre.pontarotti@univ-amu.fr](mailto:pierre.pontarotti@univ-amu.fr)>

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## Mexico SMBE CallForAbstracts DueMar15

Submission Deadline March 15, 2024

SMBE2024 Call for Abstracts - Submission Deadline March 15, 2024 -

Dear Member,

The Society for Molecular Biology and Evolution is now accepting abstracts for the 2024 annual meeting. SMBE 2024 will take place in Puerto Vallarta, Mexico

on July 7-11, 2024. Abstracts can be submitted to request participation as an oral or poster presentation on 37 different symposia. The deadline for submitting an abstract is March 15, 2024.

Please note the SMBE2024 symposium list also includes our traditional Open and Editors Symposium. If you feel your work is currently not covered by any of the featured symposia please consider submitting abstracts to the Open Symposium. Deadline March 15.

Visit the 2024 meeting website <http://smbe2024.org/> to register and submit an abstract for SMBE 2024. This year SMBE is offering registration rate discounts for low or middle income countries (LMIC). Register to SMBE 2024 before May 9 to have an Early Bird rate. Please direct any questions regarding abstract submission to [attendancesmbe2024@gmail.com](mailto:attendancesmbe2024@gmail.com).

SMBE 2024 Awards can only be applied to when submitting an abstract at <http://smbe2024.org/>. The list of awards include:

**Young Investigator Travel Award.** Attending a major conference is important for young researchers because it allows them to present their work to an expert audience and gives them the opportunity to make useful contacts. However, SMBE recognizes that travel funds may not be easily available at this career stage. Postdoctoral researchers and graduate students may apply for travel awards to attend the annual SMBE meeting.

**The SMBE Graduate Student Excellence Award.** This prize is given to the best presentation at the Graduate Student Excellence symposium which features talks from eight graduate students. Eligibility: Current graduate students and postdoctoral researchers who received their primary doctoral-level degree no earlier than one year prior to the start of the annual meeting of the society (minus any career disruption or delay). A candidate for the award must become a member of the Society at least a month before the first day of the annual meeting. You must also email your Curriculum Vitae to [tosmbe.ks@kwglobal.com](mailto:tosmbe.ks@kwglobal.com). \*\*The deadline for applications for this award is March 15th.\*\*

**The Undergraduate Mentorship Award** provides support, advice and networking opportunities for undergraduate students (including Masters students under a 3+2 system) as they navigate their first international conference. Applicants for this award must be presenting their own work as a poster or talk at the conference. Applicants must email a short explanation (250 words) of why they want to attend this meeting, including a mention of whether you fall into a group traditionally underrepresented at SMBE (e.g. enrolling in university later in life, or being the first in your family to at-

tend university). A short letter of support (250 words) should also be sent from your academic supervisor to [attendancesmbe2024@gmail.com](mailto:attendancesmbe2024@gmail.com) confirming that you are undergraduate (or a Masters student under 3+2), and that the research to be presented is your own. \*\*The deadline for applications for this award is March 15th.\*\*

Awardees are granted up to US \$2500 for travel within the same continent, and up to US \$3500 for long-haul travel. Reimbursements are processed after the meeting and awards may claim travel, accommodation and meeting registration expenses. Please review the information required to apply at the abstract registration URL. \*\*The deadline for applications for this award is March 15th.\*\*

**Caregiver award** is open for SMBE members with expenses for the care of children or dependent adults (including adult children with a disability or elderly relatives) during their attendance at the annual SMBE meeting. The amount requested can be up to \$2000 USD. Please review the information required to apply through the abstract registration URL. \*\*The deadline for applications for this award is March 15th.\*\*

The Local Organising Committee [smbe2024@gmail.com](mailto:smbe2024@gmail.com)  
Society for Molecular Biology & Evolution  
[smbe.ks@kwglobal.com](mailto:smbe.ks@kwglobal.com)

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## Mexico SMBE ComputMethodsTools DueMar15

Hello,

We invite your abstract to the SMBE 2024 Symposium (#36; [smbe2024.org](http://smbe2024.org)) for oral presentations highlighting innovative approaches, methodologies, algorithms, smarter software implementations, and sustainable analytical practices. Selected presentations will critically assess the potential of achieving computational efficiency without sacrificing accuracy or depth of analysis. The symposium aims to foster community-wide awareness and adoption of greener scientific methodologies, thereby promoting equity, diversity, and broader access to molecular evolutionary research in the era of burgeoning big datasets.

Limited funds will be made available for authors of the selected abstracts, covering airfare and/or registration fees.

This year's conference will be held in Puerto Vallarta, Mexico, with the abstract submission deadline of March 15 ([smbe2024registration.org/abstracts](https://smbe2024registration.org/abstracts)).

For any inquiries, contact: - Sudhir Kumar at [s.kumar@temple.edu](mailto:s.kumar@temple.edu) - Claudia Russo at [claudiaam-russo@gmail.com](mailto:claudiaam-russo@gmail.com)

Sudhir Kumar <[s.kumar@temple.edu](mailto:s.kumar@temple.edu)>

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## Mexico StructuralPhylogenetics DueMar15

Dear evoldir members,

We are very excited about this upcoming symposium at SMBE2024 in Mexico in July 2024, organized in part by several University of Auckland postdocs. Please forward to your networks as you see fit.

Details about deadlines and travel awards follow. Thanks very much! Cheers, Nick

**CALL FOR ABSTRACTS: Structural Phylogenetics Symposium at SMBE 2024 in Puerto Vallarta, Mexico!**

Explore cutting-edge methodologies & applications peering into evolutionary history with the lens of protein structure.

Abstracts due March 15, 2024: <https://smbe2024.org>  
Application for a travel award is also available: <https://www.smbe.org/smbe/AWARDS> Symposium description:

<https://smbe2024.org> Submission of abstracts is now open!

Deadline for abstracts: March 15th, 2024

July 7-11, 2024 Puerto Vallarta, Mexico Convention Center Puerto Vallarta SMBE 2024

SMBE 2024 Accepted Symposia

Topic 1: Phylogenetics and Comparative Genomics.

1. Structural phylogenetics: investigating deep evolutionary history using protein structure.

Organizers: Caroline Puente-Lelievre, Jordan Douglas, Ashar Malik.

Invited speakers: Betul Kacar, Martin Steinegger.

Description of the symposium:

Recent advances in AI protein structure predictions have revolutionised biological research. The implications for phylogenetics may be vast. The combination of (1) high-quality structure predictions for millions of proteins with (2) methods that can efficiently include this information in homology searches and the reconstruction of protein history (via structural distance metrics, or FoldSeek's representation of tertiary structure as a sequence of characters) raises the possibility of more accurate phylogenetics even into the "twilight zone" where amino acid sequence similarity has been lost. Structural phylogenetics thus emerges as an increasingly practicable discipline that combines structural, evolutionary, and computational biology to inform deep relationships and evolutionary events, even those that predate the last universal common ancestor. This symposium showcases structural phylogenetic methodologies and applications, either for inferring phylogeny or reconstructing the evolution of ancestral structures and functions, and is aimed at fostering state-of-the-art interdisciplinary work from researchers from a variety of disciplines and career stages.

Recent papers:

Puente-Lelievre, Caroline; Malik, Ashar J.; Douglas, Jordan; Ascher, David; Baker, Matthew; Allison, Jane; Poole, Anthony; Lundin, Daniel; Fullmer, Matthew; Bouckert, Remco; Kim, Hyunbin; Steinegger, Martin; Matzke, Nicholas J. (2023). Tertiary-interaction characters enable fast, model-based structural phylogenetics beyond the twilight zone. *bioRxiv*, 571181. December 12, 2023. <https://www.biorxiv.org/content/10.1101/2023.12.12.571181v2.full> <https://doi.org/10.1101/2023.12.12.571181> van Kempen M, Kim SS, Tumescheit C, Mirdita M, Lee J, Gilchrist CLM, Sijding J, Steinegger M. Fast and accurate protein structure search with Foldseek. *Nat Biotechnol*. doi: 10.1038/s41587-023-01773-0

Moi, David; Bernard, Charles; Steinegger, Martin; Nevers, Yannis; Langleib, Mauricio; Dessimoz, Christophe (2023). Structural phylogenetics unravels the evolutionary diversification of communication systems in gram-positive bacteria and their viruses. *bioRxiv* 2023.09.19.558401. doi: 10.1101/2023.09.19.558401

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## Montpellier MCEB MathEvolBiology Jun17-21

// EXTENDED DEADLINE FOR ABSTRACT SUBMISSION // // March 8 > March 20 //

Mathematical and Computational Evolutionary Biology (MCEB) June 17-21, 2024 Hameau de l'Etoile, near Montpellier, France

<https://mceb2024.sciencesconf.org/> Dates and deadlines:

February 1: Opening of abstract submission on the conference web site  
 March 20: End of abstract submission  
 March 27: Notification of decisions to applicants, opening of registrations  
 April 26: End of registrations and payment (~650 euro, including accommodation)  
 June 17 (evening) - 21 (early afternoon): conference

This year's meeting will put the emphasis on machine learning, in particular simulation-based inference techniques. These approaches are getting traction in population genetics, phylogenetics, phylodynamics and areas in evolutionary biology whereby the complexity of the probabilistic models at play forbid the application of classical, likelihood-driven, estimation tools. The conference will provide a good opportunity to provide an overview of the techniques themselves with a focus on their applications to shed light on interesting biological processes.

Beyond this year's theme, general concepts, models, methods and algorithms will be presented and discussed, just as in the previous editions of MCEB. As usual, the meeting will bring together researchers originating from various disciplines: mathematics, statistics, computer science, phylogenetics, population genetics, epidemiology, ecological modeling... Keynote speakers (see below) will introduce a field of research and discuss their own work in this field. Afternoon will be for short presentations and posters, with plenty of time for discussions. We will stop early every day, thus leaving time for other activities, such as hiking, rock climbing or river kayaking

Keynote speakers:

- Carolin Colijn <https://www.sfu.ca/math/people/faculty/ccolijn/> - Claire Guinat <https://envt.fr/chercheur/claire-guinat/> - Jean-Michel Marin <https://imag.umontpellier.fr/~marin/> - Tal Pupko <https://www.tau.ac.il/~talp/> - Claudia Solís-Lemus <https://solislemuslab.github.io/>

- Yun S. Song <https://people.eecs.berkeley.edu/~yss/> For more information and abstract submission, visit the website at: <https://mceb2024.sciencesconf.org/> We are looking forward to seeing you all at the Hameau in June!

Best regards,

The MCEB organizing team –

Stephane Guindon <stephane.guindon@lirmm.fr>

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## Montreal Adaptive Epigenetics Jul26-30

Dear colleagues,

We are organizing a symposium “Adaptive Epigenetics” at the 3rd Joint Congress on Evolutionary Biology, which is taking place July 26-30 in Montreal, Canada. The goal of this symposium is to feature talks focused on the various ways that epigenetic mechanisms could contribute to evolutionary processes, especially to adaptation. We hope to assemble scientists from different fields working on theoretical and empirical questions involving adaptive epigenetics. The abstract is provided at the end of the message.

Registration is now open, and abstracts can be submitted to be considered for this symposium. Please see the 2024 Conference info (<https://www.evolutionmeetings.org>) for meeting info. Talks are accepted on a first-come-first-serve basis, and those that are not selected for a symposium will nevertheless be placed in one of the general sessions. Please don't hesitate to contact us if you have any questions about the symposium.

Hollie Marshall <hjm32@leicester.ac.uk> James Ord <james.ord@helsinki.fi> Clare Vennay <clarevenney@gmail.com> Clarissa de Carvalho <clarissa.carvalho@unifesp.br>

Symposium abstract:

The field of evolution is on the edge of a paradigm shift with the incorporation of epigenetic mechanisms changing how we view evolutionary processes. Epigenetics refers to potentially heritable chemical modifications that occur on the DNA of an organism. These chemical modifications can affect how genes function and

can be induced by the environment. This paradigm is highlighted by the Unified Evolution Theory (2021), a modification of the Extended Evolutionary Synthesis which includes heritable environmentally induced epigenetics. This newly modified theory and specifically the extent to which epigenetics can play a role in species adaptation remains highly debated in some subfields but not others. A symposium directly addressing this topic will allow researchers from all areas to learn about the latest advances and evidence (or lack thereof) within evolutionary epigenetics, facilitating debate and knowledge sharing.

Clarissa F. de Carvalho Postdoctoral fellow  
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<clarissa.carvalho@unifesp.br>

Clarissa Ferreira <clarissa.ferreira1@gmail.com>

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## Montreal Evolution Biological Noise Jul26-30

Dear colleagues,

We are excited to announce a symposium on EVOLUTION AND BIOLOGICAL NOISE at the 3rd Joint Congress on Evolutionary Biology in Montréal, July 26 - 30, 2024.

**INTELLECTUAL MOTIVATION:** Phenotypic variation is the substrate of evolution by natural selection. One source of phenotypic variation is biological noise, which can be generated both during reproduction (e.g. mutations) and development (e.g. mistranscription, mistranslation). Critically, the amount of phenotypic variation resulting from biological noise can be under heritable, genetic control. For example, DNA polymerase, RNA-polymerases and ribosomal protein alleles can differ in their accuracy of replication, transcription, and translation, respectively. This fact raises the possibility that the amount of biological noise, and hence, the amount of phenotypic variability in an evolving population may itself be subject to natural selection.

**TIMELINESS:** Interest in the evolution of biological noise goes back at least 80 years, but stimulated by rapid technological advances (e.g., single-cell phenotypic and genetic characterization), the past 20 years have seen an explosion of work. Today, biological noise is under active investigation in diverse intellectual communities includ-

ing molecular modelling, gene expression and functional biology, developmental biology, transmission genetics, biophysics, systems and synthetic biology, and population genetics. There is also a growing appreciation of the role of biological noise in human health.

**OBJECTIVES:** The purpose of this symposium is to draw workers together from across communities in order to develop a greater understanding of the empirical and conceptual similarities and differences among these many domains of inquiry into the evolution of biological noise. The organizers are especially interested in developing a deeper qualitative and quantitative understanding of the selective tension between the deleterious and beneficial consequences of biological noise.

Questions? Contact the symposium organizers Nacho Bravo (ignacio.bravo@cnr.fr) or Dan Weinreich (daniel.weinreich@brown.edu).

**Important dates:** \* Registration is now open. \* Early-bird registration rates available until May 1. \* Talk submissions due by May 1. \* Conference dates: July 26 - 30. (Also perhaps of interest: the Montreal Jazz Festival opens July 27...)

This is the link to the instructions for registering and submitting an abstract, and then choosing the symposium of your interest: <https://www.evolutionmeetings.org/registration.html> Please note there is no risk in applying to symposia—talks not selected for symposia will be scheduled in concurrent sessions. <https://www.evolutionmeetings.org/instructions-for-presenters.html> Please join us in making some (biological) noise this summer in Montréal!

daniel.weinreich@brown.edu

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## Montreal Limits PhylogCompMeth Jul26-30

Dear Colleagues,

We are organising a symposium at the upcoming joint Evolution meeting in Montreal this July, entitled “What we can and cannot know through current and upcoming Phylogenetic Comparative Methods”. We are looking for enthusiastic speakers to come and add their views to the discussion and would like to encourage anyone interested in participating to submit an abstract.

The intended topics could include 1) simulation studies, 2) conceptual/theoretical work, 3) empirical work, or 4) new methods. The important thing is that it focuses on the limits of our current analytical capabilities and our understanding, and (if possible) ideas of how to overcome them (i.e., not just the presentation of a new model and how awesome it is). This could e.g. mean empirical work showing how expert knowledge can be incorporated or used to identify inferences as nonsensical, a conceptual demonstration of how the way we are addressing these questions creates a blind spot, or simulations pointing out inference limits we weren't aware of yet.

We are hoping for a diverse set of speakers from different career stages, and would thus encourage everyone to apply to be part of the symposium. The goal is for this to result in stimulating discussions, synthesis, and a vision of the future directions of the field.

Note that there is no dedicated funding to attend this symposium, so potential in-person presenters should apply for travel support from the societies or other sources. However, virtual attendees can apply to be included for the symposium too, and if selected get to have their recorded talk played during the in-person session. In addition, we are happy to highlight virtual talks presented during the virtual Evolution conference which thematically fit the symposium (and also for poster presentations).

If you or your lab members are interested, follow the instructions here ([https://twitter.com/Evol\\_mtg/status/1760696207372881977](https://twitter.com/Evol_mtg/status/1760696207372881977)) and on the conference website (<https://www.evolutionmeetings.org/instructions-for-presenters.html>), register and indicate your interest in participating in our symposium.

If anyone is unsure whether an intended talk topic fits the symposium, or plan to submit a poster on a related topic, feel free to reach out to us with questions and suggestions! And of course feel free to share this with whomever you feel might be interested.

Best wishes,

Orlando Schwery (schwery.macroevo@pm.me /  
oschwery@vt.edu) and Mariana P. Braga (mari-  
ana.pires.braga@slu.se

schwery.macroevo@pm.me

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## Montreal MarineEvolution Jul26-30

Dear friends and colleagues,

As part of the 3rd Joint Congress on Evolutionary Biology 2024 in Montreal, Canada, 26-30 July (<https://www.evolutionmeetings.org/>), we are organising a symposium on “Advances in marine evolutionary biology” (<https://www.evolutionmeetings.org/-symposia.html>). The goal of the symposium is to bring together evolutionary biologists working in marine systems across the globe and highlight scientific and technological advances in the field (See a more detailed summary below)

If you work with evolutionary marine biology we would be very happy if you consider submitting your talk to our session! Talks that are not selected for a symposium will nevertheless be placed in one of the general sessions.

Please do not hesitate to contact us if you have any questions:

Ellika Faust [ellika.faust\[at\]eawag.ch](mailto:ellika.faust@eawag.ch)

Pierre De Wit [pierre.de.wit\[at\]bioenv.gu.se](mailto:pierre.de.wit@bioenv.gu.se)

Summary:

Around 500 million years ago life had not yet colonised land and was exclusively found in the oceans. Despite the rich diversity of life found in our oceans, much has yet to be described and put into an evolutionary context. Practical hurdles of working in the marine environment, as well as the complexity of marine systems, have historically impeded our ability to study them. However, with recent theoretical and technological advancements, these hurdles are diminishing, now allowing for in-detail studies of biological processes such as speciation, local adaptation, connectivity, and genotype-phenotype associations in diverse marine systems. This symposium will broadly feature studies that advance our understanding of these phenomena and their underlying mechanisms. It aims to highlight similarities and interconnections of study systems across different coastlines and oceans, thereby building a base for future collaborations across networks and societies in a world undergoing dramatic change.

“Faust, Ellika” <[Ellika.Faust@eawag.ch](mailto:Ellika.Faust@eawag.ch)>

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## Montreal Mutation Rates Jul26-30

Dear evoldir community,

We would like to attract your attention to the following symposium at the Evolution 2024 conference in Montreal.

Title: From mutation rate to mutations rates: how uncovering the mutation rates variations change our understanding of adaptation

Description: Mutations are the raw material on which selection acts and the origin of biodiversity. Until recently, much of the research on the contribution of mutations to adaptation has been focused on genome wide base substitution rate ( $\mu$ ) and the evolutionary forces shaping it. Now, the easier and cheaper access to whole genome sequences and the improvement of genomic analyses allows to better document the variation of the mutation rate across the tree of life, but also to measure the rate of other mutation types, in particular structural mutations. Recent researches have also unraveled variations of mutation rates and spectrum with environmental factors and genomic context, sometimes of greater amplitude than the variation in mutation rate observed between closely related species. The picture of the evolution of mutation rates and the contribution of mutation rates to adaptation is thus becoming more colourful and more complex. In this symposium, we hope to bring together theoretical, genomic and experimental approaches to integrate the different facets of mutation rate and of its contribution to determining the adaptive paths taken.

Organizers:

Marc Krasovec (marc.krasovec@obs-banyuls.fr)

Stephanie Bedhomme  
(stephanie.bedhomme@cefe.cnrs.fr)

We hope to see you in Montreal!

Stephanie  
<stephanie.bedhomme@cefe.cnrs.fr>

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

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## Montreal Plasticity Social Evolution Jul26-30

Evoldir title: Montreal.PlasticitySocialEvolution.Jul26-30

Subject: Symposium on the role of phenotypic plasticity in social evolution

Dear colleagues,

We are excited to announce the symposium “Interacting in a changing world: the role of phenotypic plasticity in social evolution” at this year’s 3rd Joint Congress on Evolutionary Biology in Montreal on 26-30 July 2024. We would like to invite anyone interested in sharing their research and joining the discussion on the topic to submit an abstract. We welcome researchers from all career stages and backgrounds. You can register here: <https://www.evolutionmeetings.org/registration.html>. Please don’t hesitate to contact us if you have any questions on the symposium, The organizers

Francesca Santostefano F.Santostefano2@exeter.ac.uk  
Tom Ratz tom.ratz@uzh.ch

Symposium title Interacting in a changing world: the role of phenotypic plasticity in social evolution

Symposium Abstract Interacting with conspecifics is an important part of an organism’s life, often crucial to reproduction and survival. Traits mediating social interactions can have a genetic basis and be under selection, a process known as social evolution. Theory in social evolution has highlighted how interactions can affect the rate of evolution by accelerating or constraining the response to selection. Current models, however, do not yet fully capture the dynamic nature of social interactions: individuals typically differ in social behavior and adjust it to social partners. As a result, we still poorly understand how between- and within-individual variation, which determines heritable variation on which selection can act upon, affects the direction and speed of evolution. This symposium seeks to showcase recent advances in the field, focusing on individuality and plasticity. In doing so we aim to stimulate discussion and identify potential gaps and future directions of research on social evolution.

Goal of the Symposium Social evolution is a central topic in evolutionary biology. The field has recently made exciting conceptual advances to clarify how indirect ge-

netic effects and social selection affect the evolution of phenotypes, and developed powerful statistical tools (random-slope GLMMs, social animal models) to analyze complex data on social behavior. Yet empirical studies are lagging due to limited exchange between theoreticians and empiricists on one hand, and between quantitative geneticists and behavioral ecologists on the other hand. Given that the Congress will attract a broad crowd of theoreticians and empiricists from both backgrounds, a symposium on social evolution will be a unique opportunity to present the latest theoretical advances and ongoing empirical research in the field. We will look forward to fostering discussion and exchange of ideas in social evolution, which is an essential step to drive progress in understanding the central role that social interactions play in evolution.

“Santostefano, Francesca”  
<F.Santostefano2@exeter.ac.uk>

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## Montreal Speciation Jul26-30

We are organizing a symposium on “The completion of speciation: coupling, persistence and the micro-macro link” at the 3rd Joint Congress on Evolutionary Biology < <https://www.evolutionmeetings.org/> > (July 26-30, 2024, Montreal, Canada) and would like to encourage you to submit an abstract.

The focus of the symposium will be on integration. Speciation is central to evolutionary biology. However, major issues remain unresolved concerning the evolution of strong and robust reproductive isolation that leads to the persistence of new lineages over macroevolutionary time scales. Completion of speciation usually involves the coincidence of multiple barriers to gene exchange but many processes can generate this coupling and their contributions are not well understood. Some types of barrier might be critical for lineage persistence: perhaps intrinsic barriers are critical or strong assortative mating is needed to allow coexistence, for example. A wide range of approaches to these issues is needed, ideally covering a diversity of taxa. Therefore, this symposium will welcome contributions from all areas of evolutionary biology, fostering interactions among subfields in order to understand the evolution of strong reproductive isolation and the persistence of lineages across micro to macroevolutionary scales.

Registration and abstract submission are open now.

Please distribute this information to your networks. We aim for a wide diversity of contributors to the symposium across all dimensions, including gender, nationality, career stage and specialist field.

Roger Butlin (r.k.butlin@shef.ac.uk) and Jonna Kulmuni (j.k.kulmuni@uva.nl)

Roger Butlin

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<https://littorina.sites.sheffield.ac.uk/> Roger Butlin  
<r.k.butlin@sheffield.ac.uk>

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## Montreal UnPredictableEvolution Jul26-30

EvolDir title: Montreal.(Un)PredictableEvolution.Jul26-30

Subject: Symposium on the (Un)Predictability of Evolution

Dear colleagues,

We are happy to announce the symposium “Empirical and Conceptual Insights on the (Un)Predictability of Evolution” at this year’s 3rd Joint Congress on Evolutionary Biology in Montreal on 26-30 July. Submission of talks for the symposium is open to anyone attending the conference. You can register here: <https://www.evolutionmeetings.org/registration.html> . The goal of this symposium is to bring together empirical, theoretical, conceptual and philosophical insights on the predictability of evolution. With a long tradition in evolutionary biology, the “predictability topic” has recently gained greatly renewed interest, with growing attention also in other (sub-)fields such as ecology, speciation, and genomics. This is in part due to the advent of powerful recent technologies (for example, investigations involving aDNA or in silico and synthetic experimental approaches), several long-term field studies and experiments, controlled evolve-resequence experiments, as well as drastic real-life experiences for many of us in form of the COVID-19 pandemic. It therefore also seems of particular importance to re-consider and clarify the conceptual framework of predictability in science in general, and in evolutionary research specifically.

We hope this symposium will bring together broad and diverse empirical, theoretical and conceptual perspectives on the types, function and value of predictions in evolutionary research, the aspects that limit or facilitate predictability, as well as examples demonstrating the relevance of predictions in our research. If your work is relevant to any of these or related questions, please consider submitting an abstract to our symposium! For some more information, the symposium abstract is attached below.

In case of questions, please don't hesitate to contact us.

Lead Organizers: Marius Roesti (marius.roesti-AT-unibe.ch) and Brian Langerhans (langerhans-AT-ncsu.edu)

Additional Organizers: Andrew Hendry and Jonathan Losos

Symposium abstract:

The ability to make accurate predictions is often taken as a hallmark of strong scientific understanding. How good are we in making predictions about evolution and how can we actually test these predictions? What do we want to predict and how do we generate predictions? What limits our predictability and are these limits inherent or surmountable? And what might we gain by accurately predicting evolution? Our symposium will foster crosstalk among researchers with different perspectives on and approaches to these questions. We are excited to welcome innovative empirical (e.g., large-scale/long-term experimental or novel comparative), theoretical (e.g., synthetic, mathematical), and philosophical contributions, as well as historical perspectives on the (un)predictability of evolution. We further encourage submissions addressing predictability of evolutionary change across all levels of biological organization (e.g., genomic, cellular, morphological, behavioral, ecological communities).

“marius.roesti@unibe.ch” <marius.roesti@unibe.ch>

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## Montreal UrbanEvolution Jul26-30

We are organizing a symposium on “Urban Evolutionary Dynamics and Species Interactions” at the 3rd Joint Congress on Evolutionary Biology (July 26-30, 2024, Montreal, Canada) and would like to encourage you to submit an abstract. <https://www.evolutionmeetings.org/> The focus of the symposium will be on urban evolution. Urbanisation demands organisms rapidly respond to environmental changes including new microclimates, novel stimuli, pollution, unique synthetic habitat, and fragmented natural landscapes. These documented evolutionary changes have impacts beyond the focal species, providing an exciting study question for ecological and evolutionary patterns, processes, and principles. Complicating these “eco-evolutionary feedbacks” is the fact that city landscapes are not randomised, but fundamentally intertwined with human society, politics, and culture. This symposium will highlight how urbanisation influences (1) evolutionary and plastic (mal)adaptive genetic and trait response (e.g. physiological, life-history, morphological, behavioural, reproductive success, survival, phenology), (2) non adaptive evolutionary processes (e.g. gene flow, genetic drift) and (3) how these evolutionary and plastic changes shape species interactions in cities.

We aim to make our symposium as diverse as possible, therefore we encourage researchers at all career stages (undergrad to full professor), nationalities, gender, and focal taxa to submit an abstract to be included in the symposium.

Elizabeth Carlen, PhD website:  
[www.elizabethcarlen.com](http://www.elizabethcarlen.com) “Carlen, Elizabeth”  
 <carlen.e@wustl.edu>

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## Montreal VisualSystemEvolution Jul26-30

We are excited to announce the symposium “A Vision of the Future: Integrating Perspectives in the Evolution of Visual Systems” at the 3rd Joint Congress on

Evolutionary Biology in Montreal on 26-30 July 2024. Submission of talks for the symposium is open to anyone attending the conference, and we encourage you to submit an abstract. You can register here: <https://www.evolutionmeetings.org/registration.html>.

The symposium is meant to bring together diverse perspectives and approaches to understanding the evolution of visual systems. We hope the symposium will facilitate productive inter-disciplinary dialogue amongst researchers studying different aspects of vision, promoting integration and synthesis in the field.

Sensory systems constitute some of the most important organismal traits due to the many critical links between sensing the environment and fitness-related activities. Image-forming eyes provide the windows into the visual world for most animals, and visual systems exhibit striking diversity at multiple scales. Research in visual ecology has grown dramatically during the 21st century, leading to new insights into how animals have evolved visual systems to acquire, process, and respond to visual information. Important discoveries range from proximate effects of genes and cells to ultimate drivers of adaptive changes in visual-system components to effects of visual evolution on ecological interactions and speciation. Yet, these discoveries involve studies conducted at very different biological scales using disparate approaches in diverse taxa hence, the benefits of gathering together for this symposium.

This symposium aims to gather diverse researchers together, with special focus on (1) environmental influences on variation in the visual system (e.g. selective agents, proximate effects, genetics vs. plasticity), and (2) studies examining visual acuity and sensitivity (i.e. visual performance); but all relevant research is welcome! We encourage contributions to the symposium from researchers spanning any visual-system focus (e.g. eye/pupil, cells, genes, visual acuity), scale of analysis (e.g. phylogenetic comparative analyses, inter- and intra-population variation, experimental evolution, theory), selective agent (e.g. foraging behavior, predator-prey interactions, migration, mating behavior, light availability), and more. We further strongly encourage contributions from all dimensions e.g. career stages, gender, nationality, etc. Please spread the word to your networks. For questions, please don't hesitate to contact us.

Lead Organizers: Parker Hughes ([phughes@ncsu.edu](mailto:phughes@ncsu.edu)) and Matt Walsh ([matthew.walsh@uta.edu](mailto:matthew.walsh@uta.edu)) Additional Organizers: Brian Langerhans ([langerhans@ncsu.edu](mailto:langerhans@ncsu.edu)) and Kaj Hulthén ([kaj.hulthen@biol.lu.se](mailto:kaj.hulthen@biol.lu.se))

Brian Langerhans <[langerhans@ncsu.edu](mailto:langerhans@ncsu.edu)>

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## Namibia Conservation Genetics Jan5-15

ConGen2025 Course Cheetah Conservation Fund Research Center, Otjiwarongo, NAMIBIA January 5 to 15th, 2025

We are excited to announce a new offering from ConGen-GLOBAL: the “2025 Recent Advances in Conservation Genetics” course, to be held at the Cheetah Conservation Fund Research Center in Otjiwarongo, NAMIBIA, from January 5 to 15th, 2025.

This immersive course 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.

The application process is complimentary, with no registration fee required upfront. Upon acceptance by our selection committee, candidates may qualify for various sponsored scholarships that cover tuition, living expenses, or both. For optimal consideration, please submit your applications by June 6th. Complete the application form here to be considered for participation: ConGen2025 Application Form (<https://conservationgenetics.org/congen2025-congen2025-application/>).

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.

Thanks to our sponsors, ConGen2025 will have several

scholarships available to cover registration and/or tuition for the participants in need of financial support. These will be offered to the successful candidates after they are chosen by the committee based on merit. 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.

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 ConGenOrganization Committee from various prestigious institutions worldwide. The ConGenOrganization 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 ConGenGlobal-2025 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](http://www.conservationgenetics.org/-congen2025) Taras K. Oleksyk, Ph.D. Associate Professor Department of Biological Sciences Oakland University Dodge Hall, Rm. #367 118 Library Dr Rochester, MI 48309-4479 office: +1 (248) 370-3359 fax: (248) 370-4225 [oleksyk@oakland.edu](mailto:oleksyk@oakland.edu) <https://oakland.edu/biology/directory/oleksyk> Taras Oleksyk

<oleksyk@oakland.edu>

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**Oaxaca Mexico**  
**NorthAmerForestGeneticsSoc**  
**Jun10-14**

The second North American Forest Genetics Society (NAFGS) Biennial Conference will take place in Oaxaca, Mexico, from June 10th to 14th, 2024. This meeting follows the inaugural event hosted in Asilomar, California in June of 2022.

NAFGS seeks to provide a platform to discuss current research, foster collaboration, and promote education in forest genetics as it applies to forest health and productivity.

Society membership and registration are OPEN on the conference website. Early registration ends April 1st. We are also welcoming abstracts on a wide range of forest tree genetics topics through March 25th (DEADLINE EXTENDED).

\* Tree Breeding including seed orchard management, progeny testing \* Plant pathology and forest health \* Population and quantitative genetics \* Genetic conservation \* Population and community ecology \* Phylogenetics/phylogenomics \* Genomic and bioinformatic tools

Visit the website to view the preliminary program, register, submit a poster or talk abstract, view confirmed speakers, and join several hands-on bioinformatic training opportunities (offered FREE with registration) on the first day of the meeting.

<https://www.nafgs24.org/> Interested individuals can join the NAFGS mailing list here: <https://groups.google.com/g/nafgs-mailing-list> We hope to see you in Oaxaca, Mexico, in June 2024!

-NAFGS Organizing Committee

Jill L. Wegrzyn Associate Professor Computational Biology Core Director

Department of Ecology and Evolutionary Biology Institute for Systems Genomics: Computational Biology Core University of Connecticut Storrs CT 06269-3214 [jill.wegrzyn@uconn.edu](mailto:jill.wegrzyn@uconn.edu) +1 860-486-8742

Research: <http://plantcompgenomics.com> CBC Core:  
<http://bioinformatics.uconn.edu> Office (Gant West 419)  
 / Lab (Gant West 401)

“Wegrzyn, Jill” <jill.wegrzyn@uconn.edu>

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Wedell

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

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## Online ESEB InternalConflicts Mar21

Dear colleagues,

We would like to invite you to the first online seminar for the “Internal Conflicts and Organismal Adaptation” Special Topic Network (STN) funded by the European Society for Evolutionary Biology, which will take place on March 21st at 14:00 UTC.

The general aim of the STN is to unify the study of within-organism conflicts and work towards an account of organismal adaptation that explicitly integrates such conflicts. During this first seminar, we will provide an overview of our motivations and goals for the STN and outline upcoming events within the context of the STN. There will be ample time for questions and general discussion; we are particularly keen to hear how we can use this STN to the benefit of the evolutionary biology community. We expect the meeting to take approximately one hour. The meeting will be recorded and will be made available online afterward through our website.

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/1FAIpQLSeJkKjGDXh76JYjqxLSo35D_Zhpo3IG00HHD8G5o6wrzivvGQ/-viewform?usp=sf.link) < [https://docs.google.com/forms/d/e/1FAIpQLSeJkKjGDXh76JYjqxLSo35D\\_Zhpo3IG00HHD8G5o6wrzivvGQ/-viewform?usp=sf.link](https://docs.google.com/forms/d/e/1FAIpQLSeJkKjGDXh76JYjqxLSo35D_Zhpo3IG00HHD8G5o6wrzivvGQ/-viewform?usp=sf.link) > or visit <https://-internalconflictsstn.wordpress.com/> for more information.

Meeting details:

Link: Zoom < <https://georgetown.zoom.us/j/-95114311124> >.

Date: March 21st, 2024.

Time: 14:00 UTC (please note potential time differences caused by shifts to daylight savings time).

Sincerely,

The Internal Conflicts and Organismal Adaptation STN  
 Martijn Schenkel, Arvid Ågren, Manus Patten, and Nina

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## Online MicrobiomeConservation Apr18

THE MICROBIOME & CONSERVATION - WAME  
 ONLINE SEMINAR SERIES -

Thursday April 18, 2024

3 pm UK/BST (10 am US Eastern, 7 am US Pacific  
 time)

Online (Zoom)

Link: <https://aarhusuniversity.zoom.us/j/68868377912>

Dr. Candace Williams - Turning microbiome science  
 into conservation action“

Dr. Kevin Kohl - Keep One Another Close: The Impor-  
 tance

of Wildlife-Microbe Symbioses in a Changing World

Dr. Gloria Fackelmann - Studying the links between  
 microplastics and microbiomes through the One Health  
 perspective

Organised by Dr. Klara Wanelik and Prof. @stn\_wame  
 David Richardson

<https://-internalconflictsstn.wordpress.com/>  
 WAME - Wild Animal Microbiome Evolution - an ESEB  
 funded Special topics network

”David Richardson (BIO - Staff)“  
 <David.Richardson@uea.ac.uk>

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## Online Socially Transferred Materials Mar21

Dear colleagues,

Our ESEB-funded special topic network “Social Transfer Network” is organising a number of workshops (Social Transfer Evolution Workshops, aka STEWs) on topics around socially transferred materials.

Some of these are in person (e.g. symposium at Evolution in Montreal this summer), but in addition we are beginning an online seminar series:

Bring-Your-Own-Fluid Seminars (referring to either the social fluid you might study or your cup of coffee in hand)

Each BYOF session will be one hour, where we will have 3-4 short talks typically by ECRs (7 min each!) 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.

The very first in our series will happen next week, 21 March 2024

Topic: Bring Your Own Fluid Seminars - March 21st  
Time: Mar 21, 2024 11:00 UK / 12:00 Europe  
<https://us02web.zoom.us/j/89762780392?pwd=bVlN2k1WERkcUUrZU9sQmpmTnI5UT09> This session will open up the series with a brief introduction on the Social Transfer Network, our goals, future STEWs and related opportunities followed by three short talks and discussion

Male reproductive proteins in hermaphroditic snails - Yumi Nakadera (VU Amsterdam)  
The evolution of social regurgitation in ants - Adria LeBoeuf (Cambridge)  
Don't Sweat It, Dad! The Epigenetic Impact of Paternal Stress - Miriam Kretschmer (ETH Zürich)

We intend to have at least 6 BYOF seminars per year. If you are interested in speaking or helping to organise please attend and get in touch. The next two will be May 7th and June 12th. Fall dates and times will be announced in the 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

Adria C LeBoeuf <[acl79@cam.ac.uk](mailto:acl79@cam.ac.uk)>

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## Online Weekly Graduate Std Res Seminars Mar4-May13

SSE is pleased to announce the second round of the GREG Seminar Series, a weekly virtual seminar series featuring recipients of our

Graduate Research Excellence Grants (GREG).

Recipients of the 2022 GREG R.C. Lewontin Early Awards will present their research every Monday from 12:00 - 1:00 pm Eastern time, starting March 4 through May 13. Each talk will be 45 minutes, followed by 15 minutes for questions.

Schedule:

March 4: Robin Waterman, Michigan State University  
March 11: Matheus Januario Lopes de Sousa, University of Michigan  
March 18: Aidan Harrington, University of Minnesota, Twin Cities  
March 25: Danae Diaz, Duke University  
April 1: Danai Kontou, University of Cambridge  
April 8: Sebastian Mortimer, Oregon State University  
April 15: Fabian C. Salgado Roa, The University of Melbourne  
April 22: Sergio Serrato-Arroyo, Arizona State University  
April 29: Austin Chipps, Louisiana State University  
May 6: Josh Knecht, Binghamton University  
May 13: Verónica Reyes-Galindo, Universidad Nacional Autónoma de México

The seminar will be presented via Zoom: [Click here to join](#)

Want to receive a weekly email reminder about these talks? [Sign up here.](#)

This series is organized by the Graduate Student Advisory Committee (GSAC) and hosted by GSAC and SSE Council.

We look forward to hearing about the outstanding research of these student award winners!

Join Zoom Meeting <https://zoom.us/j/8248834624>  
Meeting ID: 824 883 4624

One tap mobile +13092053325,,8248834624# US  
+13126266799,,8248834624# US (Chicago)

Meeting ID: 824 883 4624 Find your local number:  
<https://zoom.us/j/8248834624> Society for the Study of  
Evolution <aneely@evolutionsociety.org>

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

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## Paris Conservation Genomics Jun5-6 Deadline Extended

Abstract Deadline extended to April 12, 2024! Con-  
tributed talks and posters are both welcome.

Join us at the Muséum National d'Histoire Naturelle  
in Paris on June 5-6, 2024 for a two-day conference  
dedicated to exploring the intersection of genomics and  
conservation, with a particular focus on practical appli-  
cations of genomics to immediate conservation needs.  
Participants and invited speakers include applied conser-  
vation practitioners, method developers, and genomics  
researchers. The conference aims to foster dialogue and  
encourage exchange of ideas across disciplines, especially  
between researchers and practitioners, and contributions  
from conservation managers and other applied practi-  
tioners are encouraged. Talks will explore both practical  
applications of genomics in conservation, and using ge-  
nomics to make inferences of parameters of relevance to  
conservation biology (such as recent population history  
and mutation load).

Meeting website with further details, regis-  
tration, and abstract submission: [https://  
conservgenomics.sciencesconf.org/](https://conservgenomics.sciencesconf.org/) Tim Sackton,  
on behalf of the organizing committee: Guillaume Ac-  
haz, Collège de France, Paris, France Simon Boitard,  
Centre de Biologie pour la Gestion des Populations,  
Montpellier, France Raphaël Leblois, Centre de  
Biologie pour la Gestion des Populations, Montpellier,  
France Stefano Mona, Institut de Systématique  
et Evolution, Paris, France Dmitri Petrov, Stanford  
University, Palo Alto, USA Tim Sackton, Harvard  
University, Cambridge, USA

Tim Sackton, PhD Director of Bioinformatics Infor-  
matics Group Faculty of Arts and Sciences Harvard  
University

Tim Sackton <tsackton@g.harvard.edu>

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

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## Puerto Vallarta SMBE Paleogenomics Jul7-11

Dear colleagues,

We are organizing a symposium titled

“Paleogenomics and human evolutionary history: new  
insights and novel methods”

to be held during the SMBE meeting in Puerto Vallarta,  
Mexico, between July 7-11, 2024. Deadline for abstract  
submission is March 15th, 2024.

More information about the SMBE meeting visit [https://  
smbe2024.org](https://smbe2024.org) . We are looking forward to seeing you  
in Puerto Vallarta!

Anna-Sapho, Emilia, Hannah, Mehmet, and Priya

\*\*\*

Title: Paleogenomics and human evolutionary history:  
new insights and novel methods

Invited speakers

Kay Prufer, Max Planck Institute for Evolutionary An-  
thropology

Maanasa Raghavan, University of Chicago

Abstract

Ancient genomes have opened up new possibilities for  
studying evolutionary history at varying time scales.  
Long-term evolution, including speciation patterns and  
the consequences of introgression between diverged line-  
ages, is increasingly studied using paleogenome time-  
series data. Ancient genomes have also revealed the  
existence of lineages previously unknown from the fos-  
sil record, as exemplified by the discovery of a new  
hominin group, the Denisovans. Beyond long-term  
evolution, paleogenome time series has boosted demo-  
graphic inference studies, revealing unexpected patterns  
of past population structure, admixture, inbreeding, sex-  
biased mobility, and natural selection. The symposium  
will highlight methodological developments that address  
technical challenges in the analysis of ancient genomes,  
such as genotyping, imputation, and inference of pop-  
ulation history from temporal genomics datasets and  
the resulting new insights gained into hominin evolu-  
tion, human population history, and our relationships  
with domesticated, commensal, and pathogen species.



Finally, we will showcase the importance of interdisciplinary approaches to human evolution and the ongoing co-evolution of genetics and archaeology.

#### Organizers

Emilia Huerta-Sanchez (Brown University and Trinity College Dublin, emilia.huerta-sanchez@brown.edu)

Anna-Sapfo Malaspinas (University of Lausanne, annasapfo.malaspinas@unil.ch)

Priya Moorjani (University of California, Berkeley, moorjani@berkeley.edu)

Hannah Moots (Centre for Palaeogenetics, Stockholm, hannah.moots@nrm.se)

Mehmet Somel (Middle East Technical University, somel.mehmet@googlemail.com)

#### Dates:

Abstract submission deadline: March 15, 2024

Notification of decisions: April 20, 2024

Early bird deadline: May 10, 2024

Note that this year SMBE is implementing rates for members in Low-and-Middle Income Countries (LMIC).

Abstract submission page: <https://smbe2024registration.org/abstracts> Mehmet Somel <somel.mehmet@googlemail.com>

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## Roscoff France MonodVirusEvol Oct14-18

Jacques Monod Conference Virus evolution: the mutualism-antagonism continuum of virus-virus interactions October 14-18, 2024. Roscoff, France

Registration Request and Abstract Submission Deadline: June 13, 2024 <https://cjm4-2024.sciencesconf.org>

A Jacques Monod Conference on “Virus evolution: the mutualism-antagonism continuum of virus-virus interactions” will be held from 14-18 October 2024 in Roscoff, France. The goal of this Monod conference is to convene virus researchers of varying expertise (epidemiology, theory, empiricism, bioinformatics), who work on myriad types of viruses that infect a wide variety of hosts. We will discuss classic and novel ideas about virus evolution, and the importance of within-host interactions among

viruses and how they may impact virus evolution. This conference is extremely timely due to the increased realization of the importance of interactions not only among viral species and strains, but also among viral components, be they ‘normal’ or semi-infectious or defective interfering particles, viral satellites or genomic segments, in modulating and determining viral phenotypes and infections outcomes. Importantly, the ecological context of such interactions is extremely relevant but (in our opinion) largely overlooked in virus research. Therefore, our hope is that this unique conference will contribute to expanding the integration of virus evolutionary ecology into virology studies.

“Turner, Paul” <paul.turner@yale.edu>

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## Roscoff France PhenotypicPlasticity Jun17-21

DEADLINE FOR ABSTRACT SUBMISSION EXTENDED TO MARCH 21 (midnight CET)

Dear colleagues,

We are organizing a Conference Jacques Monod (CJM) entitled:

Life is plastic: How phenotypic plasticity makes us rethink central problems in biology.

It will held in Roscoff (Brittany, France), from 17 to 21 June 2024.

CJMs are organized by the CNRS, and include ~100 participants who all present their work (oral presentation or poster) to foster scientific exchange.

The scientific scope and list of invited speakers is available here: <https://www.insb.cnrs.fr/fr/life-plastic-how-phenotypic-plasticity-makes-us-rethink-central-problems-biology>

The conference venue is a historical marine biology station in a beautiful village in Brittany: [https://en.wikipedia.org/wiki/Station\\_biologique\\_de\\_Roscoff](https://en.wikipedia.org/wiki/Station_biologique_de_Roscoff)

The registration process involves sending an abstract and CV on this website:

<https://cjm2-2024.sciencesconf.org/?forward-action=index&forward-controllerindex&lang=en>

After the deadline (March 21), selected applicants will

be invited to finalize their registration (note that conference fees include accommodation and meals).

Looking forward to seeing you there !

Luis-Miguel Chevin et Cameron Ghalambor

Luis-Miguel Chevin

Directeur de recherche CNRS Centre d'Ecologie Fonctionnelle et Evolutive 1919 route de Mende, 34293 Montpellier Cedex 5, France +33 (0)4 67 61 32 11

Luis-Miguel CHEVIN <luis-miguel.chevin@cefe.cnrs.fr>

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### SMBE Mexico AnimalPaleogenomics Jul7-11

Dear all,

We invite you to submit abstracts to the SMBE 2024 symposium "Animal paleogenomics beyond higher latitudes". This year SMBE will take place from July 7 to 11, 2024, in Puerto Vallarta, Mexico.

We aim to provide a platform to share animal paleogenomics research (including historical DNA) in the tropics and sub-tropics, including fields such as population genetics, evolutionary biology, sedimentary DNA and conservation biology, to name a few. We are excited to have as invited speakers Dr. Selina Brace (Natural History Museum, London, UK) and Dr. Viviane Slon (Tel Aviv University, Tel Aviv, Israel). You can find more information about the conference at: <https://smbe2024.org/> (we are topic 4, session 13).

If you want to participate in this symposium, submit your abstracts before the 15th of March at this link: <https://smbe2024registration.org/abstracts>. Don't forget to register by May 10 for Early Bird for registration rates!

This year SMBE has special registration discounts for LMIC. You can also apply to the usual SMBE travel awards while submitting your abstract. This list includes: Graduate Student Excellence Award, Undergraduate Mentorship Award, Young Investigator Travel Award, Caregiver award. Please visit the <https://smbe2024registration.org/abstracts> and <https://smbe2024registration.org/> for more information.

We are looking forward to reading all your abstracts, and to welcome you in Puerto Vallarta in July!

Sincerely,

Maria Zicos, J. Camilo Chacajón-Duque, Deon de Jager and Federico Sánchez Quinto

Camilo Chacajón-Duque <camilo.chaconduque@su.se>

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### SMBE Mexico SpatialPopulationGenetics Jul7-11

Hi all,

We are writing to encourage you to submit an abstract to the SMBE 2024 Symposium "Spatial Population Genetics: Where Are We Now?" The abstract for the symposium is below. This year, SMBE will be held in Puerto Vallarta, Mexico (<https://smbe2024.org/>). Talk abstracts are due by March 15th (<https://smbe2024registration.org/abstracts>).

Feel free to reach out via email with any questions (bradburd@umich.edu).

Spatial Population Genetics: Where Are We Now? Symposium #11 Organizers: Gideon Bradburd & John Novembre Abstract: Geography is fundamental to evolutionary biology because many of the processes that shape patterns of genetic variation within and between species are inherently spatial. Although the importance of space to the study of evolution has been clear from the inception of the field, many of the early models used for generating predictions or analyzing data in population genetics assumed discrete, well-mixed populations. In the past two decades, falling sequencing costs have driven the generation of more and more datasets with spatially continuous sampling; these datasets, in turn, have demanded and inspired concomitant advances in the simulation, analysis, and theory of population genetics in continuous space. The purpose of this symposium is to highlight recent advances - theoretical, methodological, and empirical - in spatial population genetics, as well as to identify key challenges at the expanding wavefront of the field. Our confirmed keynote speakers are Alison Feder (University of Washington) and Andy Kern (University of Oregon).

-Gideon Bradburd

Gideon Bradburd (\*he/him\*) Dept. of Ecology & Evolutionary Biology University of Michigan genescape.org  
< <http://www.genescape.org/> >

Gideon Bradburd <bradburd@umich.edu>

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## Verbania Cladocera Systematics Oct6-12

Registration to the traditional Symposium on Cladocera (aka Cladocera XII Conference, [www.cladocera2024.org](http://www.cladocera2024.org)) that will take place in Verbania, Italy, on October 6 to 12, 2024, is open. The early bird deadline has been set for April 30, applications for student support are to be submitted by April 1, 2024.

All information is available on the conference website: <https://www.cladocera2024.org/cladocera-xii-registration-open/> Please, spread the word among interested colleagues.

With regards

Piet Spaak & Adam Petrusek

Cladocera XII organisers

[info@cladocera2024.org](mailto:info@cladocera2024.org)

Adam Petrusek <[petrusek@cesnet.cz](mailto:petrusek@cesnet.cz)>

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## Wellcome Genome Campus UK Ancient Biomolecules Jun3-5

Wellcome Connecting Science | Ancient Biomolecules of Plants, Animals and Microbes 3-5 June 2024 Wellcome Genome Campus, UK and virtual

Developments in DNA extraction and sequencing methods have resolved many technical issues that previously hampered ancient DNA research. At this conference, global leaders will present updates in ancient DNA research from across a diverse range of evolutionary areas.

Advances in migration, adaptation, domestication, and

admixture will be highlighted, as will new insights into phylogeny and population history. Discussions will explore theoretical topics, such as rates of evolutionary change, in addition to more practical issues about species and population response to climate change and anthropogenic impacts. Conservation and extinction will be discussed, as well as best practices and novel approaches to data generation and analysis.

We invite abstract submissions on all areas relevant to the themes of the meeting for the selection of podium presentations. Posters and poster pitch talks will provide further opportunities to present research findings or discuss ongoing work with others working in related fields.

This friendly meeting aims to be highly interactive and improve knowledge dissemination between different areas of ancient biomolecule research. Face-to-face networking opportunities are facilitated at Hinxton Hall Conference Centre with optional on-site accommodation.

Deadlines Abstract & bursary 09 April 2024 In-person registration 07 May 2024 Virtual registration 27 May 2024

Visit the conference webpage <https://coursesandconferences.wellcomeconnectingscience.org/-event/ancient-biomolecules-of-plants-animals-and-microbes-20240603/?1> Questions? Email the Organiser conferences [at] wellcomeconnectingscience.org

The Wellcome Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is Wellcome Sanger Institute, Wellcome Genome Campus, Hinxton, CB10 1SA.

Jane Murphy <[jane.murphy@wellcomeconnectingscience.org](mailto:jane.murphy@wellcomeconnectingscience.org)>

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## Yosemite Natl Park Symbiosis Apr19-21

EARLYBIRD REGISTRATION EXTENDED FOR ONE WEEK to March 7

Dear Colleagues,

The TWELFTH annual Yosemite Symbiosis Workshop

will take place on April 19-21st, 2024 at the Sierra Nevada Research Institute, Yosemite National Park. In the previous 11 years, this meeting became a great venue for a diversity of symbiosis researchers.

We hope to continue to attract a diverse group in 2024!

**KEYNOTE SPEAKER:** Kabir Peay, Stanford University <https://mykophile.stanford.edu/> **REGISTRATION WILL OPEN IN EARLY 2024** Find updates here: <https://www.sachslab.com/symbiosis-2015.php>

**Why:** Our goal is to better integrate scientists that focus on symbiosis research, including researchers that study animal-microbe and plant-microbe systems, as well as broader topics related to the microbiome, cooperation, and mutualism. This will be our 12th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

**Who:** The meeting is small and intimate by design (~50 participants). We would like to make room for a diverse group of people so we will initially accept up to 3 lab members per group (including the PI) on a first come first served basis. In the past we have covered a range of symbiosis topics from ecology and evolution to molecular mechanisms in different model and non-model systems.

**What:** The meeting will be made up of two half-days of talks and one poster session. Other than the keynote (~1 hour), talks are 15 minutes long (including time for questions). Posters are flexible for size, but the ideal poster should be no larger than ~4 feet square. When you apply for the meeting, you will provide your preference for a talk or poster.

**When:** Participants generally arrive Friday afternoon or evening (April 19) and depart Sunday early afternoon (April 21). Though some attendees often extend their stay at the station to spend more time at the National Park.

**Where:** This is the best part! The meeting takes place at the Sierra Nevada Research Station, in Wawona California, within the borders of Yosemite National Park!

**What will it cost?** More good news here! We have received continued generous funding from the Gordon and Betty Moore Foundation. This will allow us to provide **FREE REGISTRATION** to graduate students and postdoc presenters.

Even without the awards, we have been good at keeping costs low (<\$300 total for PIs, includes all fees: registration, room and board).

Please direct any questions to the organizers:

Joel Sachs [joels@ucr.edu](mailto:joels@ucr.edu) A. Carolin Frank [cfrank3@ucmerced.edu](mailto:cfrank3@ucmerced.edu)

\*Joel L. Sachs\* \*Professor & Chair, \* Evolution Ecology & Organismal Biology University of California, Riverside Chair's Office 2745 Life Sciences Building Office (951) 827-6357 / Fax (951) 827-4286 / <http://www.sachslab.com> Zoom: <http://ucr.zoom.us/my/-Sachsevolution> \*Post address\*: Sachs Lab - UC Riverside 3401 Watkins Dr., 1229 Spieth Hall, Riverside, CA 92521

[joels@ucr.edu](mailto:joels@ucr.edu)

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## AarhusU ArthropodVariationAdaptation

Title: Functional variation in arthropod performance across agro-ecosystems

Applications are invited for a fully funded PhD fellowship/scholarship at Graduate School of Natural Sciences, Aarhus University, Denmark, within the Biology programme. The position is available from August 2024 or later.

Research area and project description: The specific PhD project takes an experimental approach to understand the factors that drive variation in arthropods and its consequences for arthropod performance across agro-ecosystems. It tests hypotheses about the link between land use, distribution of genetic diversity and population declines in selected arthropod species with essential roles as pollinators and decomposers. The key focus is therefore on measuring population variation in life history and stress-related phenotypic traits in populations of springtails and butterflies, and interpreting these results in relation to already available data on population genomic variation as well as spatial and temporal data on land use. Specifically, the project will 1) investigate population variation in reproductive traits, decomposition, immune performance and population growth in species of Collembola, 2) use common garden experiments to test hypotheses about local adaptation in species of Collembola, 3) test hypotheses about adaptation and plasticity of dispersal ability in species of butterflies. The details of the project will be planned with the interests of the successful candidate in mind.

The successful applicant will participate in a project lodged within the work of the Centre for Ecological Genetics (<https://bio.au.dk/forskning/forskningscentre/-centre-for-ecological-genetics>). The centre, led by Prof. Trine Bilde, investigates the population genetic consequences of the dramatic declines observed in insect diversity and abundance, and the potential consequences for their ability to perform ecosystem services such as pollination and natural pest control. The centre provides an active and diverse international group of researchers and

students with groups in Aberdeen, Helsinki and Aarhus. In addition to colleagues at the Department of Biology, Aarhus University, particularly Prof. Marjo Saastamoinen, University of Helsinki (<http://www.helsinki.fi/life-history-evolution>), provides potential close collaboration and opportunity for exchange. The work will be done under the supervision of Prof. Jesper Givskov Sørensen (AU). Co-supervision will be provided by Prof. Trine Bilde and Assoc. Prof. Tove Hedegaard Jørgensen (AU), and Prof. Marjo Saastamoinen (Helsinki), depending on the developed PhD project.

For technical reasons, you must upload a project description. When - as here - you apply for a specific project, please simply copy the project description above, and upload it as a PDF in the application. If you wish to, you can indicate an URL where further information can be found.

Qualifications and specific competences: Applications to the PhD position must have an MSc or BSc degree in Biology or a similar relevant subject. A strong interest in experimental work and data analysis is required - along with the ability to communicate scientific work. Experience with insect (eco)physiology, and a strong background in evolutionary biology is highly valuable.

Place of employment and place of work: The place of employment is Aarhus University, and the place of work is Department of Biology, Section for Genetics, Ecology and Evolution, Ny Munkegade 114, 8000 Aarhus C, Denmark.

Contacts: Applicants seeking further information for this project are invited to contact: Professor Jesper Givskov Sørensen, [Jesper.soerensen@bio.au.dk](mailto:Jesper.soerensen@bio.au.dk) or Professor Trine Bilde, [trine.bilde@bio.au.dk](mailto:trine.bilde@bio.au.dk)

How to apply:

For information about application requirements and mandatory attachments, please see the Application guide < <https://phd.nat.au.dk/for-applicants/-application-guide/> >. Please read the Application guide thoroughly before applying.

When ready to apply, go to <https://phd.nat.au.dk/for-applicants/apply-here/> 1) Choose May 2024 Call with deadline 1 May 2024 at 23:59 CET.

2) You will be directed to the call and must choose the

programme “Biology”.

3) In the boxed named “Study”: In the dropdown menu, please choose: “Functional variation in arthropod performance across agro- ecosystems (Fvapaa)”

Please note: The programme committee may request further information or invite the applicant to attend an interview.

At the Faculty of Natural Science at Aarhus University, we strive to support our scientific staff in their career development. We focus on competency development and career clarification

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## AuburnU BehaviorEvolution

MS or PhD position in Termite Behavior and Evolution

The Mizumoto lab ([mizumoto-lab.com](http://mizumoto-lab.com)) at the Department of Entomology & Plant Pathology at Auburn University (<https://agriculture.auburn.edu/research/enpp/>) is looking for a Master’s or Ph.D. student. Graduate students are fully funded through research assistantships and conduct research, as advised by Dr. Nobuaki Mizumoto, on the topic relating to the evolutionary process of termite collective behavior. The primary project is the evolution of nest building in termites, but it can be adjustable if it is aligned with our research interests (see publications and research on the lab website). The research will combine field work, behavioral observations, video tracking, and computational data analysis. Graduate students are expected to present their research at national and international conferences, write papers in international peer-reviewed journals, and physically participate in laboratory and departmental events.

For consideration, please send (1) a CV and (2) a cover letter addressing research interests and research experience (if any). Prior experiences with any behavioral studies, social insects, or code writing are not necessary, but please describe them if you have.

Contact: Nobuaki Mizumoto, Assistant Professor  
E-mail: [nzm0095@auburn.edu](mailto:nzm0095@auburn.edu) Website: [mizumoto-lab.com](http://mizumoto-lab.com)

Nobuaki Mizumoto <[nzm0095@auburn.edu](mailto:nzm0095@auburn.edu)>

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## Berlin EvolutionMobileElements

PhD Candidate (3-year contract)

We are seeking an enthusiastic and motivated individual for a PhD position in the team of Dr. Zsuzsanna Izsvák, Head of the Mobile DNA Laboratory at the Max Delbrück Center for Molecular Medicine in the Helmholtz Association Society, Berlin, Germany.

The Max Delbrück Center is one of the world’s leading biomedical research institutions.

Our common goal is that we want to understand the molecular basis of health and disease and bring our discoveries to patients as quickly as possible - for better prevention, diagnostics and treatment.

The Mobile DNA Laboratory forms an effective bridge between basic research on the non- coding genome and transposable elements, also the technological implementation of state of art gene transfer and stem cell technologies for clinical application. The position will involve the use of cutting-edge, including high-throughput techniques in molecular and cell biology.

There are currently three exciting research programs:

1) Investigating/testing the “Unwanted transcript hypothesis”:

<https://www.mdc-berlin.de/research/publications/-selection-synonymous-sites-unwanted-transcript-hypothesis>

2) “Repurposed retroviral sequences for human physiology”

3) Sleeping Beauty transposon-based technology platform

Candidates need to have a solid background in Biology, Genetics, Biochemistry, Molecular and/or Cellular Biology, Biotechnology, Bioinformatics and/or demonstrated prior experience in the broader area of research of non-coding, transposable elements or artificial intelligence (A.I.), which is most welcome.

If you have an excellent background in biological sciences and enjoy intellectual challenges, feel free to send in your application.

Furthermore, applicants should have strong analytical and problem-solving skills, as well as first-rate organizational skills. In addition, first-class written and

verbal communication skills, as well as the ability work excellently as part of a team, are required.

Please check the website of Dr. Izsvák's Mobile DNA group for more information, also on recent publications and the current projects being carried out in the lab:

<https://www.mdc-berlin.de/izsvak> The funds for this post are available for 36 months at present. The expected start date is around 1st June 2024.

Kindly send your informal enquiries and applications to Dr. Zsuzsanna Izsvák:

[zizsvak@mdc-berlin.de](mailto:zizsvak@mdc-berlin.de)

Berlin, Germany, March 2024

The Mobile DNA Laboratory values diversity and is committed to providing equal opportunity.

The Max Delbrück Center in Berlin has a responsibility to guarantee the egalitarian treatment of its employees. Eligibility both to reside and work in Germany are a prerequisite of the hiring process.

Laurence D. Hurst Professor of Evolutionary Genetics

The Milner Centre for Evolution University of Bath  
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## Berlin Three VirulenceEvolInsectImmunity

Berlin, Germany Three open PhD positions Application deadline: 29.03.24

We are advertising three doctoral candidate positions as part of the “Insect Infect” Research Unit FOR 5026 funded by the DFG, which brings together the fields of host-microbiota interactions, insect innate immunity, and bacterial resistance evolution. The Research Unit gives the opportunity to interact with a diverse group of doctoral candidates, post-docs, and PIs, to obtain methodological training, and to receive statistical and bioinformatics support. Furthermore, the projects will entail close collaboration with theoreticians. There will

be yearly retreats and access to a graduate training programme. The deadline for applications is 29.03.2024 and the positions will start in early summer 2024 or as soon as possible thereafter. The positions are fixed term and available for 4 years.

Position 1: Decomposing virulence: host, pathogen, and microbiota contributions

Position 2: Parasite life history trade-offs and the evolution of virulence - a test of the trade-off hypothesis

Position 3: Evolution of symbiont, pathogen and immune system interactions in Blattodea

See below for details of each project:

Position 1: Decomposing virulence: host, pathogen, and microbiota contributions

The Evolution and Ecology of Insect Defences group (<https://armitagelab.com/>) at the Institute of Biology, Freie Universität (FU) Berlin, Germany, would like to invite applications for the research project: Decomposing virulence: host, pathogen, and microbiota contributions.

— Project background: Our research lies in the field of eco-evo-immunology. Virulence describes the negative health or fitness effect of a pathogen, and there is long-standing interest in understanding how virulence changes over evolutionary time. Virulence will be determined by pathogen<sup>1,2</sup> and host factors<sup>3</sup>, but it is not trivial to understand the degree to which each partner affects virulence patterns. Nonetheless, we can start to understand the drivers of virulence changes by “decomposing” virulence into pathogen and host components (e.g. 1,2). More recently there has been a blossoming of interest in the tripartite interaction between host, pathogen and microbiota, and the role that microbiota play in pathogen virulence evolution<sup>4</sup>. In the project we will decompose virulence into host and pathogen components, whilst taking the interaction with microbiota into account. Experimentally evolved pathogens will be used in this project. Infection assays and measures such as bacterial load, survival and transcriptomics will be used. This project will— give insight into the generalisability of virulence patterns, it will help us to uncover hidden drivers of virulence, and it will give insight into the generalisability of the components of virulence. The host organism will be *Drosophila melanogaster* and the pathogen and microbiota will be bacteria. The position is fixed term and available for 4 years, paid according to TV-L E13, 65 %, and will start in early summer or as soon as possible thereafter. — The project will involve: §——— Literature research §——— Experimental design and hypothesis formulation §——— Preparation and execution of experiments, including infection of insects (*Drosophila melanogaster*) with bacteria, molec-

ular biology (RNA extractions), and analysis of host fitness §——— Statistical data analysis, including transcriptomic data analysis and manuscript writing §——— Collaboration with researchers of the Insect-Infect research group — Essential criterion: §——— A completed University master's degree in biology, microbiology, or similar topic — Desirable criteria: §——— We would like applications from enthusiastic students with a background/interest in evolutionary ecology, e.g., in host-microbiota-pathogen interactions and virulence evolution §——— Laboratory experience with bacteria and insects §——— Experience with molecular biology or transcriptomic analyses §——— Good basic knowledge of statistics (e.g., using "R") and experimental design §——— Proficient in spoken and written English §——— Good team-working and communication skills and ability to work independently §——— Completed projects/internships on topics relevant to the research area are advantageous — How to apply: Applications should be written in English, submitted as one single PDF, and include the following documents: (1) a one-page (maximum) letter of motivation with details of previous research experience and future goals, (2) your CV (if applicable, including any publications). Please include the names of 2-3 possible contact people who can provide a reference for you and explain why you

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## BSPGMunich VirtualPalaeontologyAI

3-year PhD position at Bavarian State Collection of Palaeontology and Geology, Munich

At the Bavarian State Collection of Palaeontology and Geology Munich, in the frame of a DFG-funded project the position of a research assistant (f/m/d) in the field of virtual palaeobiology for 3 years (75%) is to be filled as soon as possible.

More than 250 years after Linnaeus described the first species, there is still disagreement about how to define and delimit species. This discrepancy is particularly evident when comparing fossil and living species, for

which different types and amounts of information are typically available, which has led to a variety of different species concepts over the centuries. To compare past, present, and projected rates of biodiversity turnover, reconstruct biogeographic patterns, and realistically infer evolutionary processes, a standardized species classification system that considers fossils and living taxa equally is required. The aim of this project is to develop a new machine learning approach that uses image data for extant species for which species boundaries have been established based on molecular data to enable standardized and consistent species delimitation of related fossil species. Extant and fossil freshwater gastropods with comparable, high morphological plasticity are used as a model group. The data obtained are used to reconstruct biodiversity patterns and diversification processes of the fossil representatives.

Tasks: - Development of a neural network for image recognition of extant and fossil species of gastropods - Reconstruction of biodiversity patterns and diversification processes - Travel to national and international palaeontological collections to acquire image material - Participation in national and international conferences to present research results - Cooperation with national and international research teams

Required qualifications: - Completed qualifying university studies (MSc, Diploma) in the field of palaeobiology, palaeontology, theoretical biology, evolutionary biology or bioinformatics - Sound knowledge of machine learning, with a focus on neural networks - Knowledge of Python - Communication, organizational and team skills - Ability to express yourself verbally and in writing (German and English)

Desirable skills: - Experience in biodiversity informatics and systematic taxonomy - Knowledge of convolutional neural networks and Siamese neural networks - Experience in statistical analysis using R - Experience in writing scientific publications

We offer: - A stimulating working environment with various departments of natural history collections and museums, as well as in close cooperation with the Chair of Palaeontology and Geobiology at the Department of Earth and Environmental Sciences at the LMU, where you can pursue a doctorate - A diverse research environment with diverse expertise, cooperation opportunities and state-of-the-art research infrastructure - International networking and exchange opportunities - Remuneration according to the collective agreement of the federal states (TV-L E13 75%)

We look forward to receiving your meaningful and complete application documents with a letter of motivation, CV (including list of publications) and certificates,



which must be sent to [bewerbung@snsb.de](mailto:bewerbung@snsb.de) by April 30, 2024 at the latest.

If you have any questions regarding the content, please contact Dr. Thomas A. Neubauer ([neubauer@snsb.de](mailto:neubauer@snsb.de)), who will supervise this project. If you have any questions about the procedure or application process, please contact Ms. Susann Windisch ([personal@snsb.de](mailto:personal@snsb.de)).

Severely disabled applicants will be given preference if their suitability is otherwise essentially the same. In order to achieve equality between women and men, there is a particular interest in applications from women.

We would like to point out that once the process has been completed, the application documents will be destroyed and not returned. Travel costs for traveling to a possible job interview will not be covered.

Thomas A. Neubauer, PhD habil. SNSB - Bavarian State Collection for Paleontology and Geology Richard-Wagner-SträÙe 10 80333 Munich Germany Phone: 0049 (0)89 2180 6541

“Neubauer, Thomas A.” <[neubauer@snsb.de](mailto:neubauer@snsb.de)>

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## CaliforniaPoly Humboldt PlantEvolution

Master’s Students Positions: Genetics and origins of rare plants, Cal Poly Humboldt

Two Master’s positions are available to study rare species in the California Floristic Province as part of an NSF-sponsored project

Requisites: - Have a B.Sc. in Biology, Botany, or a related field - Have taken classes in genetics, evolution, and plant diversity (although some of these classes can be taken during the Master’s program) - Strong interest in learning bioinformatics (Students are expected to take Phylogenetic Systematics and Bioinformatics during the program)

Additional information: - Partial financial support is available - Our research group is committed to diversity, students from all backgrounds are encouraged to apply - Each student will study a focal rare species?¿‘ collecting it, sequencing its DNA, analyzing the data, and writing a scientific paper. - Students are expected to work independently with the support of the lab members. A

main aim of the project is to inform conservation.

Application: CV, letter of intent (two pages max.), and two professional references (emails). Send application packages to [ov20@humboldt.edu](mailto:ov20@humboldt.edu) Deadline to apply March 31.

[oscarvargash@gmail.com](mailto:oscarvargash@gmail.com)

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## CEFE-Montpellier EvolutionSexChromosomes

Hello,

I have \*two\* fully funded PhD opportunities in my lab (to start Oct 2024), to work on the evolution of sex chromosomes, with genomics and population genetics theory. This is part of the ERC RegEvol project dedicated to better understand the multifaceted evolutionary consequences of cis and trans regulatory variation.

The PhDs will be based in the GEE < <https://www.cefe.cnrs.fr/en/research/evolutionary-ecology/-genetique-et-ecologie-evolutive-3> > team in CEFE lab in Montpellier, a large and international group of evolutionary geneticists and will interact with several close collaborators (Aline Muyle, Christoph Haag, Denis Roze, Sylvain Gli¿½min).

The project description, and application instructions can be found here:

<https://bit.ly/48Czpzu> Interested candidates can contact me informally for extra details if needed.

Thanks to spread the word to interested master students!

Thomas Lenormand CNRS research director PI ERC RegEvol < <https://www.cefe.cnrs.fr/fr/recherche/ee/-gee/800-c/193-thomas-lenormand> > Lab website < <https://www.cefe.cnrs.fr/en/> > CEFE Lab, Montpellier France

“thomas.lenormand@cefe.cnrs.fr”  
<[thomas.lenormand@cefe.cnrs.fr](mailto:thomas.lenormand@cefe.cnrs.fr)>

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## Greifswald Germany DiapauseEvolPhysiology

The Institute of Zoology, Department of Animal Physiology, Faculty of Mathematics and Natural Sciences at the University of Greifswald is seeking to fill two PhD-positions within the next six months for a limited period of 3 years. Payment will be made according to pay group 13 TV-L Wissenschaft.

The post holders will work in a joint project of the Department of Animal Physiology (Zoological Institute and Museum), the Department of Cellular Biochemistry & Metabolomics (Institute of Biochemistry) and the Department of Microbial Proteomics (Institute of Microbiology) in the German Scientific Foundation (DFG)-funded project “Life on hold: a physiological model of a low temperature clock in a diapausing insect” to answer the question of how cold temperatures drive the physiological development of pupae of the butterfly *Pieris napi* as they progress through winter diapause. The position holder will work interdisciplinary in both research groups and be part of a highly motivated team of international young scientists within the research groups. The position to be filled is suitable as a qualification position for obtaining the Dr. rer. nat. (Phd equivalent) degree.

The Department of Animal Physiology is concerned with adaptations of animals to the seasons. The work is integrative, focussing on evolutionary and ecological aspects of physiological function. The main taxa are insects, especially butterflies.

Position 1 - Diapause eco-physiology and molecular biology

Work tasks: - Travel to catch *Pieris napi* butterflies - Breeding and husbandry of butterflies in the lab - Hormone analyses with immunofluorescent and mass-spectrometric methods - Western blot analyses of protein abundances and interactions - Transfection of cells and production of recombinant proteins - Physiological interpretation of data - Presentation of the results at regular project meetings

- Writing scientific articles disseminating the results  
Recruitment requirements: - Master’s or comparable scientific university degree in biology, physiology, biochemistry or a related life science - Excellent applicants with a strong interest in experimental scientific work -

Interest in the fields of animal physiology and molecular biology - During candidate selection, special emphasis will be put on scientific excellence and personal suitability

Desirable are: - A strong background in animal physiology and molecular biology - Experience with insect rearing, or work with insects in general - Experience with protein analyses, including protein sample preparation, western blot, immunohistochemistry - Experience with metabolomics and data processing of mass-spectrometric data are an asset but may be learned on the job - Very good computer skills Excellent English language skills (can be demonstrated with an IELTS score of 6.5 or equivalent) - Sound knowledge of writing scientific texts and presentations - Qualities such as reliability, self-organisation and the ability to work in a team

Position 2 - Diapause evolutionary proteomics

Work tasks: - Breeding and husbandry of the butterfly *Pieris napi* - In vitro measurements and manipulation of enzyme activities - Independent preparation of proteome samples for quantitative expression analysis with a special focus on post-translational protein modifications - Mass spectrometric measurement - Routine work on mass spectrometers (calibration, tuning) - Bioinformatic analysis of the collected data - Physiological interpretation and categorisation of the data - Presentation of the results at regular project meetings - Writing scientific articles disseminating the results — Recruitment requirements: - Master’s or comparable scientific university degree in biology, biochemistry or a related life science - Excellent applicants with a strong interest in experimental scientific work - Interest in the fields of animal physiology and proteomics - During candidate selection, special emphasis will be put on scientific excellence and personal suitability

—Desirable are: - Sound knowledge/experience in the fields of microbiology, protein chemistry and bioinformatics - Very good computer skills - Experience in proteome analysis (protein sample preparation, HPLC, mass spectrometry) and data processing of proteomic data (e.g. MaxQuant, Mascot) - Excellent English language skills (can be demonstrated with an IELTS score of 6.5 or equivalent) - Sound knowledge of writing scientific texts and presentations - Qualities such as reliability, self-organisation and the ability to work in a team

The positions are open to all persons, irrespective of gender. The University would like to increase the proportion of women in areas in which they are underrepresented and thus applications from women are particularly welcome and will be treated with priority if they have the same qualifications and as long as there are no clear reasons which make



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

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## LundU MicrobialEvolutionAnaerobicLife

Dear all,

We're looking for a PhD student to join our team at Lund University (Sweden) to study how microbial eukaryotes - 'protists' - live without oxygen. The position is set to start in the Autumn of 2024, but is flexible per agreement.

Details about the position and how to apply (including specific instructions for the cover letter) can be found here: <https://thelabupstairs.online/open-positions/>. THE PROJECT Oxygen-depleted environments are more than just "anoxic dead zones" - they are home to a diverse array of life, including eukaryotic microbes. This PhD project aims to explore the mitochondrial biology in anaerobic eukaryotes, shedding light on how their metabolism and organelle function have evolved to thrive in oxygen-free environments. The focus will be on the electron transport chain and other electron transferring strategies like hydrogen generation. We will investigate the functional diversity of anaerobic respiratory chains in eukaryotes and explore the evolutionary mechanisms that contribute to this adaptations including lateral gene transfer and neofunctionalization. Additional projects related to environmental anaerobic eukaryotes are also available.

THE ORGANISMS We study unicellular eukaryotes - or 'protists' - that often have peculiar biology compared to what our textbooks teach us. This project will centre on protists from the Breviatae and Amoebozoa phyla that have taken different evolutionary trajectories towards anaerobic life. Instead of depositing electrons onto oxygen, these protists can make hydrogen gas or succinate which can be consumed by prokaryotic organisms in a form of metabolic co-operation known as 'syntrophy'. Your task will be to help us follow the electrons and understand the basic cell biology of these protists.

RESEARCH METHODS This project will use cell biological methods, including super-resolution microscopy, proteomics, and metabolomics of quinone molecules.

Moreover, there is potential to develop expertise in bioinformatic methods such as transcriptomics, comparative genomics, and phylogenetics as well as environmental microbiology.

SUPERVISION The successful candidate will join the Molecular Cell Biology Division in the Biology Department at Lund University, under the supervision of Dr. Courtney Stairs, an expert in eukaryotic microbiology. The project will also be co-supervised by Dr. Olivier van Aken, a leading researcher in mitochondrial biology. This project is part of the European Research Council 'TANGO2' StG project, awarded to Dr. Stairs.

Best wishes, Courtney

Courtney Stairs Biträdande Universitets Lektor

Lund University Department of Biology  
[www.thelabupstairs.online](http://www.thelabupstairs.online) Courtney Stairs  
<courtney.stairs@biol.lu.se>

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## MacquarieU FlowerColourEvolution

3-year PhD scholarship in Flower colour Genomics

The Field lab at Macquarie University in Sydney Australia, is recruiting a PhD student who is enthusiastic about plant evolutionary and conservation genetics to join our project on the iconic plants known as kangaroo paws (*Anigozanthos*) of Western Australia.

The goal of the 'flower power' project is to unlock the genetic and biochemical potential of flower colour in kangaroo paws which display remarkable flower colour variation among and within species. The successful candidate will contribute to a broad project using genome assemblies, whole genome re-sequencing and phylogenomic analyses, genetic mapping and transcriptomics of flower colour genes and pathways, and population and evolutionary genomic analyses of flower colour variation in hybrid zones in nature. We will identify independent sources of colour variation across the entire group of kangaroo paw species to understand how this remarkable colour diversity is generated and maintained. This research will be important for improving programs for conservation and develop novel colours for horticulture. The PhD student will have the capacity to develop a project in these each of these areas.

The successful candidate will join a diverse team of

people working on kangaroo paws including researchers from Macquarie University, Kings Park and University of Western Australia in Perth. The broader group works on a range of plant systems (e.g. snapdragons, Eucalypts) and research questions related to speciation, adaptation, genetic rescue and conservation of threatened species and plant-pollinator interactions. We utilise an integrated approach using bioinformatics, population and evolutionary genetics, field ecology and glasshouse experiments, molecular biology, biochemistry and mathematical modelling.

#### Eligibility:

The successful applicant will ideally have an MSc involving molecular lab work, although other pathways via BSc are possible if significant research experience can be demonstrated. Previous experience working with plant DNA and genomic data is preferred. Willingness to contribute to field work. For further details see the link below

Macquarie University is situated in the northern part of Sydney. The city is a diverse and vibrant place to live, a beautiful harbour city with vast entertainment options and outdoor activities on your doorstep. Gold sandy beaches and vast National Parks circle the city (e.g. Blue Mountains, Ku-ring-gai Chase national parks) situated in a global biodiversity hotspot are easily accessible by train.

The PhD scholarship is fully funded (and a tax free salary) for 3 years (extensions possible) and all international student tuition fees are waived. Opportunities to teach in undergraduate classes are also available.

For more details on selection criteria see the link below.

Enquiries: A/Professor David Field,  
 david.field[@mq.edu.au To Apply: <https://www.mq.edu.au/research/phd-and-research-degrees/how-to-apply/scholarship-opportunities/scholarship-search/harnessing-genomics-for-australian-plants>  
 Closing Date: End of May 2024 or until filled

David Field <david.field@mq.edu.au>

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## MacquarieU Sydney EcolEvolGenomics SuperSeed

A fully funded 3-year PhD scholarship (including all tuition) in EcolEvol and conservation Genomics on Australian plants.

The Field lab at Macquarie University in Sydney Australia, is recruiting a PhD student who is enthusiastic about plant evolutionary ecology, conservation genetics (including genetic rescue) to join our project on local adaptation and admixture in Native Seed Production Areas in Australian plants.

This project aims to understand how we can produce 'Super Seed' - optimising genetic diversity and admixture in native seed orchards for Australian plants used in restoration projects. The establishment of Seed Production Areas (SPA) for native Australian plants has become increasingly important to fill the gap between seed supply and demand. However, key knowledge gaps remain in understanding the genetic diversity and composition of SPAs compared to natural populations and how this translates to resilient seeds suitable for changing climates. We are particularly interested in how plant mating systems, pollination systems and demographic factors such as range size and neighbourhood size impact seed quality and quantity and extent of admixture between provenances. As part of a collaboration with Greening Australia and other research groups across Australia, we aim to provide basic research findings and practical guidelines for improving native seed quality across diverse plant life histories, mating and pollination systems. Ultimately this will help standardise and guide SPA development to improve the likelihood of success and the production of genetically healthy seed appropriate for changing climates. This PhD student project will be able to design a project within the main goals of the larger project, using population genomic analyses in SPAs and native populations to understand the demographic and evolutionary history of each species, and eco-evol models, paternity analyses and GEA of provide practical solutions to SPA design.

The broader group works on a range of plant systems (e.g. snapdragons, kangaroo paws, Eucalypts) and research questions related to speciation, adaptation, genetic rescue and conservation of threatened species and plant-pollinator interactions. We utilise an integrated approach using bioinformatics, population and evolution-

ary genetics, field ecology and glasshouse experiments, molecular biology, biochemistry and mathematical modelling.

Macquarie University is situated in the northern part of Sydney. The city is a diverse and vibrant place to live, a beautiful harbour city with vast entertainment options and outdoor activities on your doorstep. Gold sandy beaches and vast National Parks circle the city (e.g. Blue Mountains, Ku-ring-gai Chase national parks) situated in a global biodiversity hotspot are easily accessible by train.

Eligibility:

The successful applicant will ideally have an MSc involving molecular lab work, although other pathways via BSc are possible if significant research experience can be demonstrated. Previous experience working with plant DNA, plant-pollinator interactions and population genetic data is preferred. Willingness to contribute to field work. For further details see the link below

Macquarie University is situated in the northern part of Sydney. The city is a diverse and vibrant place to live, a beautiful harbour city with vast entertainment options and outdoor activities on your doorstep. Gold sandy beaches and vast National Parks circle the city (e.g. Blue Mountains, Ku-ring-gai Chase national parks) situated in a global biodiversity hotspot are easily accessible by train.

The PhD scholarship is fully funded (and a tax free salary) for 3 years (extensions possible) and all international student tuition fees are waived. Opportunities to teach in undergraduate classes are also available.

For more details on selection criteria see the link below.

Enquiries: A/Professor David Field, david.field[[@](mailto:david.field@mq.edu.au)]mq.edu.au To Apply: <https://www.mq.edu.au/research/phd-and-research-degrees/how-to-apply/scholarship-opportunities/scholarship-search/building-resilient-seed-production-areas> Closing Date: End of 1st July 2024 or until filled.

David Field <david.field@mq.edu.au>

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## MainzU EvolutionaryBiology

Introducing a New Master's Degree Programme in "Evolutionary Biology" at Johannes Gutenberg University in Mainz, Germany

We are pleased to announce the launch of our new English-language Master's degree programme in Evolutionary Biology at Johannes Gutenberg University in Mainz starting in October 2024.

One of the key features of this programme is its integration of molecular laboratory work with computational biology and genomics. Students will have access to cutting-edge facilities and equipment, allowing them to conduct hands-on research in evolutionary processes while leveraging advanced computational techniques for data analysis. The curriculum is structured to provide students with a comprehensive understanding of evolutionary theory, molecular ecology, biotic interactions, genomics, and anthropology. Courses are taught by experienced faculty members who are actively engaged in research within the field, offering students valuable insights and mentorship. The application phase for the programme is may 1st to May 15th 2024. Interested students are encouraged to apply through the university's online portal.

Further information can be found here: <https://www.blogs.uni-mainz.de/fb10-biologie-eng/master-evolutionary-biology/> The participating research groups introduce themselves here: <https://iome.biology.uni-mainz.de> If you have any further questions, please contact the programme coordinator Prof. Joachim Burger:evolbiol@uni-mainz.de

EvolutionaryBiology <evolbiol@uni-mainz.de>

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## MPIBI Seewiesen EvolutionCognition

Opportunity!

Projects available for Master's students and self-funded

guest researchers in Comparative Cognition Research Station at Tenerife, Spain, run collaboratively between the Max-Planck Institute for Biological Intelligence and the Loro Parque Foundation

The Max-Planck Comparative Cognition Research Group (CCRG)

<https://www.bi.mpg.de/von-bayern> invites applications from Postgraduate/Undergraduate students and Interns who want to assist in research projects and bird care, enrichment and management. The CCRG is part of a collaboration between the Max-Planck Institute for Biological Intelligence, Germany, and Loro Parque Fundacion (LPF) in Tenerife, Spain. We are currently carrying out several projects on parrot intelligence. We work with mostly tame, captive parrots of LPF, which owns the largest collection of parrots and genetic reserve in the world (approximately 350 subspecies) for conservation and research purposes. Interested candidates are encouraged to contact us to request information about ongoing projects. Selected applicants will gain experience in the field of cognitive research, as well as working with and training exotic parrots in a highly dynamic international research environment. A unique opportunity!

Preferable time of joining: It is highly preferable if students can join by April/May 2024

Logistics: The projects for Master's theses and guest researchers require a minimum of 4 months but ideally 6 months of continuous commitment at the research station in Tenerife, Spain.

Accommodation can be provided in a shared student apartment (Puerto de la Cruz, Tenerife, Spain), with affordable facilities. Students with their own funding or grants can apply for the posts.

Important skills/qualifications:

Selected candidates need to have:

- High motivation and commitment to the care of our birds - Preferably pursuing a Master's degree in Biology/ Psychology/Animal Science or related subjects. - Reliability, efficiency and ability to work independently
- Confidence to interact with animals - Good verbal English skills - Good teamwork attitude and social skills

Submit your request!

For more information on how to apply, please email Dr. Anastasia Krasheninnikova ([akrasheninnikova@bi.mpg.de](mailto:akrasheninnikova@bi.mpg.de))

“Krasheninnikova, Anastasia”  
<[AKrasheninnikova@bi.mpg.de](mailto:AKrasheninnikova@bi.mpg.de)>

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## MPI Germany PolygenicAdaptation

A doctoral researcher position is available in Neda Barghi's group at the Max Planck Institute for Evolutionary Biology- Plön, Germany. The position is fully funded for 3.5 years at 65% TVöD E13, and will start in Autumn/Winter 2024. The doctoral researcher will be part of The International Max Planck Research School for Evolutionary Biology (IMPRS EvolBio). Further information about IMPRS EvolBio can be found here: <http://www.evolbio.mpg.de/imprs> Deadline to apply: April 15, 2024

Project title: Genetic and adaptive architecture of polygenic traits

Project description: The genetic architecture of quantitative traits comprises of all the contributing alleles and their effect sizes. Factors such as the distance to the new trait optimum, starting frequencies and pleiotropy determine which of the underlying alleles are potentially adaptive. Therefore, only a subset of the underlying alleles responds to selection, these alleles comprise the adaptive architecture. While the genetic architecture has been the focus of many quantitative trait loci (QTL) and genome-wide association (GWA) studies, the adaptive architecture of polygenic traits is not well characterized.

The aim of this project is to compare the genetic and adaptive architectures of a polygenic traits, *Drosophila simulans* female body size. We will determine the genetic architecture of female body size using GWAS with 1000 heterozygous individuals. Additionally, in an evolve and re-sequence (E&R) experiment we will experimentally evolved *Drosophila simulans* populations for larger body size. In this E&R project, for the first time, the shift in trait optimum, i.e. body size, is experimentally defined. Availability of this E&R dataset allows us to distinguish alleles with adaptive potential, and to compare the adaptive and genetic architectures of female body size.

This project is suitable for evolutionary biologists interested in understanding the genetic basis of adaptation. The doctoral researcher will have access to a large dataset consisting of GWAS and time-series genomic data from E&R experiments. The doctoral researcher should have strong programming skills (Python, R, etc) and experience with handling large data sets. Back-

ground in either population genetics or quantitative genetic is essential. The project is a great opportunity for researchers who are interested in analyzing time-series data and combining bioinformatics methods with population genetic theory.

This project is part of a joint research program (SFB) on polygenic adaptation (<https://www.vetmeduni.ac.at/-sfb-polygenic-adaptation>) and faculty in this program will be co-supervisors of the project.

Please send 1) your CV, 2) motivation letter (describing your education, your research interests, why you want to pursue a Ph.D., and why you are suitable for the position, max. 2 pages), and 3) contact details of at least three referees (email addresses and phone numbers) to Dr. Neda Barghi: [barghi.neda@gmail.com](mailto:barghi.neda@gmail.com).

For more information about our research/group visit: <https://www.vetmeduni.ac.at/populationsgenetik/-forschung/gruppe-barghi> Neda Barghi, Ph.D. Group leader Institute of Population Genetics, Vetmeduni Vienna, Austria

<https://www.vetmeduni.ac.at/en/population-genetics/> \*My working hours might be different from yours, please do not feel obliged to reply outside of your normal work schedule.\*

Neda Barghi <[barghi.neda@gmail.com](mailto:barghi.neda@gmail.com)>

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## NatlUSingapore EvolutionButterflyLearning

I am looking for an enthusiastic student who wants to perform research on sound communication in adult butterflies or on odor learning in butterfly larvae, at the organismal and/or molecular levels (e.g., brain circuitry and single-cell gene expression levels). This work will be supported by a Fellowship from the Ministry of Education, Singapore.

The latest from our lab on these two topics can be found here:

Tiong GJJ, L Nailin, E Ng, E Dion, and A Monteiro (2024) Tympanal ears mediate male-male competition, courtship and mating success in *Bicyclus anynana* butterflies. *R. Soc. Open Sci.* 11231386231386 (<http://doi.org/10.1098/rsos.231386>)

Gowri V and A Monteiro (2024) Hemolymph transfusions transfer heritable learned novel odor preferences to naïve larvae of *Bicyclus anynana* butterflies. *bioRxiv* (doi: <https://doi.org/10.1101/2023.12.20.572719>)

Applications need to be submitted to our graduate program (<https://www.dbs.nus.edu.sg/education/-graduates/>) and the deadline is May 15 for January 2025 entrance.

Students with previous relevant research experience are preferred. The Department of Biological Sciences is a large unified department with diverse expertises ranging from ecosystem ecology to structural biology, and an ideal environment for those who like to do integrative work and expand their minds.

If interested please visit the lab's web site (<https://lepdata.org/monteiro/>) and contact Antonia Monteiro ([antonia.monteiro@nus.edu.sg](mailto:antonia.monteiro@nus.edu.sg)).

Antonia Monteiro <[antonia.monteiro@nus.edu.sg](mailto:antonia.monteiro@nus.edu.sg)>

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## NTNU Norway ArcticAlienPlantGenomics

PhD position in genomics of Arctic alien plants at NTNU University Museum, Trondheim, Norway. Start date spring 2024, fully funded for 4 years.

Extended deadline: April1st2024

Supervisory team: Associate Professor Kristine Bakke Westergaard (main)

Dr. Simone Fior, ETH Zürich, Switzerland (co)

Professor Mike Martin (co)

Please find all details and link to apply here:

<https://www.jobbnorge.no/ledige-stillinger/stilling/-255087> About the project: We are seeking a highly qualified, ambitious, and motivated PhD candidate for a project focusing on genomics of Arctic alien plants. The project will focus on target alien plant species and seek to uncover their genomic basis of adaptation to the Arctic environment and how it relates to their invasiveness.

A warming climate, changes in soil properties, and rising human activity in the Arctic increase the probability of introduction and establishment of alien plant species.

In high-Arctic Svalbard and other Arctic regions, the wintercress (*Barbarea vulgaris*) is an established and naturalised alien species. Hypotheses for its success include multiple introductions from different genetic sources, enemy release advantage related to plant defense compounds, and shifts in adaptive traits. The PhD project will develop genomic datasets, making use of field collections and herbarium resources, and develop experimental evidence to examine links between the genomic basis of successful establishment and potential invasiveness in the high-Arctic. The wintercress will be a primary focus of the project, but complementary research on parallel systems may be developed. The project will add an important evolutionary component to ongoing interdisciplinary research on Arctic greening.

The work of the PhD candidate will consist of arctic field work, herbarium work, green house experimental work, DNA lab and bioinformatics in an international interdisciplinary team. More specifically, the successful candidate will:

Manage and supervise third-party services to achieve high-quality reference genomes suitable for population genomic analyses  
 Assemble a spatial and temporal sampling of herbarium and fresh specimens  
 Produce NGS libraries and sequencing data using clean-lab facilities and third-party services  
 Analyse sequencing data combined with available genomic resources and complementary experimental evidence to unravel the evolutionary history of parallel Arctic invasions, including the phylogeography of established populations, the genetic architecture of adaptation to the Arctic environment, and the role of different chemotypes in the context of the enemy release hypothesis  
 Analyse temporal data to assess turnover of allele frequencies following introduction and bottlenecks  
 Design and perform common garden experiments to test the adaptive role of shifts in enemy pressure, breeding system and life-history traits underlying invasiveness under current and future climate  
 Disseminate results in scientific literature, to relevant stakeholders and the public

The candidate will use the NTNU University Museum's herbarium, genomics laboratory facilities and computational resources, and the work will be closely associated with a project on Arctic greening (<https://geobiology.ethz.ch/research/arctic-greening.html>) based at ETH Zürich. The work will also be part of the newly established Nordic Borealization Network that seeks to understand the processes, drivers, and consequences of changes in the species composition of tundra ecosystems.

As a PhD candidate you are normally paid from gross NOK 532 200 per annum before tax, depending on qualifications and seniority. From the salary, 2% is deducted

as a contribution to the Norwegian Public Service Pension Fund.

The position is available from spring 2024. The period of employment is four years, with 25% of the time allocated to collection work, teaching and public outreach.

Please feel free to reach out with any enquires -  
[kristine.b.westergaard@ntnu.no](mailto:kristine.b.westergaard@ntnu.no).

Kristine Bakke Westergaard  
 <[kristine.b.westergaard@ntnu.no](mailto:kristine.b.westergaard@ntnu.no)>

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## UC Dublin TreeDiseaseEvolution

We have a fully funded 4-year Walsh Scholarship PhD program available in my group. This initiative focuses on investigating the transcriptomic responses, genetic diversity, and virulence factors of *Hymenoscyphus fraxineus*, the causal agent of dieback disease in ash trees.

This collaborative project between Teagasc and University College Dublin, Agri-Food and Biosciences Institute is jointly funded by the Department of Agriculture, Food and the Marine, and the Department of Agriculture, Environment and Rural Affairs.

For more details: [https://www.teagasc.ie/media/-website/about/walsh-scholarships/2023262-Web-Advert\\_AshPath.pdf](https://www.teagasc.ie/media/-website/about/walsh-scholarships/2023262-Web-Advert_AshPath.pdf) Closing date: 24th March, 2024

“Jie Huang (Walsh Scholar)” <[Jie.Huang@teagasc.ie](mailto:Jie.Huang@teagasc.ie)>

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## UEdinburgh ModellingAntibioticResistanceEvo

A funded PhD position (October 2024 start) is available in the research group of Helen Alexander, Institute of Ecology & Evolution, University of Edinburgh. The PhD topic is “Modelling bacterial evolution of antibiotic resistance” and a full description is available



here: <https://www.ed.ac.uk/biology/study-with-us/postgraduate-research/apply-for-a-phd/findaphd>. The ideal candidate will have strong mathematical skills and a keen interest in biology, with at least an undergraduate degree in mathematics, physics, biology, or another relevant field. For more information about our research group, please see: <https://www.ed.ac.uk/biology/groups/alexander> The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336. Is e buidheann carthannais a th' ann an Oilthigh Dh'À'n Àideann, clàraichte an Alba, àireamh clàraidh SC005336.

Helen Alexander <Helen.Alexander@ed.ac.uk>

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## UIdaho ConservationGenomic- PygmyRabbits

Two PhD Research Assistantships in Wildlife Ecology & Conservation at the University of Idaho

**Project Description:** Despite being considered narrow specialists in sagebrush habitats, pygmy rabbits exhibit substantial variability in habitat associations across their range. Projections of potential habitat under future climate models suggested a severe reduction in distribution of suitable habitat for the species in Idaho. However, the degree to which local adaptations and behavioral or physiological plasticity might influence persistence and distribution is unknown. This research will support a team of 3 PhD students working with multiple faculty with diverse expertise. The overall goal of the research is to explore adaptive capacity in response to climate change for a small-bodied mammal of conservation concern.

Specific PhD student project objectives include: Project 1) Apply genomic techniques to address questions about adaptive variation and examine physiological variation in thermal and energetic responses to the environment; Project 2) Develop and integrate physically-based surface energy and biological models of pygmy rabbit habitat and fitness under climate change; and Project 3) Model occupancy, behavior, and habitat selection to refine understanding of the current distribution, factors influencing distribution patterns, and potential future distribution under climate change (this PhD position is filled).

The Doctoral Research Assistantships include a 12-month stipend, tuition, and health insurance, and are funded for 3 years, with an additional 2 semesters of Teaching Assistantship support available.

**Start date:** Fall 2024 **Location:** University of Idaho, Moscow Campus. Remote work not possible. Application review will start 11 March 2024 and continue until filled.

**Project 1: Required qualifications:** - Scientific curiosity, a positive attitude, and strong work ethic. - A master's degree in Ecology, Biology, Wildlife Science, or a related discipline and evidence of academic productivity (e.g., publications, presentations at professional meetings, contributions to research teams). - Demonstrated communication (writing and speaking) and quantitative skills. - Strong organizational skills and experience working in research teams. - Experience and/or training in genetics. - Experience in molecular techniques, genomics, and/or physiology is a plus, but not required.

**Project Supervisors:** Drs. Janet Rachlow, Lisette Waits, Paul Hohenlohe ([hohenlohe@uidaho.edu](mailto:hohenlohe@uidaho.edu)) **Application:** Please email a brief cover letter, CV, transcripts (unofficial are fine), GRE scores (if available), and names and contact information for 3 references to Dr. Janet Rachlow at [jrachlow@uidaho.edu](mailto:jrachlow@uidaho.edu).

**Project 2: Required qualifications:** - Interest in becoming a scientist who advances the understanding of integrated physical and biological processes by integrating observational data and numerical modeling. - Interest in developing practical solutions to wildlife management problems. - Experience, knowledge, and/or interest in the following areas: (1) writing R code to process data and model systems; (2) ecological challenges related to climate dynamics; (3) basic GIS skills to manipulate geospatial data; (4) theory and models of population dynamics and individual behavior, and (5) cultivation of collaborative professional relationships with researchers and managers. - Knowledge of GIS and/or stochastic dynamic programming is preferred but not required.

**Project Supervisors:** Drs. Matt Falcy ([mfalcy@uidaho.edu](mailto:mfalcy@uidaho.edu)) and Tim Link ([tlink@uidaho.edu](mailto:tlink@uidaho.edu))

**Application:** Merge the bulleted items below into a single PDF and email to [tlink@uidaho.edu](mailto:tlink@uidaho.edu) and [mfalcy@uidaho.edu](mailto:mfalcy@uidaho.edu) by March 11, 2024 using the subject line Pygmy Rabbit Opportunity:

- Cover letter describing (i) qualifications (ii) a specific research question that you might be interested in pursuing within the general project described above, and (iii) a statement of work ethic/philosophy that you intend to implement in this position to achieve your longer-term goals. Do not exceed three pages. - CV/resume

that includes contact information for three professional references. - Photocopy of GRE general test scores, if available. - Unofficial or official transcripts of all coursework.

Paul Hohenlohe Professor, Biological Sciences Director, BCB Graduate Program University of Idaho <http://hohenlohelab.github.io> "Hohenlohe, Paul (hohenlohe@uidaho.edu)" <hohenlohe@uidaho.edu>

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## UIdaho Two Rabbit Conservation Genomics

Two PhD Research Assistantships in Wildlife Ecology & Conservation at the University of Idaho

**Project Description:** Despite being considered narrow specialists in sagebrush habitats, pygmy rabbits exhibit substantial variability in habitat associations across their range. Projections of potential habitat under future climate models suggested a severe reduction in distribution of suitable habitat for the species in Idaho. However, the degree to which local adaptations and behavioral or physiological plasticity might influence persistence and distribution is unknown. This research will support a team of 3 PhD students working with multiple faculty with diverse expertise. The overall goal of the research is to explore adaptive capacity in response to climate change for a small-bodied mammal of conservation concern.

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Project Supervisors: Drs. Janet Rachlow, Lisette Waits, Paul Hohenlohe Application: Please email a brief cover letter, CV, transcripts (unofficial are fine), GRE scores (if available), and names and contact information for 3 references to Dr. Janet Rachlow at jrachlow@uidaho.edu.

Project 2: Required qualifications:

\* Interest in becoming a scientist who advances the understanding of integrated physical and biological processes by integrating observational data and numerical modeling. \* Interest in developing practical solutions to wildlife management problems. \* Experience, knowledge, and/or interest in the following areas: (1) writing R code to process data and model systems; (2) ecological challenges related to climate dynamics; (3) basic GIS skills to manipulate geospatial data; (4) theory and models of population dynamics and individual behavior, and (5) cultivation of collaborative professional relationships with researchers and managers. \* Knowledge of GIS and/or stochastic dynamic programming is preferred but not required.

Project Supervisors: Drs. Matt Falcy (mfalcy@uidaho.edu) and Tim Link (tlink@uidaho.edu) Application: Merge the bulleted items below into a single PDF and email to tlink@uidaho.edu and mfalcy@uidaho.edu by March 11, 2024 using the subject line Pygmy Rabbit Opportunity:

\* Cover letter describing (i) qualifications (ii) a specific research question that you might be interested in pursuing within the general project described above, and (iii) a statement of work ethic/philosophy that you intend to implement in this position to achieve your longer-term goals. Do not exceed three pages. \* CV/resume that includes contact information for three professional references. \* Photocopy of GRE general test scores, if available. \* Unofficial or official transcripts of all coursework.

LISETTE WAITS Distinguished Professor Department of Fish and Wildlife Sciences College of Natural Resources [University of Idaho] lwaits@uidaho.edu 208-885-7823 875 Perimeter Drive MS1136 | Moscow ID 83844-1136

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## ULausanne EvolutionaryBiology

Introduction UNIL is a leading international teaching and research institution, with over 5,000 employees and 17,000 students split between its Dorigny campus, CHUV and Epalinges. As an employer, UNIL encourages excellence, individual recognition and responsibility.

Presentation The Group of Prof. Charles Mullan is proposing a Doctoral Student SNSF position in Theoretical Evolutionary Ecology / Biology at the Department of Ecology and Evolution, University of Lausanne, Switzerland. The PhD Students will join a dynamic team working mainly on developing and analyzing mathematical models to understand the evolutionary dynamics of traits that mediate interactions among individuals and with the environment. Interests include, but are not limited to, the evolution of sexual traits, genetic architecture, ecological interactions, niche construction, and social behaviour. For more information on the lab, visit <https://lab-mullan.github.io/> Job information Expected start date in position : 01.07.2024 or to be agreed (up to 01.01.2025) Contract length : 1 year, extendable to a total of 4 years Activity rate : 100% Workplace : Lausanne-Dorigny Annual gross salary : CHF 47'699.- (1st year)

Your responsibilities The successful candidate will be based at the Department of Ecology and Evolution of the University of Lausanne, under the supervision of Prof. Charles Mullan. The research project will be defined together with the group leader based on the candidate's interests and competences in the field of theoretical evolutionary ecology. Understanding of and confidence with mathematical modelling and evolutionary concepts are highly desirable. Most of the time will be dedicated to the realization of the doctoral thesis (85%) but a contribution to teaching activities will be asked (15%). The University of Lausanne offers a world-class international

research environment with state-of-the-art facilities.

Your qualifications In order to complete our team, we are looking for someone with the following skills:

Essential: - Master's degree in a relevant area (e.g., biology, mathematics, physics, computer science)

- Scientific research motivation and experience in evolutionary biology

- Excellent spoken and written English proficiency

Desirable: - Confidence in evolutionary biology (e.g., population and quantitative genetics, sexual selection, social evolution, evolutionary game theory)

- Experience with mathematical modelling (e.g., dynamical systems, applied probabilities)

- Programming skills (e.g., in Python, R or C)

Interpersonal skills : - Good cooperative skills with other researchers and team members

- Good communication skills, ability to keep an open mind and to communicate your ideas

- Be motivated and be able to motivate others

What the position offers you We offer an outstanding working place in a multicultural, diverse and dynamic academic environment. Opportunities for professional training, a lot of activities and other benefits to discover. The Department of Ecology and Evolution in Lausanne University hosts research groups working on a broad range of topics, producing a rich intellectual and social life. Although French is the common language in Lausanne region, the department research activities and seminars are conducted in English. The campus is located on the shore of the Geneva Lake, with the view on the Alps.

Contact for further information For further information, please contact Prof. Charles Mullan : charles.mullan@unil.ch

Your application Deadline : 12.04.2024 Formal applications should include: - a cover letter containing a short description of your research interests and research experience explaining why you reply to this job offer (max. 2 pages);

- your CV;

- a copy of your master certificate (if already available);

- master's thesis summary (~one paragraph, max. one page);

- the contact details of 2-3 referees.

To receive full consideration, application documents should be uploaded online through the University of Lau-

sanne recruitment platform. Only applications through this website will be taken into account: <https://bit.ly/3x4zYVm> Additional information UNIL is committed to equal opportunities and diversity. We actively encourage applications from individuals of diverse backgrounds, including but not limited to race, ethnicity, gender, sexual orientation, disability, and age. [www.unil.ch/egalite](http://www.unil.ch/egalite) Charles Mullon <charles.mullon@unil.ch>

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## UMainz Behavioural Evolution Ants

PhD position Behavioral neurobiology of ants

We are recruiting a motivated and talented student interested in understanding the evolution and organization of the olfactory system in ants (and other insects). The student will join an interdisciplinary team composed by Carlotta Martelli (neurobiology and computational biology), Susanne Foitzik (behavior and evolution) and Hugo Darras (evolution and genomics), two PhD students and one postdoc.

The project aims to unravel the organizational logic of the olfactory system in *Temnothorax* ants, from genes to neurons to behavior. The long-term goal is to identify evolutionary signatures of non-canonical organizations of the olfactory system and to understand the computational consequences of different architectures for odor coding and behavior. This innovative, interdisciplinary project combines neurobiological and behavioral experiments, molecular genetic analysis, genomics, transcriptomics, and theory.

This call is intended to fill a PhD position that will focus on the analysis of behavior, with the goal to link molecular and anatomical features of the olfactory system to the behavior of individual ants within a colony.

The project will be co-supervised by S. Foitzik and C. Martelli, in collaboration with H. Darras.

The PhD student should have a strong interest in behavior and neurobiology, ideally with experience in quantitative behavioral analysis. Training in evolutionary biology, neuroanatomy and experience in handling insects would also be an advantage but are not a prerequisite.

Funding for this position is secured over 3 years, with potential of extension.

The PhD student will have the opportunity to be in-

tegrated into the GenEvo graduate program (<https://www.genevo-rtg.de/>), which offers a close-knit community of graduate students and provides training in molecular and evolutionary biology, as well as methodological courses such as on bioinformatics.

To apply, please send a letter of motivation, CV and contact information of two referees to [cmartell@uni-mainz.de](mailto:cmartell@uni-mainz.de) and [foitzik@uni-mainz.de](mailto:foitzik@uni-mainz.de)

DEADLINE: 27.03.2024 For additional information, please contact us! Carlotta Martelli [cmartell@uni-mainz.de](mailto:cmartell@uni-mainz.de), <https://mrtlllab.uni-mainz.de/> Susanne Foitzik [foitzik@uni-mainz.de](mailto:foitzik@uni-mainz.de), Group Foitzik | Behavioural Ecology and Social Evolution Hugo Darras [hdarras@uni-mainz.de](mailto:hdarras@uni-mainz.de), Group Darras | Behavioural Ecology and Social Evolution iDN and iomE, Johannes Gutenberg University Mainz, Germany

Prof. Dr. Susanne Foitzik Institute of Organismic and Molecular Evolution Johannes Gutenberg University Mainz Biozentrum Hanns Dieter Hesch 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](mailto:foitzik@uni-mainz.de)

“Foitzik, Susanne” <[foitzik@uni-mainz.de](mailto:foitzik@uni-mainz.de)>

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## UMainz EvolPlantHerbivore

PhD Position available (50% E13 TV-L) University of Mainz, Institute of Organismic and Molecular Evolution Supervisor: Prof Dr Meret Huber (<https://plant-evolutionary-ecology.uni-mainz.de/>) Starting date: July 2024 or to be agreed upon

Real-Time Evolution of Plant-Herbivore Interactions

Background: One of the central paradigms in plant-herbivore interactions states that plants and their herbivores co-evolve. Yet, experimental evidence for this prediction is scarce. In this project, we aim to fill this knowledge gap by experimentally evolving duckweeds and one of its major native herbivores, the water lily aphid. By taking advantage of the rapid life cycles and the genetic and experimental manipulation possibilities in these species, we will observe and manipulate evolution in both interaction partners in real-time and thereby experimentally test a central hypothesis in plant-herbivore interactions. We look for an enthusiastic and ambitious PhD student with strong interest in plant-

herbivore interactions and evolution. The applicant should have a solid background in ecology or evolution and have interest in combining genetic engineering, chemical analytics and experimental evolution. Experience in plant-environment interactions is advantageous. The applicant must be fluent in English and hold a MSc degree in Biology or related fields.

We offer a stimulating and interdisciplinary research environment including state-of-the-art facilities in a dynamic and international research group that ensures extensive supervision. The candidate can join the graduate school GenEvo (“Gene Regulation in Evolution”) and fully benefit from its tailored programme. The Institute of Organismic and Molecular Evolution is located at the University Campus of Mainz, close to the lively city center of Mainz. Mainz is situated in the picturesque Rhine valley, which can easily be explored through various cultural and outdoor activities.

How to apply: Please send a single pdf containing i) a motivation letter (max. 2 pages), ii) detailed CV, iii) copies of BSc and MSc degree, and iv) names and addresses of two referees to meret.huber@uni-mainz.de until 31.03.2024. The successful candidate may start in July 2024 or to be agreed upon.

For further information, please contact: Prof. Dr. Meret Huber Institute of Organismic and Molecular Evolution Johannes Gutenberg University Mainz Johann-Joachim-Becher-Weg 7 D - 55128 Mainz Phone: 0049 (0)6131 3930260 meret.huber@uni-mainz.de

“Huber, Prof. Meret” <mehuber@uni-mainz.de>

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## UMarburg Germany TibetanBeetleEvol

Exciting PhD opportunity at the University of Marburg! Dive into the DFG funded project TransTibet, exploring the evolution and genomic adaptation of ground beetles in high mountain ecosystems. Starting ASAP for 3 years. Join us in unraveling the secrets of High Asia’s biodiversity and uplift history. Apply by March 10, 2024. Details: <http://www.opgenoorth.org/TransTibet/> Lars Opgenoorth <opgenoorth@uni-marburg.de>

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## UniGE Switzerland EvolutionFishParasites

I am advertising for a PhD student to join my group at the Natural History Museum of Geneva and the University of Geneva. Please find the full advertisement attached and in the link: <https://lifesciencesphd.unige.ch/-jobs> The PhD project will examine the ecology and evolution of parasites of freshwater fish in Europe, within the framework of an internationally and interdisciplinary Biodiversa project “IMPACT: Integrated Monitoring of PARasites in Changing environmenTs”

Parasites are typecast as biological villains due to their threats to human health and wildlife conservation, despite most metazoan parasites having no zoonotic potential, and constituting an overwhelming proportion of current biodiversity. Re-evaluation of European freshwater fish diversity has led to an increase in recognised fish diversity, often linked to the discovery of local endemism. Conversely, surveys of their associated parasites have been slow to follow, and their diversity is likely underestimated. New assessments of fish parasite biodiversity status are desperately needed at a time when both parasites and their fish hosts face the impacts of global change and invasive species.

Deadline 1st April 2024.

Very happy to hear from interested candidates

Dr Isabel Blasco Costa Conservatrice / Curator T. +41 22 418 6387 isabel.blasco-costa@ville-ge.ch

Muséum d’histoire naturelle (MHN)

Département de la culture et de la transition numérique

Route de Malagnou 1 1208 GENEVE [www.museum-geneve.ch](http://www.museum-geneve.ch) Notre environnement est fragile, merci de n’imprimer ce message qu’en cas de nécessité.

“Isabel.Blasco-Costa@ville-ge.ch” <Isabel.Blasco-Costa@ville-ge.ch>

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## UPorto Portugal Population Genomics

Call of interest for a Doctoral (PhD) Fellowship in population genomics of freshwater mussels.

The Interdisciplinary Centre of Marine and Environmental Research (CIIMAR) and the Research Centre in Biodiversity and Genetic Resources - InBIO Associate Laboratory (CIBIO) are advertising the Call for PhD Studentships of the Portuguese Foundation for Science and Technology (FCT).

### Background

Advancements in genomics allow for linking DNA variation with diversification, adaptation, and survival, providing unprecedented tools to aid conservation efforts for highly threatened and underrepresented organisms. Freshwater mussels are a diverse and widespread group of strictly freshwater bivalves. These organisms have evolved remarkable adaptations to freshwater environments, including internal fertilization and a unique larval stage known as glochidia, which parasitizes fish for dispersion and nutrition until metamorphosis occurs. Freshwater mussels are also among the most threatened taxa worldwide. In Europe, all species are imperilled. Besides the numerous known threats that contribute to the global decline of freshwater mussels, the Climate Crisis is also becoming a serious concern for their survival, particularly in warmer regions like the Mediterranean. Therefore, there is an urgent need for comprehensive genomic surveys, which are currently unavailable, to understand the genetic basis of the decline of these species and their adaptive potential.

### Work plan description

We are looking for PhD candidates who are motivated, enthusiastic, and hardworking, and who are interested in addressing scientific problems with rigour and creativity. The ideal candidate should have a graduate degree in natural sciences, biology, genetics, or a closely related field, and a strong interest in bioinformatics. The work will focus intensively on bioinformatics, so learning shell script will be mandatory.

The candidate will conduct whole genome assemblies and population genomics to:

- 1) Characterize the genetic diversity and demographic history of European freshwater mussels and 2) identify

the genomic features that underlie freshwater mussels' adaptation to the Climate Crisis.

The project will mainly use existing samples, but there will be opportunities for fieldwork to support project objectives or if the candidate is willing to participate in them. Also, the candidate is expected to be involved in some molecular laboratory work (DNA/RNA extractions for NGS sequencing). The PhD candidate will join a multidisciplinary team of motivated researchers in the field of aquatic ecology and evolution. They will also benefit from and be integrated into a network of collaborations with other national and international institutions. This proposal aims to provide new insights into the adaptation of freshwater species with broad geographical ranges to local environmental conditions. Additionally, it seeks to enhance our understanding of the evolutionary history of these imperilled organisms. The ultimate goal is to inform future management actions aimed at conserving these extraordinary organisms.

### IMPORTANT:

This is just a call of interest!

Interested candidates should contact us for a preliminary interview. Selected candidates will after have to apply to the FCT PhD scholarships, which will be evaluated at a national level. This application will require the submission of a comprehensive proposal plan by 18 April. Therefore, we will only consider expressions of interest up to 18 March. We will provide assistance to the successful candidate in developing the final proposal.

More details on the candidature plan can be found at the FCT website at - <https://www.fct.pt/en/concursos/-concurso-bolsas-de-doutoramento-2024-linha-de-candidatura-especifica-em-ambiente-nao-academico> For more information, please contact.

Dr. Elsa Froufe (efroufe@ciimar.up.pt)

Dr. Manuel Lopes-Lima (mplopeslima@cibio.up.pt)

Dr. André Gomes-dos-Santos (asantos@ciimar.up.pt)

—  
\*André Santos \*

PhD

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André Santos <andrepousa64@gmail.com>

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## UppsalaU MicrobialEvolution

A PhD student position in evolutionary microbiology, with focus on the evolution of intracellular bacteria, is now available at Uppsala University, Sweden. The position is fully funded for four years. Start date: Summer/autumn 2024. Deadline to apply: 8 April 2024.

Please find all the details and instructions on how to apply at: <https://uu.varbi.com/en/what:job/-jobID:708285/> The Department of Medical Biochemistry and Microbiology (IMBIM) at Uppsala University provides a broad international environment for research and teaching. Research at IMBIM broadly spans the areas of biochemistry, cell and molecular biology, tumour biology, comparative genetics, functional genomics, immunology, bacteriology, and virology. The research is essentially of fundamental nature, but with relevance and application in health and disease in both animals and humans. More info: <https://www.imbim.uu.se/research-areas/>. We are looking for a highly motivated PhD student to be involved in the project “A two-billion-years history of infections: evolution of host-adaptation in early Gammaproteobacteria”, funded by the Swedish Research Board. The project is led by Lionel Guy, and the PhD student will be located at the Biomedical Centre, Uppsala, Sweden.

### Project description

The ability to feed on other organisms through phagocytosis is a crucial step in the evolution of eukaryotes, a prerequisite for food webs, multicellularity and, arguably, the acquisition of mitochondria. It also paved the way for intracellular parasitism, as some bacteria avoided digestion by their hosts and multiplied in the nutrient-rich cytoplasm.

Here, we focus on the Deep-branching Intracellular Gammaproteobacteria (DIG), a large group of related bacteria (e.g. *Legionella* and *Francisella*) with a wide variety of host-adaptation strategies. We hypothesize that the last common ancestor of DIG, appeared during eukaryogenesis, 2 Ga ago, and was among the first bacteria to infect eukaryotes.

In this project, the PhD student will gather a solid set of DIG genomes, reconstruct their evolutionary his-

tory, assess their metabolic potential, and identify their host-adaptation genes. They will screen genomes for horizontal gene transfers from early eukaryotes or Asgard archaea.

Through a better understanding of the relationships between the first eukaryotes and their early invaders, the gained results will shed light on eukaryogenesis, particularly the role of phagocytosis.

### Duties

The main duties of PhD students are to devote themselves to their research studies, which includes participating in research projects and third cycle courses. The work duties can also include teaching and other departmental duties (not more than 20 % of full time).

### Requirements

To meet the entry requirements for doctoral studies, you must - hold a Master's (second-cycle) degree in bioinformatics, molecular biology, microbiology, microbial ecology or similar field, or - have completed at least 240 credits in higher education, with at least 60 credits at Master's level including an independent project worth at least 15 credits, or - have acquired substantially equivalent knowledge in some other way. - Documented coding skills in Python or R - Experience in using and/or developing methods in metagenomics and molecular evolution - Background understanding of, and interest in, microbial evolution - Proficiency in spoken and written English; Ability to conceive, execute, and complete research projects independently Creativity and good group-working skills

Additional qualifications - Experience in creating pipelines for use with high performance computing clusters - Competence in large dataset handling

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

Lionel Guy [lionel.guy@imbim.uu.se](mailto:lionel.guy@imbim.uu.se)

Lionel Guy <[guy.lionel@gmail.com](mailto:guy.lionel@gmail.com)>

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## Vienna Population Genetics

Reminder: 2 weeks to application deadline (April 1):

Over the past years, Vienna has developed into one of the leading centres of population genetics. The Vienna Graduate School of Population Genetics has been founded to provide a training opportunity for PhD students to build on this excellent on-site expertise.

We invite applications from highly motivated and outstanding students with a love for evolutionary research and a background in one of the following disciplines: evolutionary genetics, functional genetics, theoretical or experimental population genetics, bioinformatics, mathematics, statistics.

Topics include: - Adaptation from reduced genetic variation. - Adaptation to complex environments. - Inference of selection signatures from time-series data. - Long-term dynamics of local *Drosophila* populations. - Making sense of whole-genome polymorphism data - The role of deleterious mutations for adaptation and

maintenance of variation. - Unraveling the impact of gene flow during species divergence.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by April 1st will be considered. Two letters of recommendation need to be sent directly by the referees.

PhD students will receive a monthly salary based on currently euro 2.464,80 before tax according to the regulations of the Austrian Science Fund (FWF).

All information about the about available topics, the training program and the application procedure can be found at [www.popgen-vienna.at](http://www.popgen-vienna.at) Dr. Julia Hosp

Vienna Graduate School of Population Genetics Coordinator

[www.popgen-vienna.at](http://www.popgen-vienna.at) <https://twitter.com/PopGenViennaPhD> c/o Institut für Mathematik, Universität Wien & Institut für Populationsgenetik, Veterinärmedizinische Universität Wien

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## Arizona State University Computational Biology

Teaching Assistant Professor - Computational Biology  
School of Life Sciences Arizona State University

The School of Life Sciences (SOLS) invites applications for two full-time, benefits-eligible, non-tenure-eligible Teaching Assistant Professor positions with an anticipated start date of August 16, 2024. Both positions are 80% teaching and 20% service. Subsequent academic year renewals (Aug. 16 to May

15) are contingent upon satisfactory performance, availability of resources, and the needs of the unit. Supplementary summer teaching may be available.

Applicants should have a broad grasp of computational biology, coding, genomics, and biostatistics, and experience in college or university-level teaching and student mentoring. Ideally, applicants will also have experience in research, in the fields of computational life sciences, bioinformatics, biostatistics, biological computing, or genomics.

The School of Life Sciences is a broadly interdisciplinary community of undergraduates, M.S. and Ph.D. students, staff, and faculty members. We are committed to transforming science education and research by making learning more accessible, inclusive, and impactful through innovations in teaching and connections to nationally recognized research and education programs such as the Research in Inclusive STEM Education (RISE) Center. The School of Life Sciences is also home to a growing Computational Life Sciences program for undergraduate and graduate students including online and immersion MS students. SOLS is embedded within the larger community of ASU, a dynamic, progressive university dedicated to interdisciplinary collaborations, rethinking university education, and integrating excellence in research and teaching. The university has been ranked #1 in innovation by US News & World Report for the past nine years. We invite you to learn more about the School of Life Sciences and Arizona State University by visiting <https://sols.asu.edu>, and <https://newamericanuniversity.asu.edu>, respec-

tively. Learn more about what The College of Liberal Arts and Sciences has to offer by visiting <https://thecollege.asu.edu/faculty>.

Successful applicants will contribute to SOLS' innovative online MS programs in Computational Life Sciences and in Biology. They will be responsible for providing instruction in online Master's-level and undergraduate courses in genomics, genetics, coding, biostatistics, quantitative and computational biology. This includes supervising coursework for Applied Projects and Capstones for the Computational Life Sciences MS program. Responsibilities will include supervising graduate teaching assistants and updating/developing course materials with other faculty & staff. This person will also provide service within the school, college, and university in capacities appropriate for the position.

Minimum qualifications: - PhD in computational biology, quantitative biology, genomics, bioinformatics or related field by the time of appointment. - Demonstrated experience with applying computational approaches to life sciences questions. - Demonstrated evidence of organizational and communication skills. - Demonstrated commitment to working with faculty, staff, students and/or communities to advance the ASU Charter.

Desired qualifications: - Three (3) years of post-secondary teaching experience. - Demonstrated experience teaching college-level biology courses in a traditional classroom and alternative delivery modalities such as hybrid or online. - Two (2) or more years of research experience in computational life sciences, biostatistics, or genomics. - Experience creating curriculum and teaching online. - Experience in using technology to supplement and improve pedagogy.

- A record of using evidence-based methods of teaching that promote mastery of computational biological concepts and advance higher-order critical thinking, as evidenced by instruction and assessments.

- Demonstrated commitment to serving and understanding the particular needs of online students. - Demonstrated success meeting the needs of underrepresented student populations or reaching out to diverse communities. - Experience supervising and mentoring teaching assistants.

- Evidence of collaborative activities with other faculty and staff.

- Participation in the higher education community and professional development activities (for example, authoring educational and scientific publications, presenting at conferences, attending workshops, etc.).

To apply, please click here <http://apply.interfolio.com/143402> to submit the following materials electronically: Materials shall include (1) a cover letter, (2) a comprehensive curriculum vitae, (3) a teaching statement, (4) evidence of teaching excellence (e.g., summative assessments, lesson plans,

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## ArizonaStateU TeachingEvolutionaryMedicine

Teaching Assistant Professor - Evolutionary Medicine  
School of Life Sciences Arizona State University

The School of Life Sciences (SOLS) invites applications for a full-time, benefits-eligible, non-tenure-eligible Teaching Assistant Professor position with an anticipated start date of August 16, 2024. This position is 80% teaching and 20% service. Subsequent academic year renewals (Aug. 16 to May 15) are contingent upon satisfactory performance, availability of resources, and the needs of the unit. Supplementary summer teaching may be available.

Applicants should have a broad grasp of evolutionary biology, general biology, medicine, and global health, and experience in college or university-level teaching and student mentoring. Ideally, applicants will also have experience in research, in the fields of evolutionary medicine, evolutionary biology, or global health.

The School of Life Sciences is a broadly interdisciplinary community of undergraduates, M.S. and Ph.D. students, staff, and faculty members. We are committed to transforming science education and research by making learning more accessible, inclusive, and impactful through innovations in teaching and connections to nationally recognized research and education programs such as the Research in Inclusive STEM Education (RISE) Center. The Center for Evolution and Medicine at ASU supports a vibrant evolution and medicine community including a

seminar series. The School of Life Sciences is also home to a thriving Evolutionary Biology PhD program. SOLS is embedded within the larger community of ASU, a dynamic, progressive university dedicated to interdisciplinary collaborations, rethinking university education, and integrating excellence in research and teaching. The university has been ranked #1 in innovation by US News & World Report for the past nine years.

We invite you to learn more about the School of Life Sciences and Arizona State University by visiting <https://sols.asu.edu>, <https://evmed.asu.edu>, and <https://newamericanuniversity.asu.edu>, respectively. Learn more about what The College of Liberal Arts and Sciences has to offer by visiting <https://thecollege.asu.edu/faculty>. Successful applicants will contribute to SOLS' innovative online MS programs in Biology and Computational Life Sciences. They will be responsible for providing instruction in online Master's-level and undergraduate courses in evolutionary medicine and global health, maternal and child health, evolutionary biology, genetics, and general biology. This includes supervising coursework for Capstones and Applied Projects for the MS degree programs.

Responsibilities will include supervising graduate teaching assistants and updating/developing course materials with other faculty & staff. This person will also provide service within the school, college, and university in capacities appropriate for the position.

Minimum qualifications: - PhD in evolutionary biology, evolutionary medicine, global health or related field by the time of appointment. - Demonstrated experience with evolutionary research approaches. - Demonstrated evidence of organizational and communication skills. - Demonstrated commitment to working with faculty, staff, students and/or communities to advance the ASU Charter.

Desired qualifications: - Three (3) years of post-secondary teaching experience. - Demonstrated experience teaching college-level biology courses in a traditional classroom and alternative delivery modalities such as hybrid or online. - Two (2) or more years of research experience in evolutionary medicine. - Experience creating curriculum and teaching online. - Experience in using technology to supplement and improve pedagogy. - A record of using evidence-based methods of teaching that promote mastery of evolution and medicine concepts and advance higher-order critical thinking, as evidenced by instruction and assessments. - Demonstrated commitment to serving and understanding the particular needs of online students. - Demonstrated success meeting the needs of underrepresented student populations or reaching out to diverse communities. -

Experience supervising and mentoring teaching assistants. - Evidence of collaborative activities with other faculty and staff. - Participation in the higher education community and professional development activities (for example, authoring educational and scientific publications, presenting at conferences, attending workshops, etc.).

To apply, please click here <http://apply.interfolio.com/143404> to submit the following materials electronically: Materials shall include (1) a cover letter, (2) a comprehensive curriculum vitae, (3) a teaching statement, (4) evidence of teaching excellence (e.g.,

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## Barcelona Two BioinformaticsMalariaSepsis

Bioinformatician for Malaria Physiopathology & Genomics Group

Description The Barcelona Institute for Global Health (ISGlobal) is a cutting-edge institute addressing global public health challenges through research, translation into policy and education. ISGlobal has a broad portfolio in communicable and non-communicable diseases including environmental and climate determinants, and applies a multidisciplinary scientific approach ranging from the molecular to the population level. Research is organized in five programs: Climate, Air Pollution, Nature and Urban Health; Environment and Health over the Lifecourse; Global Viral and Bacterial Infections; Malaria and Neglected Parasitic Diseases and Maternal Child and Reproductive Health. ISGlobal is accredited with the Severo Ochoa distinction, a seal of excellence of the Spanish Science Ministry. The overall goal of the Malaria Physiopathology and Genomics group at ISGlobal is to contribute to developing new tools for the control and eventual elimination of malaria through understanding key physio-pathological events of malaria in children and pregnant women. To this end, the team combines genomics, epidemiology, molecular biology, immunology, and clinical medicine to study parasite and host factors influencing malaria infections.

Venue

Barcelona

What We Are Looking for

ISGlobal is seeking a talented individual who is experienced in bioinformatics analysis of next generation sequencing (NGS) data for Genmoz project. GenMoz project (<https://www.isglobal.org/en/-/genmoz>) aims to build and consolidate genomic capacities in Mozambique for malaria surveillance and public health response. The goal is to advance malaria control and eradication through the identification of key drivers of malaria transmission using innovative genomic and analytical tools. The project proposes a participatory approach engaging all parts of the health system to promote a culture of genetic data use and increase the public health impact, while leveraging ongoing activities and existing capacity in Mozambique. We aim to integrate genomic intelligence in the National Malaria Control Program (NMCP) strategic and operational activities through a) embedding genetic surveillance on ongoing and future routine control and elimination strategies (e.g. use of routine samples) and b) the integration of genomic surveillance onto the Integrated Malaria Information Storage System (iMISS) for analysing, visualising and generating data for action (e.g. through surveillance dashboards) at the appropriate granularity level. The project is led by the Malaria Physiology & Genomics group at ISGlobal and Manhica Health Research Center (CISM, Mozambique), in collaboration with the NMCP, the University of California-San Francisco and the Institute of Disease Modelling (USA). The candidate will be based at the Malaria Physiopathology & Genomics Group at ISGlobal, and will work in close collaboration with CISM (Mozambique), the EPPICenter at the University of California-San Francisco (USA) and the Institute of Disease Modelling (USA).

Field research

Biological sciences Computer science

KEY RESPONSIBILITIES

Develop and apply bioinformatics approaches to interrogate parasite populations from Mozambique to derive epidemiologically actionable information for malaria molecular surveillance. Explore genetic metrics as proxy indicators of changes in malaria transmission intensity in both low and moderate-to-high transmission settings. Provide bioinformatics support to the team at ISG and CISM.

SPECIFIC DUTIES

Analysis of malaria parasites targeted amplicon sequencing data to get insights into best approaches for the control and elimination of the disease. Develop, op-

timize and/or troubleshoot scripts, analysis pipelines and reports for routine NGS data processing at ISG and CISM. Extend the analytics and visualization of capabilities of in-house developed or existing dashboards. Publication curation and data entry into to public repositories. Contribute to build bioinformatics capacity at CISM (Mozambique) by remote and/or in person interaction with team. Interact with key partners (CISM, EppiCenter-UCSF, Wellcome Sanger Institute) on data analysis approaches, exchange of sequencing data, design of training content and harmonization purposes. Additional duties as assigned. This job description reflects the present requirements of the post but may evolve at any time in the future as duties and responsibilities change and/or develop providing there is appropriate consultation with the post-holder.

#### TRAINING AND EXPERIENCE /QUALIFICATIONS

MSc in bioinformatics, computer science, mathematical modeling, data analysis or related areas.

#### SPECIFIC REQUIREMENTS

Required:

Knowledge and demonstrated experience in management and analysis of genomic data. Availability to travel to Mozambique and/or USA for

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## California Oregon FieldTech PlantAdaptation

Job posting: <https://jobs.wisc.edu/jobs/eco-evo-botanical-field-technician-california-united-states> Job Summary: Help us study adaptation and resilience to climate change in action! The Muir Lab in the Department of Botany at the University of Wisconsin-Madison is seeking summer field technicians to assist with trait and fitness measurements at field sites in California and Oregon.

The technicians will contribute to a collaborative study of eco-evolutionary responses to climate change in the scarlet monkeyflower, *Mimulus cardinalis*, a perennial herb that grows in riparian habitats in western North

America. The primary responsibilities involve collecting trait and fitness data at three field sites in California and Oregon. Training will be provided on eco-evo techniques such as measuring leaf traits, phenology, and fitness. Conditions are mostly dry and can include cool mornings and hot, sunny afternoons. The technicians will have opportunities to work collaboratively with undergraduate and graduate students, other technicians, a post-doc, and the research teams of Dr. Seema Sheth at North Carolina State University, Dr. Lluvia Flores-Rentera at San Diego State University, Dr. Jay Sexton at UC Merced, and Dr. Jeff Diez at the University of Oregon.

Education: Bachelor's Degree in Botany, Biology, or related field with university coursework and strong interest in evolution and/or ecology.

Qualifications: - Must be available to work in remote field locations in California and Oregon for all or the majority of May 1 - October 15. There is some flexibility in start/end dates as well as unpaid time off - Ability to work outdoors in challenging conditions for long days involving lots of bending and crouching - Ability to pay attention to detail and follow instructions of research protocols - Ability to perform repetitive tasks - Excellent problem-solving and communication skills - Able to work with a diverse team living in shared spaces - Preference for someone who is willing to drive a large 7-passenger vehicle off road

License/Certification: Required: Drivers License - Valid and Meets UW Risk Management Standards

Work Schedule: It is anticipated that the position will work 40 hours per week, but may include varied schedules depending on location and weather conditions.

Work Type: This work will take place in remote field locations in California and Oregon. Transportation to and from field sites as well as lodging in a mix of field stations, Airbnb's, motels, and camping will be provided.

Salary: \$17.50 HOURLY

Field safety: We take field safety very seriously. We will conduct field safety trainings at the beginning of the season. You will always work with a team of 3-4 people and we will address safety risks and mitigation at each site.

How to Apply: Go to: <https://jobs.wisc.edu/jobs/eco-evo-botanical-field-technician-california-united-states> Click on the "Apply Now" button to start the application process.

Please upload a brief cover letter explaining your interest, a resume/CV, unofficial transcripts, and contact

information for 2-3 references.

If you have questions, particularly if you have constraints on your availability that you want to discuss before applying, please contact Chris Muir at [cdmuir@wisc.edu](mailto:cdmuir@wisc.edu).

Contact: Chris Muir [cdmuir@wisc.edu](mailto:cdmuir@wisc.edu)

Chris Muir <[cdmuir@wisc.edu](mailto:cdmuir@wisc.edu)>

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## Colombia UNALMedellin Twelve EvolutionaryBiology

The Faculty of Agricultural Sciences at Universidad Nacional de Colombia (UNAL Medellin;  $\frac{1}{2}n$ ) invites applications for 12 full-time permanent Faculty Professorships (Tenure, some of them related to Plant Taxonomy, Evolution, and Molecular Biology) with a yearly 15-month appointment beginning in the fall of 2024.

### JOB DESCRIPTION

Applicants will be considered for the faculty title of Assistant or Associate Professor, depending on qualifications. Positions will be based across all four Departments of the Faculty, as follows:

Department of Agricultural Sciences: Four positions in the areas of Botany, Plant Evolution and Taxonomy (FCA-1), Rural Economics and Policy (FCA-2), Molecular Biology and Biotechnology (FCA-3), and Entomology (FCA-4).

Department of Forestry: Four positions in the areas of Forest Management (FCA-5), Forest Innovation and Extension (FCA-6), Forest Protection (FCA-7), and Soil Sciences (FCA-8).

Department of Food Science and Agricultural Engineering: One position in the area of Rural Constructions (FCA-9).

Department of Animal Sciences: Three positions in the areas of Animal Well-Being (FCA-10), Sustainability (FCA-11), and Soil and Water Resources (FCA-12).

### KEY RESPONSIBILITIES

The successful candidates are expected to teach undergraduate and graduate courses in the corresponding fields. They are also expected to advise graduate students, execute research and extension projects, and engage in other on- and off-campus professional activities.

ties.

### QUALIFICATIONS

Candidates must have (1) an earned doctorate degree in the applicable discipline, (2) teaching experience of at least 200 hours, and (3) professional experience of at least 2,000 hours. Fluency in Spanish and English proficiency, an established record of peer-reviewed publications, and the ability to secure extramural research funding and contribute to professional service activities will also be assessed.

### TERMS OF OFFICE

Salary is commensurate with research experience and accomplishments, as follows: [https://personal.manizales.unal.edu.co/fileadmin/user\\_upload/ACUERDO.023.2008.CSU.pdf](https://personal.manizales.unal.edu.co/fileadmin/user_upload/ACUERDO.023.2008.CSU.pdf) The full package of benefits includes 30 vacation days per year, 50% income tax deduction, and full health and retirement insurance. Life and long-term care insurance, as well as savings plans are also available, <https://www.fodun.com.co/> Salaries are highly competitive by Colombian standards, see cost of living here: [https://www.numbeo.com/cost-of-living/country\\_result.jsp?country=Colombia&displayCurrency=USD](https://www.numbeo.com/cost-of-living/country_result.jsp?country=Colombia&displayCurrency=USD) The position will be based in Medellin, the second largest city of Colombia located in the province of Antioquia (northwestern Andes), a vibrant place for living with an exciting cultural, gastronomic and natural scene, besides all modern facilities (including state-of-the-art hospitals and well-ranked international schools). A top spot in the nation to raise a family and enjoy an excellent quality of life.

### APPLICATION PROCESS

Applications will be received in Spanish until April 15. The application also must include a Research Statement (Essay) and a Teaching Statement (a draft of a Syllabus). During interviews the candidates will defend the former, and offer a Trial Lecture. Results will be disclosed by August 8. More details, including dates and the application portal, are available at <https://cienciasagrarias.medellin.unal.edu.co/-concurso-profesoral.html> For enquiries, do not hesitate to contact the committee chair, Natalia Lizpezo-Loaiza at [concurso.fcamed@unal.edu.co](mailto:concurso.fcamed@unal.edu.co)

Concurso Profesoral <[concursoprofesoral@gmail.com](mailto:concursoprofesoral@gmail.com)>

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

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## FortHaysStateU TeachingEvolutionaryAnatomy

Assistant Professor, Department of Biological Sciences  
Fort Hays State University

**JOB DESCRIPTION:** Our new colleague must have the expertise to teach and mentor students pursuing health-related careers. We are seeking someone who can teach some combination of Anatomy and Physiology, Advanced Cell Biology, Microbiology, and Science Writing, as well as Introductory Biology courses for majors and non-majors. Individuals with discipline-based education research and/or assessment experience are encouraged to apply. Opportunities will exist to develop courses in the candidate's area of specialty that complement our current courses and fulfill departmental needs. The typical teaching load for this position is 12 credit hours during each of the spring and fall semesters. Candidates must have a strong desire to teach undergraduate and graduate courses, mentor undergraduate and M.S. graduate research, and contribute to departmental and university service. There will also be opportunities to develop outreach and community engagement activities. FHSU and the Department of Biological Sciences are committed to building an environment that is inclusive and representative of our students and state. We encourage women and members of underrepresented groups to apply.

**APPLICATION PROCESS:** To apply for this position, please visit: [https://fhsu.wd1.myworkdayjobs.com/-en-US/CAREERS/details/Assistant-Professor-Department-of-Biological-Sciences\\_R-04147](https://fhsu.wd1.myworkdayjobs.com/-en-US/CAREERS/details/Assistant-Professor-Department-of-Biological-Sciences_R-04147) Only electronic applications submitted through the webpage will be accepted.

**APPLICATION MATERIALS:** Qualified candidates should submit a single PDF that includes the following:  
- A cover letter highlighting the candidate's qualifications to teach a combination of the listed courses and mentor undergraduate and graduate research.  
- A CV listing teaching, scholarship, mentoring, and service experiences.  
- Contact information for three professional references.

**MINIMUM QUALIFICATIONS:** - Ph.D. in biology or a closely related field. Candidates who are ABD will be considered. - Evidence that the candidate can teach general biology courses (majors and non-majors) and at

least one other course listed in the ad.

**PREFERRED QUALIFICATIONS:** - Evidence of teaching (lecture and/or lab) effectiveness in higher education. Teaching assistant experience is acceptable. - Proficiency with online learning tools and resources. - Evidence of potential for a sustained research program. - Positive experiences mentoring undergraduate and graduate students from diverse backgrounds. - Demonstrated active engagement in professional development. - Evidence of contributions to the development of course and program assessments.

**RANK:** Assistant Professor

**APPOINTMENT DATE:** August 2024

**APPLICATION DEADLINE:** To guarantee full consideration, applicants should apply by April 9, 2024. Screening of applications will begin immediately following April 9th and will continue until the position is filled.

**SALARY:** Faculty salaries are set at 90% of current College and University Professional Association (CUPA) averages by rank and discipline.

**BENEFITS:** Competitive benefits package <http://www.fhsu.edu/humanresourceoffice/Prospective-Employees/> **RESPONSIBILITIES:** - Teaching lecture and lab classes in biology (online and in-person) - Student success coaching - Mentoring undergraduate and graduate research students - Departmental service - Scholarly research

**CONTACT:** If you have questions regarding the position, please contact: Name: Eric Gillock Email: [egillock@fhsu.edu](mailto:egillock@fhsu.edu) Phone: 785-628-5965

Michael Gruenstaeudl <[m.gruenstaeudl@fhsu.edu](mailto:m.gruenstaeudl@fhsu.edu)>

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## IZW Berlin EvolutionWildlifeDisease

The Leibniz Institute for Zoo and Wildlife Research (Leibniz-IZW) in the Forschungsverbund Berlin e.V., a member of the Leibniz Association, aims to understand and, where possible, 'improve' the adaptive capacity of wild animals to cope with global change. To this end, it focuses on the diversity of lifestyles, diseases and mechanisms of evolutionary adaptation of

mammals and birds, on the limits of these mechanisms in natural and anthropogenically influenced environments, and on conservation strategies that take these into account. The Institute fulfils this mission through long-term, application-oriented, interdisciplinary basic research in evolutionary ecology, ecological dynamics, evolutionary genetics, wildlife diseases, reproductive biology and reproductive management.

For our Department of Wildlife Diseases we are seeking to appoint a

Scientist (f/m/div) in full time

in the field of wildlife disease proteomics

We will expand into the area of wildlife proteomics, particularly bacterial pathogens and immune markers, and are looking for a scientist to develop a research programme around this specialty. The successful candidate will be in charge of all aspects of method development and validation and resulting sample analysis in the field of wildlife disease research by using MALDI TOF and UHPLC-HR mass spectrometry (MS).

Main topics include building a wildlife bacteria MS database for reliable identification, developing novel approaches and applications for the use of MALDI TOF MS in wildlife bacteriology and characterising the proteomic profile of different sample types from wildlife species. The resulting proteomic platform should also allow the identification of biomarkers relevant to conservation and complement existing and future functional immune tests used in wildlife immunology.

Responsibilities include:

Key activities are proteome analyses by mass spectrometry, particularly MALDI TOF MS for the differentiation of bacteria, and shotgun and targeted serum and plasma proteomics for comparative immunological analyses (UHPLC-HRMS), including:

- \* mass spectrometric measurements, documentation and interpretation of results;
- \* creation of own reliable database entries;
- \* preparation, development and care of the internal databases;
- \* leading and co-coordinating the proteomics/metabolomics laboratory, including guiding and supervising technical staff and students;
- \* to work independently and in collaboration with other scientists and departments.

Requirements:

- \* PhD in biochemistry, biology, microbiology, veterinary medicine or similar subject;

- \* microbiological and/or immunological background and hands-on experience with mass spectrometry-based proteome analyses and/or MALDI TOF MS;

- \* experience in processing and analysis of mass spectrometry data;

- \* willingness to learn and develop skills for own improvement;

- \* strong organizational and team working abilities;

- \* excellent command of English (written + spoken) and profound skills in scientific writing;

- \* interest and ability to work in an international team and with a diverse community of scientists and stakeholders;

- \* high motivation to address scientific questions, particularly to develop and implement novel approaches and applications for proteome analyses in wildlife.

This is what we offer:

- \* An interesting and responsible position with room for manoeuvre in an international and dynamic scientific working environment in a beautiful location right next to the Tierpark Berlin-Friedrichsfelde.

- \* A comprehensive induction programme and a well-functioning team that will be happy to support you.

- \* Working on an equal footing between all those involved and respectful co-operation within the team.

- \* A full-time employment relationship of 39 hours per week in flexitime with part-time option.

- \* A salary in accordance with the public collective bargaining law TVi<sub>j</sub>  $\frac{1}{2}$  D (Bund), with an annual bonus payment, at level E13.

- \* Company pension scheme (VBL) and subsidised capital-forming benefits (VWL).

- \* Flexible working hours to allow scope for work-life balance.

- \* 30 days holiday per calendar year.

- \* Excellent connectivity with public transport, to underground stations Tierpark (U5) or Friedrichsfelde-Ost (S5, S7, S75), as well as three tram lines and several bus routes.

- \* Employer subsidy for the annual public transport  $\frac{1}{2}$  job ticket'.

- \* Free admission to the Tierpark (current agreement between Leibniz-IZW and Tierpark Berlin) from Monday to Friday.

The position will be filled preferably by 1st July 2024 and is initially limited to 3 years.

We welcome people of any gender, origin, sexual orientation and religion; there is equal opportunity. Severely disabled persons will be given

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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>

## IZW Berlin EvolutionWildlifeMetabolomics

The Leibniz Institute for Zoo and Wildlife Research (Leibniz-IZW) in the Forschungsverbund Berlin e.V., a member of the Leibniz Association, aims to understand and, where possible, 'improve' the adaptive capacity of wild animals to cope with global change. To this end, it focuses on the diversity of lifestyles, diseases and mechanisms of evolutionary adaptation of mammals and birds, on the limits of these mechanisms in natural and anthropogenically influenced environments, and on conservation strategies that take these into account. The Institute fulfils this mission through long-term, application-oriented, interdisciplinary basic research in evolutionary ecology, ecological dynamics, evolutionary genetics, wildlife diseases, reproductive biology and reproductive management.

For our Department of Reproduction Biology we are seeking to appoint a

Scientist (f/m/div) in full time

in the field of wildlife metabolomics.

We are hiring an experienced scientist to run a metabolomics research programme based on ultra-high performance liquid chromatography coupled to high-resolution mass spectrometry (UHPLC-HRMS). The successful candidate will be in charge of all aspects of method development and validation and resulting sample analysis in the field of wildlife conservation research. You will co-lead the proteomics/metabolomics laboratory together with a specialist on proteomics who will be appointed at the same time.

Main topics, but not exclusive, will be unravelling the reproductive biology of species, innovative approaches in assessing stress and research on environmental contaminants. The resulting metabolomics wildlife platform should also allow the identification and validation of

biomarkers as well as the benchmarking of existing in-house and newly developed immunoassay techniques.

Responsibilities include:

- \* UHPLC-HRMS measurements, documentation and interpretation of results;
- \* organising, processing, storing and analysing data;
- \* supporting the development and validation of immunoassays;
- \* leading and co-coordinating the metabolomics / proteomics laboratory, including guidance and supervision of technical staff and students;
- \* working independently and in close collaboration with other scientists and departments.

Requirements:

- \* PhD in Biology, Veterinary Sciences or related, related relevant area (senior PhD students can apply on the condition that they are close to finalising their thesis);
- \* a minimum of 3 years hands-on experience with UHPLC-HRMS applications, including method development and validation of targeted and untargeted screening methods;
- \* experience in processing and analysing UHPLC-HRMS data;
- \* strong organisational abilities;
- \* excellent command of English (written and spoken) and profound skills in scientific writing (manuscripts and research proposals);
- \* interest and ability to work in an international team and with a diverse community of scientists and stakeholders;
- \* a willingness to learn and develop skills for own improvement;
- \* high motivation to address scientific questions, particularly to developing and implementing novel approaches and applications for metabolomic analyses in wildlife.

Advantageous skills:

- \* Experience with UHPLC-HRMS applications in the field of conservation research.
- \* An interest in evolutionary adaptations.

This is what we offer:

- \* An interesting and responsible position with room for manoeuvre in an international and dynamic scientific working environment in a beautiful location right next to the Tierpark Berlin-Friedrichsfelde.
- \* A comprehensive induction programme and a well-



functioning team that will be happy to support you.

- \* Working on an equal footing between all those involved and respectful co-operation within the team.
- \* A full-time employment relationship of 39 hours per week in flexitime with part-time option.
- \* A salary in accordance with the public collective bargaining law TVoD (Bund) with an annual bonus payment at level E13.
- \* Company pension scheme (VBL) and subsidised capital-forming benefits (VWL).
- \* Flexible working hours to allow scope for work-life balance.
- \* 30 days holiday per calendar year.
- \* Excellent connectivity with public transport, to underground stations Tierpark (U5) or Friedrichsfelde-Ost (S5, S7, S75), as well as three tram lines and several bus routes.
- \* Employer subsidy for the annual public transport 'job ticket'.
- \* Free admission to the Tierpark (current agreement between Leibniz-IZW and Tierpark Berlin) from Monday to Friday.

The position will start soonest 1st July 2024 and latest 1st Jan 2025 and is initially limited to 3 years.

We welcome people of any gender, origin, sexual orientation and religion; there is equal opportunity. Severely disabled persons will be given preferential consideration if they are equally qualified. The Leibniz Institute for Zoo and Wildlife Research is "Total-E-Quality" certified,

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

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## Lisbon MultipleLevels GenomicEvolution

The Genome Maintenance and Evolution lab at IGC(Oeiras, Lisbon, Portugal) is recruiting at multiple levels.

WHO WE ARE: We are biologists, biophysicists and bioengineers broadly interested in the evolution of cell and molecular mechanisms.

WHAT WE DO: We study the interplay between genome maintenance mechanisms and evolutionary forces in shaping organismal features.

HOW WE DO IT: We use a multidisciplinary methodology that entails molecular, cellular, evolutionary, and synthetic biology. When possible, we take advantage of quantitative approaches to discriminate amongst different classes of models.

At this stage, we welcome applications for the following positions:

Postdoc: PhD holders eager to lead a scientific project in the lab (Start date: ASAP).

Lab Manager: Master/PhD holders who can provide administrative, technical and scientific support to lab members (Start date: ASAP).

Technician: Bachelor/Master holders who can provide technical assistance to lab members (Start date: ASAP).

PhD student: Master holders eager to join the IBB PhD program(Beginning 9/2024, joining labs in 3/2025).

Master student: Students enrolled in universities or ERASMUS training programs, who want to take part in one of the current lab projects for their thesis (Start date: 10/2024).

Eligibility: PhD holders must have received their degree within the past 3 years. Prospective candidates are encouraged to apply or inquire further information at: [mfumasoni@igc.gulbenkian.pt](mailto:mfumasoni@igc.gulbenkian.pt)

Additional details: <https://fumalab.github.io/news/>-<https://fumalab.github.io/join/> Ana Garoï<sub>1</sub>/<sub>2</sub>a Delgado Genome Maintenance and Evolution Group Instituto Gulbenkian de Ciï<sub>1</sub>/<sub>2</sub>ncia (IGC) Rua da Quinta Grande, 6, 2780-156 Oeiras, PT

Ana Garoï<sub>1</sub>/<sub>2</sub>a <[agarona@igc.gulbenkian.pt](mailto:agarona@igc.gulbenkian.pt)>

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## NotreDame Bioinformatician

Assistant Professor of the Practice in Bioinformatics

Description:

The Department of Biological Sciences at the University of Notre Dame seeks a broadly trained and innovative bioinformatician at the Assistant Professor of the Practice level to contribute to service in the Genomics

and Bioinformatics Core Facility (GBCF), and to teach courses and workshops in computation and genomics. This non-tenure track position is available starting fall semester 2024, and is renewable and expected to be a long-term, continuing position with opportunities for promotion.

The successful candidate will join a vigorous and growing genomics community anchored by the Department of Biological Sciences and distributed across the Colleges of Science and Engineering. The GBCF is a central component of this community with a mission to facilitate genomics research on the Notre Dame campus. The successful candidate will work closely with the GBCF staff to provide bioinformatic and computational consultation, expertise, and infrastructure to support faculty research. This role includes developing working relationships with faculty, exploring possible avenues for novel bioinformatics research, as well as providing basic bioinformatic services and project consultation. The successful candidate will also develop and deliver courses and workshops to enhance the educational infrastructure in bioinformatics based on departmental needs and the applicant's area of expertise. Courses may range from basic computation literacy to advanced undergraduate/graduate level genomics analysis. While this position will be service and teaching oriented, the candidate will also have opportunities to engage in collaborative and independent research.

#### Qualifications:

Preference will be given to candidates with a Ph.D. in biological sciences, computer science, or related field and experience teaching bioinformatics. Excellent communication skills, and familiarity with the analysis of genomic and transcriptomic data are required. The successful candidate will have experience with one or more of the following areas of analysis: epigenomics, proteomics, genome assembly, population genomics, microbial diversity, comparative phylogenomics, GWAS, single-cell and spatial genomics, and/or network analysis. Strong candidates will also have a solid understanding of data management practices, common software handling paradigms (e.g. conda, modules, containers), linux command line, common genomic data formats (gff, vcf, sam, etc). Broad experience troubleshooting genomic analysis and software and experience with permissions (both unix and ACLs) will be advantageous. Strong candidates will also have experience teaching computational biology or bioinformatics in the classroom or in workshops.

#### Application Instructions:

To apply online, visit: <https://apply.interfolio.com/142498> Applicants will need to provide the following

with their online application:

- Cover Letter
- Current Resume/Curriculum Vitae
- Statement of Experience and Expertise in Bioinformatics (including Research Interests is optional) (1-2 pages)
- Statement of Teaching Philosophy (1-2 pages)

The Department of Biological Sciences is dedicated to excellence in undergraduate and graduate education to develop the next generation of leaders in the life sciences. We seek to advance biological knowledge through excellence in research to solve the grand challenges that will shape the future of human health and the environment. The department is highly interdisciplinary and fulfilling the promise of innovative approaches to teaching biology at the collegiate level.

The University of Notre Dame seeks to attract, develop, and retain the highest quality faculty, staff and administration. The University is an Equal Opportunity Employer, and is committed to building a culturally diverse workplace. We strongly encourage applications from female and minority candidates and those candidates attracted to a university with a Catholic identity. Moreover, Notre Dame prohibits discrimination against veterans or disabled qualified individuals, and requires affirmative action by covered contractors to employ and advance veterans and qualified individuals with disabilities in compliance with 41 CFR 60-741.5(a) and 41 CFR 60-300.5(a).

Review of applications will begin: April 15, 2024.

The University of Notre Dame, an international Catholic research university, is an equal opportunity employer.

Michael Pfrender <Michael.Pfrender.1@nd.edu>

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## Oahu Hawaii Waterfowl Specialist

The Lavretsky Lab at The University of Texas at El Paso (UTEP) is searching for a full-time waterfowl specialist to be stationed on Oahu, Hawaii. The person will be working on a newly funded project as part of a collaboration with U.S. Fish and Wildlife Services (USFWS) to conduct novel management efforts to the conservation of the endangered Hawaiian duck (Koloa). In short, the

individual will lead a team comprised of students, private, state, and federal personnel to pilot a project that attempts to artificially reverse the genetic ancestry of a koloa x feral mallard hybrid population towards koloa through specific active management strategies (see Hernandez et al. 2023. *simRestore*: A decision-making tool for adaptive management of the native genetic status of wild populations. *Molecular Ecology Resources*. 24: e13892). More information on the Lavretsky Lab can be found here: <http://science.utep.edu/lavretskylab>. STATIONED: Oahu, HI

WORKING LOCATIONS: James Campbell National Wildlife Refuge (NWR) (Oahu, HI) & Hanalei (NWR) (Kauai, HI)

DUTIES: Live capture Koloa, feral mallards, and their hybrids using swim-in and walk-in traps in both locations. All birds will be banded with authorized USGS bird banding laboratory leg bands, as well as bled for molecular analyses to be conducted at the Lavretsky Lab. A sub-number of birds will have auxiliary GPS-GSM telemetry units attached. Lead translocation efforts of koloa from Kauai to Oahu and ensure soft release of koloa onto James Campbell NWR per research protocols. Lead monitoring of translocated and resident koloa, nest monitoring, behavioral studies, disease surveillance and response, and feral mallard removal. Assist with predator control, habitat enhancements around wetland areas, and other tasks deemed necessary by the Refuge/Project PI.

ANNUAL PAY (Employment is through UTEP): \$63,000 + Benefits for 2 years, with the potential of additional years.

START DATE: May 2024 (preferably)

MINIMUM QUALIFICATIONS:

- B.S. Degree in wildlife ecology, conservation biology, or a related field
- Must have a valid state driver's license.
- Must have the legal and physical ability to possess and discharge firearms. You must be able to pass a government background check and meet any additional requirements to carry and use firearms.
- History of waterfowl (or other avian) capture, handling, and banding
- Highly self-motivated and organized
- History of working in diverse teams

DESIRED QUALIFICATIONS:

- History of working with Hawaii's flora and fauna
- History of leading teams in field conditions

- Knowledge of working with all-terrain vehicles (UTVs, ATVs, etc)

- Analytical skills in band-recovery

APPLICATION PROCESS:

To apply, please submit: a cover letter describing experience related to or interest in as they relate to the project, a current CV/resume, and the name and full contact information for three professional references to Dr. Philip Lavretsky (plavretsky@utep.edu) and Kelly Goodale (kelly\_goodale@fws.gov). Review of applications will begin as soon as possible and continue until the position is filled.

Philip Lavretsky, PhD Associate Professor Department of Biological Sciences Birds Curator of UTEP's Biodiversity Collections University of Texas El Paso Office Phone: (915)747-6424 Cell Phone: (310)770-1758

"Lavretsky, Philip" <plavretsky@utep.edu>

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## Okinawa IST Programmer Evolutionary Genomics

Join the Model-Based Evolutionary Genomics Unit (<https://www.oist.jp/research/research-units/-modevolgenom/>) as a scientific programmer making fundamental contributions to research at the intersection of computational and evolutionary biology. Our unit works to decode the complex patterns and processes that underpin the evolution of life across its myriad forms with a significant focus on reconstructing the Tree of Life and modeling the dependency between different levels of organization in biological systems. By employing probabilistic models and leveraging the power of machine learning, we aim to unravel the co-evolutionary dynamics that have shaped the Tree of Life, from the enigmatic origins of early life forms to the sophisticated structures of modern biological systems.

As a scientific programmer, you have the opportunity to further develop phylogenetic software in C++ (e.g., ALE, ALERax, GeneRax) as well as other languages (e.g., MCMCdate in Haskell) in collaboration with researcher groups in both the Life Sciences and Computer Science, including the Stamatakis group at HITS (<https://www.h-its.org/people/prof-dr->

[alexandros-stamatakis/](#)). You will also have the opportunity to participate in projects that aim to adapt machine learning methods, including protein language models such as ESM, to genomic data work. As a Scientific programmer at OIST, you will work with the extensive HPC resources of the university and interact with the excellent Scientific Computing & Data Analysis team (<https://groups.oist.jp/scs>).

The position offers a platform for innovation and discovery in a unit that thrives on intellectual curiosity and interdisciplinary collaboration and includes funding, provided by the budget of the Model-based Evolutionary Genomics Unit, to travel to international conferences as well as extended research visits to international collaborators, including Tom Williams at the University of Bristol, Anja Spang at NIOZ in the Netherlands, Phil Hugenholtz at the University of Queensland, and others.

Okinawa Institute of Science and Technology

The Okinawa Institute of Science and Technology Graduate University (OIST; see [www.oist.jp](http://www.oist.jp)) is a dynamic new graduate university of science and technology in Okinawa Prefecture, Japan. The university is located on 85 hectares of protected forestland overlooking beautiful shoreline and coral reefs. The campus is striking architecturally, and the facilities are outstanding (OIST campus video tour: <https://www.youtube.com/watch?v=-OLeylXbZDpo>). There are no academic departments, which facilitates multidisciplinary research. Outstanding resources and equipment are provided and managed to encourage easy access and collaboration. English is the official language of the University, and the university research community is fully international, with more than 50 countries represented. OIST is rapidly gaining recognition in the worldwide academic community as a model for excellence in education and research.

Responsibilities:

Work with members of the Model-based Evolutionary Genomics Unit as well as collaborators at the University of Bristol and the University of Queensland, NIOZ in the Netherlands, and the Institute of Evolution in Budapest. Publish to maintain and develop software, in particular AleRax (<https://github.com/BenoitMorel/AleRax>) and ALE (<https://github.com/ssolo/ALE>).

Qualifications:

(Required)

Demonstrated ability to develop C++ code.

(Preferred)

Demonstrated ability to develop scientific software. Knowledge of, or ambition to learn Haskell, as well as Machine Learning libraries and frameworks such as

Pytorch. Ph.D. in Natural Science, including, but not restricted to, Life Sciences, Physics, Computer Science, and Mathematics and an interest in Evolutionary Biology.

How to Apply:

Apply by emailing your Submission to: [gergely.szollosi@oist.jp](mailto:gergely.szollosi@oist.jp). Please ensure that you mention “modevolgenom postdoc 2024” in the subject line of your email.

Submission Documents: §Cover letter §Curriculum vitae including publications and if possible, Google Scholar link §Names and contact information of 2 referees, one of which should be a previous employer

Application Due Date:

Applications will be reviewed starting April 1st, 2024 until the position is filled.

Dr. Gergely J Szöllősi

MTA-ELTE „Lendület” Evolutionary Genomics Research Group ERC “GENECLOCKS” Research Group head researcher

Model-Based Evolutionary Genomics Unit

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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>

## PennsylvaniaStateU LabManager EvolutionaryGenomics

The Toews Lab (<http://www.davetoews.com>) at The Pennsylvania State University is seeking to hire a Research Technologist / Lab Manager- Life Sciences-Advanced Professional. Link: [https://www.myworkday.com/psu/d/inst/9925\\$149944/rel-task/2998\\$16774.html](https://www.myworkday.com/psu/d/inst/9925$149944/rel-task/2998$16774.html) The tasks of this position include: - Generate and analyze high-throughput DNA sequencing data to address several evolutionary and ecological questions regarding the diversification of wood warblers. - Assist in managing two active projects: using fecal metabarcoding data to understand the diets of insectivorous birds in diverse forest communities and studying hybridization genomics of *Vermivora* warblers. The candidate will coordinate data collection

and sample storage. - Assist in helping develop and apply new molecular and analytical tools to these projects, and independently assess the feasibility and cost effectiveness of these new methods. - The candidate will be responsible for helping train students and postdocs with laboratory methods as well as some specialized equipment. - The candidate will also help foster a safe, productive, and collegial lab environment. The candidate will work with the Principal Investigator (PI Toews) on effective communication of the data and will hopefully co-author subsequent publications.

David Toews: toews@psu.edu

“Toews, David” <toews@psu.edu>

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### **RollinsC Florida 2yr MarineEvolution**

The Department of Biology at Rollins College is looking for a 2-year Visiting Assistant Professor beginning August 2024. We are looking for candidates who specialize in Marine Biology. Application review will begin on March 20th, 2024

<https://jobs.rollins.edu/en-us/job/493617/visiting-assistant-professor-biology> Pamela M. Brannock, PhD Assistant Professor Department of Biology Rollins College Bush 118B (407)646-2290

Pamela Brannock <PBRANNOCK@Rollins.edu>

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### **SouthwesternOklahomaStateU PlantEvolution**

Colleagues,

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.

Take care,

Rickey

< <https://swosu.csod.com/ux/ats/careersite/1/home/-requisition/454?c=swosu> > 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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### **SpelmanC Atlanta ResTech MicrobeEvolutionGenomics**

Job Opportunity: Full-Time Research Technician (Post-doc) at Tekle Lab, Biology Department, Spelman College We invite applications for a full-time Research Technician position at the Tekle Lab within the Biology Department at Spelman College in Atlanta, GA. The lab focuses on eukaryotic microbial evolution, emphasizing interaction and behavior, particularly in amoeboid microorganisms.

The responsibilities for this position include isolation, culturing, and maintenance of microorganisms, conducting molecular and behavior studies, and performing DNA/RNA extraction, PCR, mutagenesis, NGS, light, and fluorescence microscopy. Additionally, the successful candidate will be responsible for supervising undergraduate researchers and ensuring general lab maintenance.

We are seeking individuals with a Bachelor's degree in biology (Master's and PhD levels, including post-doctoral candidates, are encouraged to apply), along with 1-2 years of relevant research experience or an equivalent combination of experience, training, and/or education. The ideal candidate will have experience in basic molecular techniques (DNA extraction, PCR), and field experience is a plus. Strong organizational skills,

attention to detail, and the ability to work effectively with and supervise undergraduate students are essential. Previous experience working with microorganisms is desirable, and familiarity with next-generation sequencing techniques and programming (bioinformatics) skills for genome/transcriptome analysis are advantageous.

This is a grant-supported position for up to three years based on performance, offering a competitive salary commensurate with experience and includes benefits.

To apply, please email a letter of interest, CV, and the contact information for 2 references to ytekle@spelman.edu. For additional details about the lab, visit <http://faculty.spelman.edu/yonastekle/>. Feel free to contact us with any questions via the provided email address.

Yonas Tekle, Professor Department of Biology, Spelman College 350 Spelman Lane SW Atlanta, GA 30314-4399 Office: 404-270-5779

Yonas Isaak Tekle <yonastekle@gmail.com>

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### Trinidad Paid Internship Guppy Project

Paid Research Internships - The Guppy Project Research interns are needed to assist in a multi-disciplinary, multi-investigator, experimental study of the evolution of species interactions in Trinidad, West Indies. The research is led by Professors David Reznick (University of California, Riverside), Joseph Travis (Florida State University), Tim Coulson (University of Oxford), and Ron Bassar (Auburn University). We seek to integrate multiple biological fields for the study of these interactions in experimental populations of guppies and killifish in Trinidad. Duties include assisting in monthly censuses of guppy and killifish populations in montane streams and helping to execute experiments in on-site artificial streams. The monthly censuses include long hours in the field and laboratory.

Interns will be required to spend a minimum of 3 months in Trinidad, with possibility of extension, and/or promotion to field site manager. There are potential start dates in February 2024 and every month thereafter until November 2024. We will pay a monthly stipend (\$700 USD per month for first time interns), cover travel (up

to \$900 USD), and provide housing.

Qualifications: We seek interns who are entertaining the possibility of pursuing graduate studies in some area of ecology and evolution and who wish to gain some additional field research experience before doing so. Research will take place in semi-remote areas of Trinidad, sometimes under bad weather conditions. Applicants must be able to live and work well with others. Research will involve carrying heavy packs over slippery and steep terrain. Applicants must be in good physical condition and be able to meet the demands of field research under these conditions. Ability to drive a standard transmission vehicle is desirable but not required. Applicants with first-aid/first responder training, skills in automobile maintenance, and construction skills are highly desirable. Please address these skills when applying.

Please see our website <[www.theguppyproject.weebly.com](http://www.theguppyproject.weebly.com)> for more information on the project and access to reprints. Be sure to check out our video menu, which includes a “guppy censuses” as submenu VII. It details the main tasks associated with the internship.

Applicants should send a cover letter, CV, and the names and e-mail addresses of three or more professional references to David Reznick (gupy@ucr.edu). At least two of the references should be academics.

Ronald Bassar <rdb0057@auburn.edu>

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### UAntwerp RMCA Belgium Historical Epidemiology

Long-term postdoc position in Belgium on historical epidemiology of vector-borne diseases

The University of Antwerp and the Royal Museum of Central Africa (Belgium) offer a combined position (10% junior professor, 90% senior researcher) for a postdoc in Biology, Geography or a related discipline with a background in epidemiology, ecology, parasitology and/or distribution modelling. The position is of indeterminate duration but salary is secured for at least 8 years.

RECORDED: Reconstructing disease dynamics in Central Africa using historical museum collections and archives

The past century has seen unprecedented changes in nat-

ural biotopes due to human activities, in Africa perhaps even more than elsewhere. This has affected the distribution and dynamics of infectious diseases, particularly zoonotic infections, transmitted from wildlife to humans. In addition, changes in human demography, agriculture and other human activities in the environment, including health care interventions, have also changed the disease dynamics. Understanding the relative contribution of these factors may help in predicting what the effects can be of future environmental changes to the spread of diseases. The scientist we are looking for will use museum collections and historical archives to retrospectively study the impact of environmental and anthropogenic changes on vector and disease dynamics. Despite its enormous potential, this 'unexplored heritage' is vastly underused in epidemiological research. This profile will combine longitudinal series of vector collections and zoonotic disease carriers, with historical archives such as medical records, aerial pictures and scientific publications. By taking a multidisciplinary approach, combining ecology, geography, modelling and semi-quantitative methods, the changes in the presence, diversity and distribution of pathogens, vectors and animal reservoirs can be documented and related to changes in 1) human demography, 2) climate, and 3) land cover and land use on the spread of vector-borne and zoonotic diseases. By including socio-ecological studies and historical records of disease control efforts, lessons can be learned in order to improve current health policies ('historical epidemiology').

For a start, the research will focus on three vector-borne diseases that are strongly affected by environmental and anthropogenic change and that fall within the expertise of and/or historical documentation at both institutes: schistosomiasis, sleeping sickness and bubonic plague.

Profile: 3-12 years of postdoc experience

The full position announcement and instructions for applying can be found at: [https://www.uantwerpen.be/en/jobs/vacancies/academic-staff/?q=3298&descr=Senior-academic-staff-and-postdoctoral-researcher/-scientific-researcher-\(KMMA\)-RECORDED-2-%E2%80%9CReconstructing-disease-dynamics-in-Central-Africa-using-historical-museum-collections-and-archives](https://www.uantwerpen.be/en/jobs/vacancies/academic-staff/?q=3298&descr=Senior-academic-staff-and-postdoctoral-researcher/-scientific-researcher-(KMMA)-RECORDED-2-%E2%80%9CReconstructing-disease-dynamics-in-Central-Africa-using-historical-museum-collections-and-archives)

Deadline for application: 30/04/2024

More information about the research project can be obtained from Tine Huyse ([tine.huyse@africamuseum.be](mailto:tine.huyse@africamuseum.be)) or Herwig Leirs ([herwig.leirs@uantwerpen.be](mailto:herwig.leirs@uantwerpen.be)).

Tine Huyse <[tine.huyse@kuleuven.be](mailto:tine.huyse@kuleuven.be)>

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## UChicago ResAssist PlantEvolution

The Kreiner lab ([kreinerlab.com](http://kreinerlab.com)) and the Carley lab (<https://carleylab.uchicago.edu/>) in the Department of Ecology & Evolution at the University of Chicago are looking to co-hire a lab manager/research technician in plant evolutionary genomics and ecology. Responsibilities will range from molecular work in the wet lab to plant care and phenotyping to field collections around the Midwest; this will provide a great opportunity for a graduating undergraduate or recent grad to build a broad skill set that may benefit them if they are considering graduate research in the future. The target start date is July of 2024.

Full details about both positions, including instructions about how to apply, can be found here: <https://bit.ly/UChiPlantTech2024> Julia Kreiner ([kreiner@uchicago.edu](mailto:kreiner@uchicago.edu)) and Lauren Carley ([lcarley@uchicago.edu](mailto:lcarley@uchicago.edu)) also welcome informal inquiries via email.

Dr. Julia M. Kreiner (She/Her) Incoming Assistant Professor, Department of Ecology & Evolution University of Chicago

Julia Kreiner <[kreiner@uchicago.edu](mailto:kreiner@uchicago.edu)>

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## UExeter Fieldworker InsectSociality

Social Insect Paid Fieldwork Assistant in Surrey, UK:

We seek an experienced field worker to help research how helping may have evolved using a wild digger wasp population (*Ammophila*) from the start of June until mid-end of August 2024.

The assistant will be working alongside a Postdoctoral researcher and several junior field assistants at a nature reserve just outside of Guildford, Surrey, UK. *Ammophila* 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 briefly involves: observing and manipulating provisioning behaviour, handling and marking wasps, setting up video cameras, uploading video footage and data entry. The field worker will be expected to take on responsibilities such as data entry, helping with the day-to-day running of the fieldwork and sometimes managing the field site/team when the Postdoc and PI are away. 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](http://biosciences.exeter.ac.uk/~staff/index.php?web_id=Jeremy_Field)).

Candidates must have strong fieldwork experience (preferably including managing others and leading data collection in the field), a degree in Behaviour/Evolution/Ecology and experience in handling animals (particularly insects). Experience in handling data is also essential (e.g., accurate note taking, inputting data). A valid driving licence is desirable.

The candidate must be available from 1st June - mid/end August, though the exact timing of the fieldwork is unknown as it is weather condition dependent. The successful applicants must have enthusiasm for fieldwork, and will obtain excellent experience of cutting-edge research.

Shared accommodation in Surrey is provided. The position will receive £675 per week.

Please contact Dr Lucy Winder [l.winder2@exeter.ac.uk](mailto:l.winder2@exeter.ac.uk) (cc'ing Prof Jeremy Field [j.p.field@exeter.ac.uk](mailto:j.p.field@exeter.ac.uk)) to discuss these positions further, attaching a CV and covering letter (max 1 page).

Dr Lucy Winder (she/her)

Postdoctoral Research Fellow University of Exeter [www.exeter.ac.uk](http://www.exeter.ac.uk) Stella Turk Building, Treliever Road, Penryn, Cornwall TR10 9FE

“Winder, Lucy” <[L.Winder2@exeter.ac.uk](mailto:L.Winder2@exeter.ac.uk)>

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## UHKong Two Biodiversity

The University of Hong Kong. Two. Ecology&Biodiversity

Assistant / Associate / Full Professor in Ecology and Biodiversity in the Area of Ecology and Biodiversity (2 posts)

Applications are invited for appointment as Assistant Professor/ Associate Professor/ Professor in the broad area of Ecology and Biodiversity (2 posts) in the School of Biological Sciences(Ref.: 526098),to commence as soon as possible. Appointment at Assistant Professor level will be made on a three-year fixed-term basis, with the possibility of renewal and consideration for tenure before the expiry of a second three-year fixed-term contract, while appointment at Associate Professor and Professor level may be considered for appointment on fixed-term or tenure terms.

The Faculty of Science provides a supportive and friendly environment and has been undertaking programme of recruitment to invest in areas of acknowledged strength and internationally competitive activity. Information about the Faculty can be obtained from <https://www.scifac.hku.hk/> and <https://www.cpao.hku.hk/firstandforemost/rankings> . The Area of Ecology and Biodiversity (AoEB) is one of the two research areas in the School of Biological Sciences. AoEB oversees a range of projects on fundamental research in ecology and evolution, as well as applied work on environmental change, ecological restoration, and wildlife forensics and conservation. It has strengths in ecology, evolutionary and environmental biology, marine sciences, as well as global change and conservation biology. Hong Kong has a diverse array of tropical ecosystems that are rich in biodiversity, providing ample opportunities to research the ecological effects of anthropogenic change on terrestrial and aquatic biota, including both endemic and globally threatened species. For more information on AoEB, please visit:<https://www.biosch.hku.hk/research/EB-research-areas/> . Applicants should possess a Ph.D. degree in fields relevant to the positions, strong academic track records and a high level of scholarly accomplishments. The appointees will have the freedom to choose their research directions within the broad area of ecology and biodiversity, including conservation biology and ecological genetics. They are expected to build up strong research environ-



ments, supervise Ph.D. and M.Sc. students, and apply for research funding through the various funding instruments available in Hong Kong. Enquiries about the posts should be sent tobiosch@hku.hk.

A highly competitive salary commensurate with qualifications and experience will be offered, in addition to annual leave and medical benefits. At current rates, salaries tax does not exceed 15% of gross income. The appointments will attract a contract-end gratuity and University contribution to a retirement benefits scheme, totaling up to 15% of basic salary. Housing benefits will also be provided as applicable.

The University only accepts online application for the above posts. Applicants should apply online (<https://jobs.hku.hk/en/job/526098/assistant-professor-associate-professor-professor-in-ecology-and-biodiversity-in-the-area-of-ecology-and-biodiversity-2-posts>) and upload an up-to-date C.V. with the contact details of 3 referees who are able to provide written reference, a publication list, a letter of intent explaining why they would like to be considered for the positions, a teaching statement and expression of their research interests in PDF format. Review of applications will commence as soon as possible and continue until August 30, 2024, or until the posts are filled, whichever is earlier.

The University is an equal opportunities employer and is committed to equality, ethics, inclusivity, diversity and transparency

Juha Kari Kristian Merilae <merila@hku.hk>

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## Uiceland PlantEvolution

Assistant Professor in Plant Biology University of Iceland < <https://radningarkerfi.orri.is/?s=37175> >

A full-time Assistant Professor position in the field of plant biology at the Faculty of Life and Environmental Sciences, School of Engineering and Natural Sciences, University of Iceland is open for applications. The candidate should have a background in research in the field of plant biology and an interest in the education of biology students.

Field of work

\* Teaching and teaching development in various courses

in the field of plant biology, including botany, plant physiology and plant ecology. \* Guidance of research projects in undergraduate and graduate studies. \* Structure of independent research in the field of plant biology at the Institute of Life and Environmental Sciences of the University of Iceland. \* Obtaining external research grants. \* Participation in the management of the department and other academic service and administrative tasks.

### Qualification requirements

\* A Ph.D. in plant biology or related subjects. \* Experience in teaching at the university level. \* Experience in course management and teaching development at university level is an advantage. \* Research experience, having published peer-reviewed research articles in acknowledged journals in the field. \* Expert knowledge of plant characteristics, plant physiology or molecular biology is an advantage. \* Experience in managing research projects and obtaining research grants. \* Good oral and written English skills. \* Good Icelandic skills are an advantage as the department emphasizes teaching compulsory courses in Icelandic for undergraduate studies. \* Good cooperation and agility in interpersonal relations, initiative and independence.

In the hiring decision, considerations will be given to how well the applicant fits the current circumstances and needs of the Faculty of Life and Environmental Sciences.

### Application process

The tentative starting date is August 1, 2024 or according to agreement although not until after the work, of the committees involved in the recruitment process, is finished.

Applicants are required to submit the following documents with their application:

1. Cover letter where it is stated how the applicant meets the qualification requirements.
2. Certificates of education.
3. Curriculum Vitae.
4. List of publications.
5. Report on scholarly work and other work they carried out.
6. Outline of proposed research and teaching plan, if hired.
7. Contact information for three referees willing to provide a reference.

The applicant must list up to eight of their most important publications in relation to this position. The applicant must include a copy of these publications along with the application or indicate where they can be accessed electronically. When multiple authors are listed in a publication, the applicant must include an account of their contribution to the publication. Applications and accompanying documents, which are not submit-

ted in electronic form, must be sent in duplicate to the Division of Science and Innovation, University of Iceland, Main Building, Síðmundargata 2, 101 Reykjavik, Iceland.

The successful candidate will be hired for five years with the possibility of a permanent contract at the end of this period, cf. paragraph 3, Article 31 of the Regulation for the University of Iceland no. 569/2009.

Processing of applications, evaluation of applicants' competence and hiring shall be in accordance with the Act on Public Higher Education Institutions no. 85/2008 and the Regulation for the University of Iceland no. 569/2009.

All applications will be answered, and applicants will be informed about the appointment when a decision has been made. Applications can remain valid for six months after the application deadline.

Appointments to positions at the University of Iceland are made in consideration of the Equal Rights Policy < [https://english.hi.is/university/-university\\_of\\_iceland\\_equality\\_action\\_plan](https://english.hi.is/university/-university_of_iceland_equality_action_plan) > of the University of Iceland.

The University of Iceland has a special Language Policy < [https://english.hi.is/university/-university\\_of\\_iceland\\_language\\_policy](https://english.hi.is/university/-university_of_iceland_language_policy) >.

The University of Iceland is a flourishing community of knowledge and is a very dynamic and interesting workplace. Our values are academic freedom, professionalism and equality. The University strives to provide flexibility and encourages participation in the development of the study programs and research in all fields within the realm 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>

## UKansas LabTech FlyComplexTraits

A research assistant / lab technician position is available in my lab at KU to work on projects examining the genetic analysis of complex traits in flies. The position will involve both fly work and molecular biology (including approaches using high-throughput sequencing). Experience with flies would be a plus, but isn't

required. The formal announcement, and links to the institutional employment website are provided below. Feel free to email me with any questions. Stuart Macdonald ([sjmac@ku.edu](mailto:sjmac@ku.edu))

**Position Overview:** An assistant researcher position is available in the Macdonald lab in the Department of Molecular Biosciences at the University of Kansas (<https://molecularbiosciences.ku.edu/people/-stuart-j-macdonald>). We explore the genetic basis of complex trait variation using the fruit fly *Drosophila* as a model system. The successful candidate will help maintain fly strains and populations of flies, supervise and carry out large-scale phenotyping screens, and perform various molecular biology tasks, including generating next-generation sequencing libraries for various genomics applications. We are looking for an enthusiastic and organized individual who wants to learn new skills, and has excellent oral and written communication skills. Previous research assistants in the Macdonald group have undertaken independent research projects, been authors on research publications from the lab, and gone onto graduate school or positions in industry. The position is funded through a new multi-year NIH grant and has an anticipated start date of May 27, 2024 (although this is flexible/negotiable).

**Job Description:** 50% - Generate, maintain and use *Drosophila* strains/populations for genetic analysis. Examples of the work include stock maintenance, preparing media, carrying out crosses, and assaying strains/populations for phenotypic variation (e.g., stress tolerance).

30% - Carry out a range of molecular biology procedures. Examples of the work include DNA and RNA isolation, PCR, and next generation sequencing library construction (e.g., for RNAseq or whole-genome sequencing).

10% - Perform general lab tasks, including inventory and ordering of supplies, and working with undergraduate students.

10% - Keep accurate and detailed records. Maintain an up-to-date and accurate lab notebook, keep a detailed digital record of all experimental results, and regularly present data/results to Dr. Macdonald.

**Required Qualifications:** (1) A Bachelor's degree in Biology or a related field. (2) Previous experience with molecular biology techniques (e.g., PCR), as evidenced by application materials. (3) Effective written communications skills as evidenced by application materials.

**Preferred Qualifications:** (1) Experience with *Drosophila* husbandry. (2) Significant laboratory experience, including troubleshooting and optimizing protocols. (3) Experience making next generation sequencing libraries (e.g.,

RNAseq libraries). (4) Prior experience managing large scientific projects, including managing undergraduate assistants.

Application:

For a complete announcement and to apply online, go to [employment.ku.edu/staff/27466BR](http://employment.ku.edu/staff/27466BR)

A complete application includes the following: (1) A cover letter outlining relevant experience and interest in the position, (2) a CV/resume highlighting pertinent experience relative to the required and preferred qualifications, and (3) contact information for three professional references.

Only complete applications will be considered. Informal queries about the position are welcome, and can be directed to Dr. Stuart Macdonald ([sjmac@ku.edu](mailto:sjmac@ku.edu), 785-864-5362).

Review of applications will begin on April 8, 2024 and will continue until the position is filled.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the university's programs and activities. Retaliation is also prohibited by university policy. The following persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Director of the Office of Civil Rights & Title IX, [civilrights@ku.edu](mailto:civilrights@ku.edu), Room 1082, Dole Human Development Center, 1000 Sunnyside Avenue, Lawrence, KS 66045, 785-864-6414, 711 TTY (for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses); Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

Dr. Stuart J Macdonald he, him, his

University of Kansas (785) 864-5362 [sjmac@ku.edu](mailto:sjmac@ku.edu)

Professor and Associate Chair Department of Molecular Biosciences

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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>

## UKassel Germany PartTime Metabarcoding

The University of Kassel/Germany is a modern and growing University with round about 23.000 students. The university's wide range of expertise covers subjects in the natural, applied, cultural and social sciences. At the University of Kassel, Faculty of Biology, Group Botany (Prof. Dr. Birgit Gemeinholzer), the following position is to be filled by 1th of April 2024 or later:

Doctoral Researcher (m/f/d), EG 13 TV-H, temporary, part-time (currently 26 hours per week)

Application deadline: 15.03.2024

Date of hire: 01.04.2024

vacancy number: 36992

Part-time position with 65 % of a full-time employee. This is a fixed-term position for three years, corresponding to §2 Abs. 2 WissZeitVG.

TRIO (Transformative Mischkultursysteme für One Health) is a "Hessen LOEWE" excellence Project with a wide interdisciplinary scope, aiming to investigate the potential of mixed cultivation of wheat with medicinal plants to address possible solutions for climate-change-induced drought in agriculture. In the context of this project, a doctoral position is available addressing the "Development of remote sensing based methods to monitor agronomic parameters and heat-related stress of mixed cropping systems of wheat". The main place of service is Witzenhausen, but extended fieldwork in different parts of the state of Hesse, mainly during summer, will be required. Fitness for service in the field is, therefore, mandatory.

Tasks: - Collection of pollinators to identify plant-insect networks using metabarcoding analyses - Implementation of plant metabarcoding and insect barcoding - Documentation, evaluation, analysis and assessment of the experimental results - Working in partnership with project partners to develop joint research results - Participation in project-related seminars, workshops and international conferences by presenting the results - Preparation and presentation of research results in internationally recognized journals

Requirements: - Master's or Diploma degree in Biologie, or related fields The required degree must be obtained by

the recruitment date at the latest. - Knowledge and experience or willingness to learn in the field of vegetation and insect identification - Knowledge and experience in the molecular laboratory and with the analysis of molecular data - Ability to statistically analyze and publish own research - High interdisciplinary willingness to learn and cooperate - A high degree of organizational talent and ability to work in a team. - Good verbal and written communication skills in English and/or German

Advantageous are: - Experience in field surveys, experimental design, and data evaluation. - Scientific expertise, preferably demonstrated by a degree in a field of activity relevant to the project activities - Attention to detail and commitment to produce high-quality, scientifically rigorous results - EU class B driver's license - Experience in knowledge transfer and inter- or transdisciplinary collaboration

For further information please contact Prof. Dr. Birgit Gemeinholzer, University of Kassel, Tel: +49 561 8044601, Email: b.gemeinholzer(at)uni-kassel.de.

Our Offer: As an employee of the University of Kassel

you will be offered an interesting and diverse range of tasks within the framework of a modern and ambitious university, you will be part of an interdisciplinary team with a good and collegial working atmosphere, you will have the opportunity to participate in professional and interdisciplinary further education measures, is your workplace with good connections to public transport, which you can currently use free of charge. In addition, you will benefit from the advantages of employment in the public service such as:

an additional company pension (VBL), an optional child supplement in accordance with TV-Hessen, a family-friendly university (including childcare for emergencies), an annual bonus, an entitlement to capital-accumulation benefits, a promotion of voluntary commitment, low-cost participation in university sports and a full range of fitness activities as part of Unifit, as well as workplace health management

You can find more jobs at [stellen.uni-kassel.de](http://stellen.uni-kassel.de)

Please send your application with the usual informative documents, stating the reference number in the subject line, via the online form. We have compiled further information for you in our FAQ.

In exceptional cases, we will also accept your application documents in paper form addressed to: The President of the University of Kassel, 34109 Kassel, Germany, or via mail to [bewerbungen\[at\]uni-kassel.de](mailto:bewerbungen[at]uni-kassel.de), stating the reference number. In the case of postal applications, please submit only copies of your documents (no fold-

ers), as these cannot be returned. All documents will be destroyed after completion of the selection process in compliance with data protection regulations. The protection of your personal information is very important to us, so

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

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## UmeaU Modeling Adaptive Mechanisms

IceLab and the Department of Ecology and Environmental Science

Umeå University's interdisciplinary research hub, IceLab (Integrated Science Lab, [www.icelab.se](http://www.icelab.se)), has been awarded a grant by the Swedish Research Council to establish a center of excellence: Center for modeling adaptive mechanisms in living systems under stress.

We are now opening a tenure-track Assistant Professor position in ecosystem ecology with employment at the Department of Ecology and Environmental Science. The position seeks a candidate conducting ecological research including computational methods, with a focus on ecological, evolutionary, and/or biogeochemical processes. The position presents a unique opportunity to establish your research group and develop your independent line of research aligned with the Center's theme. Join our supportive environment and work at the forefront of multidisciplinary science. We integrate mathematical modeling and data science with diverse disciplines, including ecology, evolution, microbiology, plant physiology, and molecular biology. Your research will be instrumental in improving our understanding of the processes that govern the responses of living systems to environmental change and stress.

The position comes with a recruitment package. We invite interested candidates to apply on April 29, 2024 at the latest and become part of our quest to shape the scientific discoveries of the future at IceLab.

Please see the ad for more information at:

Tenure-track Assistant Professor in Ecosystem Ecology linked to IceLab's Center for modeling adaptive mechanisms in living systems under stress

umu.se

Eric Libby <eric.libby@umu.se>

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## UMelbourne Two Genomics

Role type: Full-time; Continuing (tenure track) Faculty: Science Department/School: School of BioSciences Salary: Levels B-C-D - AUD \$114,645 - \$186,288 p.a. plus 17% super (retirement savings plan)

\* Two exciting opportunities are available in the fields of computational genomics and functional genomics. \* Join The University of Melbourne's School of BioSciences.

The School of BioSciences at the University of Melbourne is seeking two enthusiastic and collaborative academic colleagues with expertise in genomics.

One appointment will focus on computational and/or computational synthetic genomics, while the other will specialise in functional or synthetic genomics (wet-lab-based research).

Applicants interested in plant, insect, and microbial systems or using established model systems from these taxonomic groups are particularly encouraged to apply.

As part of our commitment to diversity, at least one successful appointee will be female.

Both positions offer opportunities for research, teaching, and service components, with potential affiliation with the Melbourne Institute of Genomics and close interaction with the ARC Centre of Excellence in The Mathematical Analysis of Cellular Systems.

Your responsibilities will include:

\* Undertake internationally competitive independent and/or team-based research, resulting in diverse research outputs such as peer-reviewed publications, patents, license agreements, government reports, and scholarly materials for teaching and learning. \* Contribute to teaching by coordinating, developing and delivering subjects in genomics, genetics and quantitative skills for biologists. As subject coordinators, you will lead academic colleagues in curriculum development and delivery to ensure the successful implementation of course objectives at the University of Melbourne. \* Actively participate at School and/or Faculty meetings and play a leadership role in planning activities or com-

mittee work to support capacity building and strategic planning in the School. \* Participate in supervising research team members and junior academics within the School, under the direction of the Head of School. As a supervisor, actively engage in fostering learning and career development opportunities for both yourself and those you supervise, promoting a positive and supportive environment for professional growth.

Who We Are Looking For

You will ideally possess a dedication to teaching and research excellence, strong collaboration skills, the ability to think innovatively across disciplines, a research focus on genomics in plant, insect, and microbial systems, and a background in running a diverse, collaborative research programs.

You will also have:

\* PhD in genomics, synthetic biology or a related field of biology. \* Excellent track record, relative to opportunity, in conducting research and publishing in top peer-reviewed academic journals. \* Experience teaching into genetics, genomics and/or quantitative biology subjects (as a graduate student demonstrator or tutor for level B; as a member of a lecturer for level C; as a coordinator for level D) at the tertiary level. \* Track record of successfully mentoring postgraduate research students as a co-supervisor (B/C) or as a primary supervisor (Level D) \* Obtained research funding through competitive student scheme (Level B), ECR scheme from internal university sources or small external funding programs (Level B or C) or as a lead Chief or Principle Investigator for larger external funding programs (Level D).

More information here: <https://jobs.unimelb.edu.au/en/job/915977/lecturer-senior-lecturer-associate-professor-in-genomics-multiple-opportunities>  
evol\_dir@evol.biology.mcmaster.ca

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## United Arab Emirates U Molecular Evolution

The Biology Department at the United Arab Emirates University in the UAE, is seeking a dynamic and motivated individual to fill the position of Assistant Professor in Molecular Evolutionary Biology. The faculty position offers an exciting opportunity to contribute to our vi-

brant academic community and engage in cutting-edge research in the field of evolutionary biology, with a focus on molecular mechanisms. Responsibilities: Teaching: Develop and deliver undergraduate and graduate courses in molecular evolutionary biology and related subjects. Create innovative and effective teaching materials, including lectures, laboratory exercises, and assessments. Provide mentorship and academic guidance to students, fostering their intellectual growth and research skills. Research: Establish and maintain an active research program in molecular evolutionary biology, with a focus on addressing fundamental questions in evolutionary genetics and genomics. Pursue external funding opportunities to support research endeavors and contribute to the advancement of the field. Publish high-quality research findings in peer-reviewed journals and present findings at national and international conferences. Service: Participate in departmental and university service activities, including committee assignments, curriculum development, and academic advising. Contribute to outreach efforts to promote the department's initiatives and engage with the broader scientific community. Collaborate with colleagues within the department and across disciplines to enhance interdisciplinary research and educational opportunities.

Minimum Qualification:

Ph.D. in Biology or related field Expertise in molecular evolutionary biology Experience in teaching and research

Close Date:

05/05/2024

Applications need to be lodged via the official site at:

<https://jobs.uaeu.ac.ae/Postings/PostingDetails/4036>  
Assistant Professor in Molecular Evolutionary Biology  
< <https://jobs.uaeu.ac.ae/Postings/PostingDetails/4036> > UAEU Jobs [jobs.uaeu.ac.ae](https://jobs.uaeu.ac.ae)

Dr. Oliver Manlik

Associate Professor of Molecular Ecology,

Biology Department, College of Science,

United Arab Emirates University (UAEU), UAE

Tel: 971-03-7136346 Email: [oliver.manlik@uaeu.ac.ae](mailto:oliver.manlik@uaeu.ac.ae)

Web: <https://cos.uaeu.ac.ae/en/profile.shtml?email=oliver.manlik@uaeu.ac.ae> Associate Editor:

Ecology and Evolution Researchgate: [https://www.researchgate.net/profile/Oliver\\_Manlik](https://www.researchgate.net/profile/Oliver_Manlik) Oliver Manlik <[oliver.manlik@uaeu.ac.ae](mailto:oliver.manlik@uaeu.ac.ae)>

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## UOldenburg ResAssoc EvolutionAntibioticResistance

This ad was machine translated, for the original German ad see this link:

<https://uol.de/stellen?stelle=70127> Faculty VI Medicine and Health Sciences comprises the fields of human medicine, medical physics and acoustics, neurosciences, psychology and healthcare research. Together with the four regional hospitals, Faculty VI forms the University Medicine Oldenburg. There is also close cooperation with the University Medical Center of the University of Groningen.

In the Department of Medical Microbiology and Virology of the Department of Human Medicine, a position is available at the earliest possible date as a

Research Associate (m/f/d)

(E14 TV-L, 100%)

as laboratory manager for the microbiological research area, initially for a limited period of 3 years. The possibility of obtaining your own scientific qualification [habilitation] is given. The position is suitable for part-time work and can be made permanent after three years.

In the research laboratory (location: Philosophenweg) of the Institute of Medical Microbiology and Virology (Institute Director: Prof. Dr. Axel Hamprecht), Medical Campus of the University of Oldenburg, we deal with clinical-oriented and basic scientific microbiological research with a focus on antibiotic resistance, resistance mechanisms and multi-resistant pathogens in human and veterinary medicine and the environment/one health.

The tasks include

- Management and organization of the research laboratory
- Supervision of research projects from conception, acquisition of third-party funding, implementation to publication of the results
- Implementation and organization of courses at the institute

Recruitment requirements:

- Relevant university degree (Diplom (Uni)/Master) in biology, biochemistry, human biology, human or veterinary medicine or a related natural science with a

relevant doctorate

- Knowledge of microbiological-bacteriological and molecular biological methods
- Experience in carrying out genetic engineering work
- Experience in the documentation of research results as well as data management and analysis
- Experience in the supervision of theses
- Ability to prepare, present and publish scientific data
- Very good knowledge of English and German
- Commitment, independence and ability to work in a team

An advantage:

- Knowledge of bioinformatic methods and whole genome sequencing (WGS)
- Project leader license genetic engineering  $\ddot{u}$   $\frac{1}{2}$  28
- Experience in personnel management

We offer:

- A collegial environment with opportunities to develop your own research topics
- Active participation in the expansion of our research unit
- Payment in accordance with collective bargaining law (special annual payment, company pension scheme, capital-forming benefits) including 30 days' annual leave
- Support and guidance during your induction phase and your habilitation project
- A family-friendly environment with flexible working hours (flexitime) and the option of pro rata mobile working
- Company health promotion benefits
- An extensive free continuing education program as well as our own promotion of young scientists (<https://-uol.de/medizin/nachwuchs>)

The Carl von Ossietzky University of Oldenburg aims to increase the proportion of women in science. Women are therefore strongly encouraged to apply. According to  $\ddot{u}$   $\frac{1}{2}$  21 para. 3 NHG, female applicants with equivalent qualifications should be given preferential consideration.

Severely disabled persons will be given preference if equally qualified.

For further information, please contact Prof. Dr. Axel Hamprecht by e-mail at [sandra.schoebel@uni-oldenburg.de](mailto:sandra.schoebel@uni-oldenburg.de) or 0441/403 2160.

Please send your application (description of your moti-

vation, CV, certificates, further references) in electronic form (one PDF file including the usual documents) by 31.03.2024 to Carl von Ossietzky University Oldenburg, Prof. Dr. Axel Hamprecht, Institute of Medical Microbiology and Virology, Philosophenweg 36, 26121 Oldenburg, [sandra.schoebel@uni-oldenburg.de](mailto:sandra.schoebel@uni-oldenburg.de).

Timo van Eldijk <[timovaneldijk@gmail.com](mailto:timovaneldijk@gmail.com)>

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## UPennsylvania ResTech Evolution Vectorborne Pathogens

Research Technician University of Pennsylvania, Department of Biology

The Evolution and Ecology of Disease Systems laboratory (<https://web.sas.upenn.edu/brisson-lab/>) at the University of Pennsylvania is recruiting a research technician to join a multi-institutional team investigating evolutionary or ecological processes in vector-borne disease systems. Our current research aims are to identify the factors and processes that govern the population dynamics of pathogens and their vectors. The research technician will participate several ongoing projects including field-based experiments and collections, the development and application of advanced molecular tools, and generating and analyzing next generation sequence data. The ideal candidate is enthusiastic about evolutionary- or ecologically-based questions and is willing to learn and utilize both field and molecular techniques.

The Evolution and Ecology of Disease Systems laboratory is housed in UPenn's Department of Biology ([www.bio.upenn.edu](http://www.bio.upenn.edu)) - a diverse, interactive community with a long-standing tradition of maintaining an integrated research and educational program across all basic biological sciences including Ecology and Evolution, Plant Sciences, Molecular and Cellular Biology, Genomics, and Neuroscience. The Department values interdisciplinary research, collaboration, and collegiality, emphasizing Life in its Natural Context. The University of Pennsylvania has a strong group of evolutionary biologists and ecologists that frequently interact with each other and with an accomplished group of microbiologists in the Medical and Veterinary schools. The University of Pennsylvania is an equal opportunity employer. Minorities, women, individuals with disabilities, and protected veterans are encouraged to apply.

The position is available as early as Summer 2024. Salary is commensurate with experience based on the NIH guidelines.

Please send enquiries to [dbrisson \[at\] sas.upenn.edu](mailto:dbrisson@sas.upenn.edu)

To apply, please visit [https://wd1.myworkdaysite.com/en-US/recruiting/upenn/careers-at-penn/details/-Research-Specialist-A\\_JR00087394](https://wd1.myworkdaysite.com/en-US/recruiting/upenn/careers-at-penn/details/-Research-Specialist-A_JR00087394) Dustin Brisson, Professor of Biology Director, Evolution and Ecology of Disease Systems Laboratory Department of Biology University of Pennsylvania Philadelphia PA 19104-6018 <http://www.bio.upenn.edu/faculty/brisson/> <https://web.sas.upenn.edu/brisson-lab/> “Brisson, Dustin” [dbrisson \[at\] sas.upenn.edu](mailto:dbrisson@sas.upenn.edu)

“Brisson, Dustin” <[dbrisson@sas.upenn.edu](mailto:dbrisson@sas.upenn.edu)>

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## US NSF DirectorSystematicsBiodiversity

The National Science Foundation (NSF) is searching for a temporary program director (rotator) in the Systematics and Biodiversity Science cluster in the Division of Environmental Biology, with a flexible start date. Rotators typically join NSF on a short-term basis (1-3 years) and contribute to making proposal funding recommendations, influencing NSF program trajectories, interfacing with the scientific community, and relaying trends about research community directions to NSF programs.

Rotators maintain ties to their current institution during their appointment at NSF, ultimately returning with new insights about, and understanding of, the federal funding landscape after their rotation. The Rotator Program strengthens NSF’s ties with the research community and provides the talent and resources that are critical to meeting NSF’s mission. Serving as a rotator at NSF can expand your scientific world view and enable you to engage in a leadership position within the science community in a whole new way.

NSF has an Independent Research/Development (IR/D) program that permits rotators with approved IR/D plans to maintain involvement with their professional research by providing time and travel expenses for research activities.

Qualified candidates from the full range of expertise

covered by the Systematics & Biodiversity Science Program are encouraged to apply. In the short-term, SBS is particularly keen on recruiting rotators with expertise in theory/methods development, microbial and/or invertebrate systematics and taxonomy, and paleosystematics.

If you or someone you know might be interested in serving in this important role at NSF, we would like to hear from you. You can read the job posting and apply at: <https://beta.nsf.gov/careers/openings/bio/bio-18-001> Please forward this announcement to anyone you think might be interested in this opportunity. The application is straightforward. Applications can be submitted at any time, but since we have upcoming staffing needs, we encourage submissions by April 8, 2024. If your interest in rotation is in the longer term, you are welcome to apply as well. We often schedule rotations months to years in advance.

We encourage you to get in touch with these current Program Directors to learn more about the position:

Cathy Aime, [maime@nsf.gov](mailto:maime@nsf.gov) Chris Balakrishnan, [cbalakri@nsf.gov](mailto:cbalakri@nsf.gov) Carolyn Ferguson, [cferguso@nsf.gov](mailto:cferguso@nsf.gov) Matt Fujita, [mfujita@nsf.gov](mailto:mfujita@nsf.gov) Maureen Kearney, [mkearney@nsf.gov](mailto:mkearney@nsf.gov)

“Balakrishnan, Christopher” <[cbalakri@nsf.gov](mailto:cbalakri@nsf.gov)>

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

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## UVienna ArthropodMorphology

The Evolutionary Biology Department/School of Life Sciences at the University of Vienna seeks to appoint a Tenure-Track Professor in the field of Functional Morphology of Arthropods

We are seeking a scientist with a research agenda focused on material and mechanistic understanding of arthropod morphology and its function. The candidate will use state-of-the-art research methods such as high-end microscopy, tomography, and/or high-speed video analyses in combination with imaging software to reconstruct how morphological components interact and how they function in dynamic biological systems. Research organisms may encompass any terrestrial or aquatic panarthropod taxa. We welcome research that may form a link to the applied sciences such as biomechanics/bionics, the material sciences, or robotics. The position will complement existing research on evolutionary morphology, developmental biology, phylogeny, and



evolutionary theory at the University of Vienna.

The broad field of Animal Morphology at the University of Vienna is largely represented by the School of Life Sciences. The broad methodological spectrum at the School offers a fantastic infrastructure for the newly hired colleague and will allow for an immediate start of his\*her research activities. Functional research on the currently not covered arthropods will put the new colleague in a unique and prominent position within the biological disciplines of our faculty. Information on the prime research environment can be found on the homepage of the Department of Evolutionary Biology: <https://evolution.univie.ac.at/>. Several research groups in other departments work in organismal research, offering a potential for productive collaborations, e.g., in the fields of animal-plant interactions, neuro- and developmental biology, as well as ecology.

The initial contract as Assistant Professor is limited to six years, after positive evaluation of a qualification agreement the contract becomes permanent as Associate Professor; Associate Professors can be promoted to Full Professor through an internal competitive procedure. We offer a dynamic research environment, a wide range of research and teaching support services and attractive working conditions in a city with a high quality of life. Salary according to the Collective Bargaining Agreement for University Staff (level A2) and an organisational retirement plan. We expect the successful candidate to acquire proficiency in German sufficient for teaching in bachelors programmes and for participation in university committee within three years.

For details on application requirements see: <https://jobs.univie.ac.at/job/Tenure-Track-Professor-in-the-field-of-Functional-Morphology-of-Arthropods/-1041826701/> Application deadline: 04/15/2024 Reference no.: 2183

For questions, please contact: [tenure-track.personal@univie.ac.at](mailto:tenure-track.personal@univie.ac.at)

The University of Vienna has an anti-discriminatory employment policy and attaches great importance to equal opportunities, the advancement of women and diversity. We lay special emphasis on increasing the number of women in senior and in academic positions among the academic and general university staff and therefore expressly encourage qualified women to apply. Given equal qualifications, preference will be given to female candidates.

Mihaela Pavlicev

Univ. Prof. Mihaela Pavlicev, Ph D Unit for Theoretical Biology

Department of Evolutionary Biology, Chair Zoological Collection, curator

University of Vienna Djerassiplatz 1, 1030 Vienna, Austria

[mihaela.pavlicev@univie.ac.at](mailto:mihaela.pavlicev@univie.ac.at) Tel.: +43 1 4277 56700

NEW BOOK: *Evolvability: A unifying concept in evolutionary biology?*

Mihaela Pavlicev <[mihaela.pavlicev@univie.ac.at](mailto:mihaela.pavlicev@univie.ac.at)>

(to subscribe/unsubscribe the EvoDir send mail to [golding@mcmaster.ca](mailto:golding@mcmaster.ca))

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## WashingtonStateU-Vancouver LabTech PlantMicrobes

Research Technician

Washington State University - Vancouver

The Porter Lab in the School of Biological Sciences at Washington State University - Vancouver is searching for a Research Technician. Research in the lab investigates the evolution and ecology of plant-microbe cooperation in both wild and agricultural systems.

SCOPE: To reveal whether symbiosis between plants and microbes has shifted over the course of crop domestication, the technician will help design and conduct manipulative experiments in the greenhouse and laboratory (see research questions in Porter & Sachs (2020) *TREE*: <https://doi.org/10.1016/j.tree.2020.01.006>). Our lab has a large collection of wild and domesticated legume seeds and rhizobia bacteria ready for plant-microbe growth experiments to compare symbiotic outcomes for crops and wild species. Successful applicants should be experienced in cultivating plants under controlled conditions and interested in using microbial inoculations in experiments. Experience with the collection, analysis, and curation of experimental data, and training in plant science/horticulture and/or microbiology are preferred.

POSITION DETAILS: We will be working in a new, state of the art greenhouse facility with automated climate and irrigation controls, as well as an adjacent new Life Sciences Building on the Vancouver campus. This position is open until filled with potential start dates in Spring 2024. The successful applicant will be compensated with benefits and a salary commensurate with WA state guidelines (likely starting around \$36,000). The position is funded by a grant from the National

Science Foundation and will initially be for one year, with the possibility of renewal for a second year based on satisfactory performance.

**COMMUNITY:** The Porter Lab is committed to creating a diverse, equitable, and inclusive working environment. All members of the group are expected to share in this commitment. Candidates from groups historically underrepresented in biological science research are especially encouraged. The Natural Sciences community at WSUV is collaborative, supportive and conducting research on a wide variety of topics across ecology and evolution across several PhD-granting departments.

**LOCATION:** Vancouver, WA is located in the Portland, OR metro area and is a beautiful place to live and work. As the only public four-year educational institution in Southwest Washington, WSU Vancouver is dedicated to its land-grant tradition for openness, accessibility and service to people. Situated on 351 scenic acres, WSU

Vancouver is in the homelands of the Chinookan and Taidnapam peoples and the Cowlitz Indian Tribe. Employees and students alike value the beauty of campus. Recognized by Insight Into Diversity magazine as a top college for diversity, WSU Vancouver is committed to advancing equity, diversity, inclusion and belonging in all that it does.

**TO APPLY:** Interested applicants, please send a cover letter, CV, and contact information for 3 references to [stephanie.porter@wsu.edu](mailto:stephanie.porter@wsu.edu) Informal email inquiries are also welcome.

Stephanie S. Porter Associate Professor, School of Biological Sciences Washington State University, Vancouver <https://labs.wsu.edu/stephanie-porter/> [stephanie.porter@wsu.edu](mailto:stephanie.porter@wsu.edu)

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### Community Feedback Queer Micro

Hello!

I am writing about a recent preprint put together by an international team of early career microbiologists: \*["Running a queer- and trans-inclusive microbiology faculty search"](#)\*

We are currently soliciting community feedback on this piece and welcoming consortium authors onto the team. We would welcome your experience and insights! Please also feel free to distribute to your networks as appropriate.

You can find the manuscript here: <https://doi.org/10.32942/X2J310> Please record your feedback on the consortium author form: <https://forms.gle/Hn13RKchqyVuiuSX6> Have a great week!

Best, JL

\*Jackie Lee Weissman, Ph.D\* \*pronouns: they/them/theirs\* \*or\*\* she/her/hers\* \*... I'll happily accept either\* \*(see: <https://pronoun.is/-they/.../themselves>, <https://pronoun.is/she>)

[https://microbialgamut.com/-](https://microbialgamut.com/-jw4336@terpmail.umd.edu)

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 (Adjunct Assistant Professor of Biological Science at USC) [jweissman@ccny.cuny.edu](mailto:jweissman@ccny.cuny.edu) (Director of Proposal Development at City College)

JL Weissman <jw4336@terpmail.umd.edu>

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## ExcellenceInScientificCollections E-ScoRe Award

Dear EvolDir community,

I'm pleased to announce the call for the 5th edition of the E-ScoRe Award, which is open until April 15th 2024.

The E-SCORE Award - Excellence in Scientific Collections-based Research is a celebration of the new generation of scientists who have shown dedication to the use of collections that help document, describe and understand life on Earth and the processes that have shaped it. The Award also celebrates the United Nations-endorsed International Day for Biological Diversity, which falls annually on the 22nd of May to commemorate the 1992 adoption of the Convention on Biological Diversity.

More information and access to the application portal can be found here:

<https://cetaf.org/template-activities/cetaf-initiatives/-escore/> Best wishes Eva

Dr. Eva Häffner Science Policy Coordinator Botanischer Garten Berlin

Telefon: +49 30 838 59964 Mobil: +49 176 183 850 63 e.haeffner@bo.berlin<mailto:e.haeffner@bo.berlin>

Freie Universität Berlin ZE Botanischer Garten und Botanisches Museum Berlin Königin-Luise-Strasse 6-8 14195 Berlin

#BoBerlin Internationales Wissenszentrum der Botanik

"Häffner, Eva" <E.Haeffner@bo.berlin>

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## Japan FieldAssist AvianPopulations

An exciting opportunity has arisen for a highly motivated assistant to participate in fieldwork in Japan, as part of our international research team. We will be visiting Japan in May-June 2024 to sample urban and rural tree sparrow (*Passer montanus*) populations, mainly in the Tokyo area. We are now seeking a Japanese-speaking field assistant to help with tasks in the field and act as a translator throughout the field season. This expenses-paid role will give the assistant extensive experience in avian fieldwork, ideal for a future career in ecology, evolution or conservation, whilst working with a friendly team in a beautiful country.

Project summary: The tree sparrow shows geographical variation in the extent to which it associates with humans. In Japan, the tree sparrow is anthrodependent or human-commensal, depending upon human resources for population persistence. This tight association with humans likely emerged and spread with the introduction of rice agriculture out of China. Putatively, it seems the tree sparrow underwent adaptations to thrive in human-modified environments, nesting in building crevices, displaying modified behavioural traits, and transitioning to starch-rich diets.

We aim to investigate the evolutionary consequences of human-commensalism for tree sparrows, as well as their variation along urban-rural gradients. A range of measurements and samples will be collected to understand dietary, reproductive, immunological, behavioural, and genomic adaptation to a human-commensal niche. The field assistant would be involved in all aspects of data collection including mist netting, bird handling, sample collection, data recording, and note taking.

Requirements for the role: - Available for one month of fieldwork between 6th May - 6th June 2024 (ESSENTIAL) - Fluent in both Japanese and English (ESSENTIAL) - Confident with translational tasks, including but not limited to day-to-day translation of signs, timetables etc. and explaining our work to the public (ESSENTIAL) - A full driver's licence, with the option to apply for an international driving permit if necessary (ESSENTIAL) - A valid passport (ESSENTIAL) - Field experience, in particular previous experience with bird handling (DESIRABLE) - Willing to work long hours, including very early mornings and weekends (ESSENTIAL)

What we offer: - Expenses including flights, accommodation and food whilst in Japan - Stipend of euro 750 - Extensive avian field experience, including training from our experienced team members

To apply: For more information and pre-application enquiries, please contact Ruth Fawthrop (r.fawthrop@nioo.knaw.nl) or Melissah Rowe (m.rowe@nioo.knaw.nl).

Applicants should send a brief motivation letter and copy of their CV including two references to Ruth Fawthrop (r.fawthrop@nioo.knaw.nl) and Melissah Rowe (m.rowe@nioo.knaw.nl).

This advert has a rolling deadline, until the position is filled.

“Fawthrop, Ruth” <R.Fawthrop@nioo.knaw.nl>

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## NewPhytologist CallPapers

Dear all,

We are pleased to announce a joint call for papers in Plants, People, Planet and New Phytologist. We are seeking manuscripts that encourage the global scientific community to explore and showcase the uses and benefits of harnessing and synthesising digital information derived from plants and fungi. How can this emerging digital and inter-connected data resource, capturing a rapidly increasing proportion of the world's 400 million plant and fungal specimens, help us address pressing scientific, environmental and societal challenges? A selection of the peer-reviewed papers that are accepted will feed into the Royal Botanic Gardens Kew's State of the World's Plants and Fungi 2026 report. Submit abstracts for consideration by 15 April 2024.

Find more information here: <https://www.newphytologist.org/news/view/343> Best wishes, Mike

Dr Mike Whitfield (he / him), Development Coordinator The New Phytologist Foundation < <https://www.newphytologist.org/> > | Registered charity number 1154867

Twitter & Instagram: @newphyt | Facebook: fb.com/NewPhytologist

Dedicated to the promotion of plant science

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## OmennPrize BestArticleEvolMed Apr15Deadline

Nominations for the \$5000 Gilbert S. Omenn Prize are open until April 15, 2024. The Prize is awarded by the International Society for Evolution, Medicine, and Public Health <https://isemph.org> for the best article published in the previous calendar year on a topic related to evolution in the context of medicine and public health. The first author is invited, expenses paid, to present a plenary talk at the Society's annual meeting. This year's meeting will be August 6-9 in Durham, UK. Abstract submissions are welcome until March 1, 2024.

Full details at <https://isemph.org/Omenn-Prize>

The easy to complete nomination form is here <https://airtable.com/appdYBBUrtoCaFfYn/-shrRwFXDIjU0RsXBD> –Details are below–

Nominations are open until April 15, 2024 for the best article in any peer-reviewed journal on a topic related to evolution in the context of medicine and public health with a final publication date in 2023. The winning article is announced in May and the prize is awarded to the first author of the article at the ISEMPH annual meeting. The prize includes travel, lodging, and an invitation to present at talk at the ISEMPH annual meeting.

All peer-reviewed articles that use evolutionary principles to advance understanding of a disease or disease process are eligible. The prize committee will give priority to articles with implications for human health, but many basic science or theoretical articles have such implications. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome.

Please use this form to submit your nomination. <https://airtable.com/appdYBBUrtoCaFfYn/-shrRwFXDIjU0RsXBD> The prize is made possible by a generous donation by Gilbert Omenn, M.D., PhD. Director of the Center for Computational Medicine and Bioinformatics at the University of Michigan where he is a Professor of Internal Medicine, Human Genetics, and Public Health. Dr. Omenn served as Executive Vice President for Medical Affairs as Chief Executive Officer of the University of Michigan Health System from 1997-2002. He is a past president of the American Association for the Advancement of Science and

a member of the Institute of Medicine of the National Academy of Sciences.

Randolph Nesse <nesse@umich.edu>

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### Online SSE StudentSeminarSeries Mar4-13

The Society for the Study of Evolution (SSE) is pleased to announce the second round of the GREG Seminar Series, a weekly virtual seminar series featuring recipients of our Graduate Research Excellence Grants (GREG): <https://www.evolutionsociety.org/meetings/-greg-seminar-series.html> Recipients of the 2022 GREG R.C. Lewontin Early Awards will present their research every Monday from 12:00 - 1:00 pm Eastern time, starting March 4 through May 13. Each talk will be 45 minutes, followed by 15 minutes for questions.

Schedule:

March 4: Robin Waterman, Michigan State University  
 March 11: Matheus Januario Lopes de Sousa, University of Michigan  
 March 18: Aidan Harrington, University of Minnesota, Twin Cities  
 March 25: Danae Diaz, Duke University  
 April 1: Danai Kontou, University of Cambridge  
 April 8: Sebastian Mortimer, Oregon State University  
 April 15: Fabian C. Salgado Roa, The University of Melbourne  
 April 22: Sergio Serrato-Arroyo, Arizona State University  
 April 29: Austin Chipps, Louisiana State University  
 May 6: Josh Knecht, Binghamton University  
 May 13: Verónica Reyes-Galindo, Universidad Nacional Autónoma de México

The seminar will be presented via Zoom. Find the link on our website: <https://www.evolutionsociety.org/meetings/greg-seminar-series.html> Sign up for weekly email reminders here: <https://forms.gle/W7bQAJxheYEBYNI9> This series is organized by the SSE Graduate Student Advisory Committee (GSAC) and hosted by GSAC and SSE Council.

We look forward to hearing about the outstanding research of these student award winners!

\*Kati Moore\*she/her \*Communications Manager\*  
 \*Society for the Study of Evolution\*  
 communications@evolutionsociety.org  
[www.evolutionsociety.org](http://www.evolutionsociety.org) SSE Communications  
 <communications@evolutionsociety.org>

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### RoyalSocietyPubl EvolutionSustainability

The following issue from Royal Society Publishing Philosophical Transactions B is highly cited and widely read: Evolution and sustainability: gathering the strands for an Anthropocene synthesis compiled and edited by Peter Sogaard Jørgensen, Timothy M Waring and Vanessa P Weinberger and the articles can be accessed directly at [www.bit.ly/PTB1893](http://www.bit.ly/PTB1893) A print version is also available at the special price of 40.00 pounds per issue from sales@royalsociety.org

Felicity Davie Royal Society Publishing

T +44 20 7451 2647

The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG <http://royalsocietypublishing.org> Registered Charity No 207043

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### RoyalSocPubl Releases

The following issues from Royal Society Publishing Philosophical Transactions B are widely read and now FREE to access:

Sex determination and sex chromosome evolution in land plants compiled and edited by Susanne S Renner and Niels A Müller and the articles can be FREELY accessed directly at [www.bit.ly/PTB1850](http://www.bit.ly/PTB1850) Human socio-cultural evolution in light of evolutionary transitions compiled and edited by Yohay Carmel, Ayelet Shavit, Ehud Lamm and Eörs Szathmáry and the articles can be FREELY accessed directly at [www.bit.ly/PTB1872](http://www.bit.ly/PTB1872) A print version is also available at the special price of 40.00 per issue from sales@royalsociety.org

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### UTexasElPaso REU Evolution Summer2024

REU Opportunity Summer 2024: “Research Experience for Undergraduates in Chihuahuan Desert Biodiversity”  
- DEADLINE MARCH 15, 2024

The University of Texas at El Paso (UTEP) Department of Biological Sciences invites applicants for the NSF sponsored Research Experience for Undergraduates (REU) in Chihuahuan Desert Biodiversity. Mentors involved with this program conduct research in diverse aspects of ecology and evolutionary biology of extreme environments. This is a 10 week summer program. The goal of this program is to provide undergraduate students with experience in hypothesis-driven collaborative research utilizing field based and/or laboratory methods and fully engage students in projects associated with the ecology and evolution influencing Chihuahuan Desert biodiversity.

The program provides:

- High quality research experience in ecology and evolutionary biology in the field and/or lab
- Research opportunities at the Indio Mountains Research Station (IMRS), a 40,000 acre facility controlled by UTEP and/or other Chihuahuan Desert field sites
- One-on-one and group mentoring from active research faculty in multidisciplinary fields
- Training in bioethics and other relevant professional skills

The program includes:

- \$7000 stipend for 10 weeks
- Housing in shared apartments and field station
- Travel reimbursement of up to \$700

For more information on the program, research projects or to apply please visit:

<https://www.utep.edu/couri/programs/cdb-reu/>  
<https://etap.nsf.gov/award/604/opportunity/616>

Enquiries: CDB-REU@utep.edu

“Moody, Michael L” <mlmoody@utep.edu>

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## Barcelona GenomicEvolution

I have an open postdoc position in my lab at CREAM in Barcelona. The position is for evolutionary biologists with experience working in whole genome sequencing who have an interest in global change biology, potential rapid adaptation, and biological invasions. A description is at this url <https://creaf.factorialhr.com/-job-posting/postdoctoral-researcher-in-evolutionary-ecology-ref-24-010-47865-64973> The candidate will join Oriol Lapiedra's lab in the Biodiversity department at CREAM. The primary goal of our research is to shed light on how organisms adapt to rapid environmental changes with a specific focus on the role of animal behavior in this process. Our research combines approaches from behavioral ecology, evolutionary ecology, and global change biology. Ongoing research examines the ecological and evolutionary consequences of the arrival of new predators for populations of native lizards as well as for the functioning of the ecosystems they live in. The successful candidate will have experience in evolutionary ecology and/or ecological genomics. He/she will lead their own research program using already collected as well as newly collected genetic data and will participate in fieldwork campaigns in the Balearic Islands, lead lab meetings, and co-supervise Msc students.

Oriol Lapiedra, PhD Severo Ochoa Senior Researcher at CREAM Ramon y Cajal Fellow National Geographic Explorer CREAM Edifici C, Campus UAB, 08193, Spain [oriollapiedralab.com](mailto:oriollapiedralab.com)

Oriol Lapiedra <[o.lapiedra@gmail.com](mailto:o.lapiedra@gmail.com)>

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## Berlin EvolutionMobileElements

Post-Doctoral Position (2-year contract) We are seeking an enthusiastic and motivated individual for a Post-Doctoral position in the team of Dr. Zsuzsanna Izsvaïk, Head of the Mobile DNA Laboratory at the Max Delbrück Center for Molecular Medicine in the Helmholtz Association Society, Berlin, Germany.

The Max Delbrück Center is one of the world's leading biomedical research institutions. Our common goal is that we want to understand the molecular basis of health and disease and bring our discoveries to patients as quickly as possible - for better prevention, diagnostics and treatment.

The Mobile DNA Laboratory forms an effective bridge between basic research on the non-coding genome and transposable elements, also the technological implementation of state of art gene transfer and stem cell technologies for clinical application. The Post-Doctoral position will involve the use of cutting-edge, including high-throughput techniques in molecular and cell biology.

There are currently three exciting research programs: 1) Investigating/testing the "Unwanted transcript hypothesis": <https://www.mdc-berlin.de/-research/publications/selection-synonymous-sites-unwanted-transcript-hypothesis> 2) "Repurposed retroviral sequences for human physiology" 3) Sleeping Beautytransposon-based technology platform

Candidates need to hold a PhD in a relevant biological subject (preferably Biology) and have a solid background in Genetics, Biochemistry, Molecular and/or Cellular Biology, Biotechnology, Bioinformatics and/or demonstrated prior experience in the broader area of research of non-coding, transposable elements or artificial intelligence (A.I.), which is most welcome.

If you have an excellent background in biological sciences and enjoy intellectual challenges, feel free to send in your application.

Furthermore, applicants should have strong analytical and problem-solving skills, as well as first-rate organizational skills. In addition, first-class written and verbal communication skills, as well as the ability work excellently as part of a team, are required. Those applying should also have appeared on at least one high-quality, peer-reviewed first-author publication. Please check the website of Dr. Izsvaĭk's Mobile DNA group for more information, also on recent publications and the current projects being carried out in the lab: <https://www.mdc-berlin.de/izsvak> The funds for this post are available for 24 months in the first instance, with a possible option to extend. The expected start date is around 1st June 2024. Kindly send your informal enquiries and applications to Dr. Zsuzsanna Izsvaĭk: [zizsvak@mdc-berlin.de](mailto:zizsvak@mdc-berlin.de)

Berlin, Germany, March 2024

Laurence D. Hurst Professor of Evolutionary Genetics  
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## BinghamtonU NY MicrobiomeEvolution

Microbiome.Postdoctoral.Fellowship.Binghamton Univ.

Salary and details:\$76,000 (two years, with a pipeline to a Tenure-track position). This position is open until filled, but apply by April 12thfor full consideration.

The Department of Biological Sciences at Binghamton University (SUNY) seeks applicants for an independent Postdoctoral Fellowship (open for two years). The fellowship is open to anyone studying microbiomes in a wide range of plant or animal systems, focusing on how variation in microbiota impacts the way organisms interact with their environment. The postdoc will ideally work with a collaborative team of mentors that will host the fellows in their laboratories and help guide them to remain here in a tenure-track faculty position at the conclusion of the fellowship. Applicants should, therefore, have research interests that complement existing

faculty in our department. The mentorship team will be built from faculty with research most relevant to the applicant's interests. Fellows are appointed with the Postdoctoral Associate title and will receive a highly competitive compensation package, including New York State comprehensive benefits. There will also be an annual allowance to cover research expenses, conference travel, and dissemination of research findings.

The Fellowship is part of the SUNY PRODiG+ initiative that focuses on two goals: (1) increasing the number and share of excellent diverse faculty committed to advancing the ideals of diversity, equity, and inclusion; and (2) strengthening the pipeline for retention and support of these faculty. Eligible candidates must demonstrate personal, academic, or work experience engaging diversity, equity, and inclusion or a commitment to facilitating and enhancing diversity, equity, and inclusion efforts in the campus community. Such experience may include, but is not limited to, an academic/scholarly track record focused on diversity, equity, and inclusion; work, volunteer/unpaid/community service; or related experience/expertise in serving underserved or vulnerable areas and/or populations. Also, candidates must be eligible to work in the United States without a visa sponsorship, and have a Ph.D. in Biology or related discipline from an accredited institution completed prior to the start date.

More details about the position: <https://binghamton.interviewexchange.com/-jobofferdetails.jsp?JOBID=173272> All applicants must apply via Interview Exchange: <http://binghamton.interviewexchange.com/-candapply.jsp?JOBID=173272> Applicants must submit a statement, up to 750 words, that responds to the following - please describe how you've engaged, facilitated, and/or enhanced diversity, equity, and inclusion efforts in the campus community. Examples could include personal, academic, and/or work experience and may include, but is not limited to, an academic/scholarly track record focused on diversity, equity, and inclusion; work, volunteer/unpaid/ community service; or related experience/ expertise in serving underserved or vulnerable areas and/or populations - along with a cover letter, CV, brief research statement, and names and contact information for three references to: <https://binghamton.interviewexchange.com> . You may add additional files/documents after uploading your resume. After you fill out your contact information, you will be directed to the upload page. Please login to check/edit your profile or to upload additional documents: <http://binghamton.interviewexchange.com/login.jsp> . Kirsten M. Prior, Ph.D. (she/her) Associate Professor Binghamton University, SUNY Department of



Biological Sciences priorecologylab.com Sci. 4, Rm. 210  
 “Kirsten M. Prior” <kprior@binghamton.edu>  
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 ing@mcmaster.ca)

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## Brno CzechRepublic BirdEvolution

Postdoc Researcher in Avian Ecology and Conservation

The project funded by Horizon Europe (HORIZON-CL6-2023-BIODIV-01) aims to gain crucial insights into the conservation of breeding, stopover and non-breeding habitats of 14 species of hutable birds in Europe. Many of these species are facing steep declines in numbers, emphasising the urgency of understanding their habitat requirements in terms of quality and quantity. The ultimate goal of the project is to provide decision-makers and managers with robust recommendations to effectively manage and restore these habitats, and thus ensure the favourable conservation status and sustainable management of these species.

Specifically, the postdoc will use extensive tracking data and high-resolution remote sensing datasets to study how habitat selection at non-breeding grounds affects spring phenology and breeding performance. Drawing on the concept of carry-over effects, the postdoc will:

- Investigate temporal dependencies among different stages of the annual cycle in the selected species
- Develop customized R scripts to automatically identify breeding status and performance from detailed multi-sensor tracking data
- Test how temporal and spatial variation in non-breeding conditions, particularly during winter and spring stopovers, influence individual breeding status and performance and link them to population trends

Tracking data for the Eurasian Curlew (>300 individuals) are already available and the postdoc will begin by analysing these data, using this species as a proof of concept. These analyses will then provide the analytical framework to be applied to all other study species as soon as the necessary data are collected. The central task of the project, for which the Institute of Vertebrate Biology is responsible, is to establish how carry-over effects, particularly the downstream consequences of non-breeding conditions on reproductive output, influence population trends, thereby offering insights for effective conservation strategies for these species.

Working conditions The postdoc will work at the Bird

Ecology and Migration Lab led by Petr Procházka. This research group is a small team based at the Institute of Vertebrate Biology CAS (IVB), at its headquarters in Brno, Czech Republic (<https://www.ivb.cz/en/workplace/research-facility-brno/>). The primary workspace of the postdoc will be at the IVB in Brno. Brno, the second-largest city in the Czech Republic, is a modern research and innovation hub. The IVB headquarters are housed in a spacious villa located in a quiet residential district. The IVB's scientific community comprises numerous international early-career researchers, offering promising opportunities for professional networking. Furthermore, the candidate will have the chance to interact with other teams from the international HABITRACK consortium (led by Frédéric Jiguet, Pierrick Bocher, Aurélien Besnard, Andrea Kitzsch, Markus Piha, and Aleksi Lehikoinen). The postdoc will receive a competitive monthly gross salary of 55,000 CZK, with social and health insurance provided in addition. This ensures more than comfortable living standards in Brno.

**Requirements** The successful candidate will possess a deep understanding of data analysis and a strong interest in avian ecology and conservation. The ideal candidate will have good experience in data analysis in R and GIS, animal tracking, remote sensing data, habitat use, bird ecology and conservation. The primary focus of the position is on data analysis and scientific manuscript writing, though there will be opportunities for fieldwork. A valid ringing licence or experience in bird handling and tagging is thus an advantage but not a requirement. The quality of the candidate's existing work will be given priority over the number of publications. Extensive experience in R programming and data analysis, as well as excellent scientific publication skills, will be the most decisive criteria in candidate selection. All candidates, regardless of gender and background, are warmly invited to apply. We particularly encourage applications that will contribute to the diversity of our team.

**Application:** Candidates should compile a structured CV, a motivation letter, and a letter of recommendation into a single PDF file and send it to Petr Procházka (prochazka@ivb.cz) by 15 April 2024. Online interviews with shortlisted candidates will be conducted until the position is filled.

**Links:** <https://euraxess.ec.europa.eu/jobs/209202>  
<https://bit.ly/HabittrackPostdoc> More information: Dr Petr Procházka prochazka(at)ivb.cz +420 543 422 117

Petr Procházka <prochazka@ivb.cz>

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

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## CambridgeUK PandemicScalePhylogeneticMethods

We have an open 3-year postdoc position in the Goldman group at EMBL-EBI for the development of pandemic-scale phylogenetic methods, see e.g. <https://www.nature.com/articles/s41588-023-01368-0>. Please consider us for your next position, or circulate to any possibly interested candidates, in particular those with previous phylogenetic methods experience.

Links with job adverts and more information: <https://www.embl.org/jobs/position/EBI02209>

<https://www.nature.com/naturecareers/job/12814683/postdoctoral-fellow-pandemic-scale-phylogenetics/> <https://www.linkedin.com/feed/update/urn:li:activity:7174003050020270083/>

<https://twitter.com/EBIgoldman/status/1768245265532604610> Apologies if you get multiple notifications of this via different routes. Thank you very much,

Nick Goldman Nicola De Maio EMBL-European Bioinformatics Institute

Nick Goldman <[goldman@ebi.ac.uk](mailto:goldman@ebi.ac.uk)>

(to subscribe/unsubscribe the EvolDir send mail to [goldman@mcmaster.ca](mailto:goldman@mcmaster.ca))

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## CzechRepublic ClimateAdaptationGenomics

Opportunity for Postdoctoral Researchers: Population Genomics and Climate Change Adaptation

A postdoctoral position for up to 2.5 years is available in population genomics and climate change adaptation at the Czech Academy of Sciences. This position is funded by the MERIT Programme, a regional initiative for incoming mobility of postdoctoral researchers from all over the world. MERIT is co-funded by the

European Commission under the Horizon Europe Marie Skłodowska-Curie Actions (MSCA) - COFUND. The call is open until April 15, 2024.

Research environment: Join the research team of Dr. Petr Kotlik at the Institute of Animal Physiology and Genetics. Our team investigates animal responses to climate change with the aim of predicting species coping mechanisms based on both current and past adaptive capabilities.

Lab website: <https://www.iapg.cas.cz/en/laboratories/lme/Research> ResearchGate: [https://www.researchgate.net/profile/Petr\\_Kotlik](https://www.researchgate.net/profile/Petr_Kotlik) Your role:

As a postdoctoral researcher, you will develop your own project within the scope of our lab. Research areas include:

Identifying post-glacial population history and genetic adaptations. Exploring physiological mechanisms, such as resistance to oxidative stress mediated by haemoglobin and other systems. Assessing the significance of past and present adaptations for future resilience using climate models

Research infrastructure: Our facilities support investigations at multiple levels, including population genomics, gene expression, protein structure-function relationships and physiology.

Collaboration and networking: Benefit from collaborations with scientists in Europe and the USA. There is the possibility of a secondment to a collaborating institution.

Ideal candidate: We are looking for candidates with solid publications in peer-reviewed journals and a background in population/ecological genomics or related fields. Enthusiasm, motivation, and the ability to work independently and as part of a team are essential.

Location: Choose between living in the historic town of Melnik or in Prague. Good written and spoken English skills are required.

Application process: Applications should be submitted through the MERIT Programme online system. Visit [www.meritcb.eu](http://www.meritcb.eu) for more information on the application process, eligibility criteria and deadlines.

Salary: The selected candidate will receive an internationally recognized MSCA COFUND fellowship covering up to 30 months of research. The minimum gross salary is 3,188 EUR per person per month.

Representative publications from our lab: Markova et al. (2023) Nature Communications <https://doi.org/10.1038/s41467-023-43383-z> Escalante et al. (2022) Communications Biology <https://doi.org/10.1038/s42003-022-03935-3> Kotlik et al. (2022) Frontiers

in Ecology and Evolution <https://doi.org/10.3389/fevo.2022.866605> Markova et al. (2020) Molecular Ecology <https://doi.org/10.1111/mec.15427> Kotlik et al. (2014) Proceedings of the Royal Society B <https://doi.org/10.1098/rspb.2014.0021> If you are intrigued by our research and believe you could be a valuable addition to our team, we encourage you to contact Dr. Kotlik at [kotlik@iapg.cas.cz](mailto:kotlik@iapg.cas.cz) if you have any questions or would like to discuss the position further. We look forward to hearing from passionate and motivated individuals who would like to contribute to our exciting research endeavours.

Petr Kotlik <[Kotlik@iapg.cas.cz](mailto:Kotlik@iapg.cas.cz)>

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### **Eawag Switzerland AquaticEcoEvolution**

The call for the prestigious “Eawag-Postdoc”, a 2-year postdoctoral fellowship at Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is open:

<https://apply.refline.ch/673277/1136/pub/1/-index.html> The deadline for applications is 11 April 2024. Please refer to the advert for details. The call is open for researchers in any field within the area of aquatic sciences, and we encourage ecologist and evolutionary biologists to apply.

Information on our research in these fields is available via the following links: <https://www.eawag.ch/en/-department/eco/organisation/> <https://www.eawag.ch/en/-department/fishec/organisation/> <https://www.eawag.ch/en/-department/umik/organisation/> <https://www.eawag.ch/en/-department/siam/-organisation/> Interested candidates have the opportunity to define their own research project at Eawag. Feel free to contact me or any of Eawag’s other department heads or group leaders to discuss possibilities.

Christoph Vorburger Eawag, Swiss Federal Institute of Aquatic Science and Technology & Institute of Integrative Biology, ETH Zürich  $\frac{1}{2}$ berlandstrasse 133 8600 Dübendorf Switzerland

Phone: +41 58 765 5196 e-mail: [christoph.vorburger@eawag.ch](mailto:christoph.vorburger@eawag.ch) or [vorburgc@ethz.ch](mailto:vorburgc@ethz.ch) group homepage: [http://](http://homepages.eawag.ch/~vorburger/)

[homepages.eawag.ch/~vorburger/](http://homepages.eawag.ch/~vorburger/) “Vorburger, Christoph” <[Christoph.Vorburger@eawag.ch](mailto:Christoph.Vorburger@eawag.ch)>

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### **FordhamU GenomicsRiceAdaptation**

Postdoctoral Associate, Genomics of local adaptation in rice

A postdoctoral position will be available in the lab of Steve Franks in the Department of Biology at Fordham University in New York City. The position will involve performing population and evolutionary genomic analyses of local varieties of rice grown experimentally under different conditions. The project is in collaboration with Michael Purugganan at New York University (NYU) and Amelia Henry at the International Rice Research Institute (IRRI). The position will be based at the Rose Hill campus of Fordham in the Bronx. The postdoc will also conduct research projects on related topics, and will have access to the institutions affiliated with Fordham, including NYU, the New York Botanical Gardens, Bronx Zoo, American Museum of Natural History, and Fordham’s Louis Calder Field Station.

The candidate should have a Ph.D. in ecology, evolution, genetics or a related field and knowledge of these subject areas, with a background in evolutionary ecology particularly important. The candidate should have skills in genomic and bioinformatics analysis, biological statistics, and should be able to use programs such as R and Python. The postdoc will be expected to participate in research projects, help to mentor graduate and undergraduate students, and contribute to scientific publications. The postdoc must be eligible to work in the United States, and will undertake a background check and drug screening. The salary range is \$64,000-65,000 per year, and includes benefits.

The start date for the position is September 1, 2024. The initial appointment will be for one year and can potentially be extended for an additional year.

To apply, please upload a C.V. and a cover letter that includes a statement of research interests and goals and contact information for 3 references to this link (<https://careers.fordham.edu/postings/7026>), which can be found on the career opportunities website of Fordham University. For questions, please contact Steve Franks

at [franks@fordham.edu](mailto:franks@fordham.edu).

The application materials should be received by May 15, 2024.

Steven J Franks Professor and Chair Department of Biology Fordham University Bronx, NY 10458 Lab website-<https://franks91.wixsite.com/sfrankslab> Project Baseline- <http://www.baselineseedbank.org> Steven Franks <[franks@fordham.edu](mailto:franks@fordham.edu)>

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## IndianaU PlantEvolEco

Postdoctoral Position Available in Plant Evolutionary and Community Ecology

A Postdoctoral Research Associate position is available to conduct collaborative research at Indiana University in the Delph lab in the Department of Biology. The research associate will work on an NSF-funded project, investigating interactions of closely related North American *Lobelia* species and mechanisms affecting co-existence within communities. Our collaborative research team is taking a wide variety of approaches, including manipulative greenhouse, common-garden studies, and range-wide characterization of species niches, traits, and phylogenetic history.

We are looking for an individual to collaborate on a range-wide common garden experiment, with replicate gardens in Florida, Indiana, and Michigan. The postdoc will interact with the research teams of Drs. Andrea Case and Chris Blackwood at Michigan State University. We will plant our study species and their hybrids in semi-natural outdoor settings inside and outside the center of species richness (the Atlantic Gulf). The postdoc will collaboratively coordinate the establishment and maintenance of all three common gardens over two seasons and lead the investigation into questions related to reproductive isolation and interference. The postdoc will also conduct additional experiments in the field and greenhouses in Indiana. This position presents a great opportunity to leverage existing datasets, field sites, and resources, as well as develop additional research projects related to the overall objectives of the project.

The position requires fieldwork for extended periods away from home. The postdoctoral associate will be responsible for managing and analyzing data, writing publications, and communicating effectively with other

scientists, students, and the public. I seek someone who exhibits curiosity and enthusiasm for discovery and who would enjoy being part of a collaborative team working with plants.

Salary starts at \$55,000, and full benefits are included. Start date is negotiable, preferably between 6/1/2024 and 9/1/2024. Inquiries about this position can be directed to Dr. Lynda Delph at [ldelph@iu.edu](mailto:ldelph@iu.edu). Indiana University has an interactive and highly ranked Evolution, Ecology, and Behavior program that is part of a large Department of Biology. Bloomington is an affordable mid-sized city situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater. To apply, please submit a letter of application describing interest and previous experience, a curriculum vitae, and the contact information for three references to <https://indiana.peopleadmin.com/postings/23067>. For best consideration, please apply before April 15, 2024.

The College of Arts and Sciences is committed to building and supporting a diverse, inclusive, and equitable community of students and scholars.

Indiana University is an equal employment and affirmative action employer and a provider of ADA services. All qualified applicants will receive consideration for employment based on individual qualifications. Indiana University prohibits discrimination based on age, ethnicity, color, race, religion, sex, sexual orientation, gender identity or expression, genetic information, marital status, national origin, disability status or protected veteran status.

Minimum Requirements (1) Ph.D. (Evolutionary Biology, Ecology, Plant Biology, or a related field); (2) Record of publishing in peer-reviewed scientific journals; (3) Evidence of the ability to work independently as well as part of a team; (4) Evidence of skills in experimental design and statistical analysis; (5) Excellent communication skills; (6) Valid driver's license or ability to obtain one within 30 days of employment.

Desired Qualifications (1) Experience with and interest in fieldwork, sometimes in adverse conditions, and ability to work from field sites for extended periods; (2) Expertise in plant organismal biology, including experience with plant cultivation; (3) Evidence of successful project management and research mentoring.

"Delph, Lynda F." <[ldelph@iu.edu](mailto:ldelph@iu.edu)>

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## Kew Gardens UK Five4yr Fellows Plant Evolution

Royal Botanic Gardens, Kew is now accepting applications for 5 early-career researchers to join the annual Future Leader Fellowship scheme in Plant and Fungal Science.

This is a 4-year fellowship which allows for scientists to undertake their own research project, aligned with one of Kew's priorities of: Ecosystem Stewardship Trait Diversity & Function Digital Revolution Accelerated Taxonomy Enhanced Partnerships

Line managed by a senior researcher, the candidate will benefit from opportunities for development that include - but are not limited to - training workshops on topics from grant writing to research impact, a mentorship programme, bi-annual meetings with the Director of Science, and other chances for researcher-led training. They will also be able to apply for secondment and research funding internally and are encouraged to use this funding to travel for their research.

Applications close on 21st April, please submit your application via Kew's career site, attaching a research plan and CV. <https://careers.kew.org/vacancies.html#> Interviews are likely to take place toward the end of May with the position commencing in September 2024.

Please contact [FLFscience@kew.org](mailto:FLFscience@kew.org) with any enquiries.

FLF Science <[flfscience@kew.org](mailto:flfscience@kew.org)>

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## LMU Munich Evolutionary Genetics

Postdoctoral Researcher in Evolutionary Genetics

The Wolf lab is recruiting a postdoc to join our international research team at the University of Munich (LMU Munich). This multi-year postdoc position offers the opportunity to make an impact in the broad field of evolutionary genetics and build a successful research career.

The position. We are seeking a skilled scientist with a solid background in evolutionary genetic theory, proficiency in bioinformatic processing of large -omics data sets and familiarity with common population/comparative genetic software tools. The postdoc will develop and apply computational approaches to existing data sets and co-develop future research activities characterize patterns and processes of evolution. Beyond research, responsibilities include service of IT infrastructure and mentoring students in computational BSc and MSc courses (4 h / week during the semester). This is a multi-year postdoc position initially restricted to three years with possibility of extension of up to seven additional years. Remuneration is according to German public payment scale TV-L E13 100 % commensurate with qualifications and experience.

Research environment. We use computational methods to study fundamental demographic and evolutionary processes in natural and experimental populations. A central goal of the lab is to understand the evolutionary processes involved in adaptation and speciation. Data sets exploring different aspects of natural variation in ancient and current-day samples are generally sequence-based (WGS, ATACseq, RNAseq, WGBS, EMseq) and are used to test evolutionary theory, often by intersection with quantitative phenotypes and other metadata. Model organisms include birds, marine mammals, fission yeast and a meadow. The lab is located at LMU Munich and Max-Planck Institute of Biological Intelligence and maintains close ties to a growing evolutionary genetics community representing the breadth of the field (EvoGenMunich). With the Leibniz Supercomputing Centre and its local partners, we have access to state-of-the-art computing facilities. Munich is Bavaria's capital, with many traditions still alive, and is a vibrant but relaxed city offering a high quality of living.

How to apply. Applicants holding a PhD with a proven publication record in a relevant field are encouraged to apply. Applications including a statement of motivation, a CV and the contact details of at least two references should be sent as a single .pdf file to [evolution@bio.lmu.de](mailto:evolution@bio.lmu.de) subject term 'EvoGen postdoc'. The position is open until filled with an anticipated start date in summer 2024.

Links. Wolf Lab, LMU Munich: [https://www.evol.bio.lmu.de/research/j\\_wolf/index.html](https://www.evol.bio.lmu.de/research/j_wolf/index.html); MPI Biological Intelligence: <https://www.bi.mpg.de/wolf>; Evolutionary Genetics community Munich: <https://evogenmunich.de/>; Leibniz Compute centre: <https://www.lrz.de/english/>; Biology Campus: <http://www.campusmartinsried.de/en/336-2/> Prof. Dr. Jochen B. W. Wolf Head of Evolutionary Biology Division, LMU Munich MPI fellow, Max Planck Institute

for Biological Intelligence

mail to: Jochen Wolf Division of Evolutionary Biology  
Faculty of Biology LMU Munich Grosshaderner Str. 2  
82152 Planegg-Martinsried Germany

office phone: +49 (0)89 / 2180-74102 fax:  
+49 (0)89 / 2180-74104 Lab website: [http://-  
www.evol.bio.lmu.de/research/j\\_wolf/index.html](http://www.evol.bio.lmu.de/research/j_wolf/index.html)  
MPI: <https://www.bi.mpg.de/wolf/de> Jochen Wolf  
<j.wolf@bio.lmu.de>

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ing@mcmaster.ca)

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## MacquarieU EcolEvolGenomics SuperSeed

2.5-year Postdoctoral Fellowship in Plant Ecology and  
Evolutionary Genomics

The Field lab at Macquarie University is recruiting a  
postdoctoral fellow to join our project on local adapta-  
tion and admixture in Native Seed Production Areas in  
Australian plants.

This project aims to understand how we can produce  
'Super Seed' - optimising genetic diversity and admix-  
ture in native seed orchards for Australian plants used  
in restoration projects. The establishment of Seed Pro-  
duction Areas (SPA) for native Australian plants has  
become increasingly important to fill the gap between  
seed supply and demand. However, key knowledge gaps  
remain in understanding the genetic diversity and com-  
position of SPAs compared to natural populations and  
how this translates to healthy seeds suitable for chang-  
ing climates. We are particularly interested in how plant  
mating systems, pollination systems and demographic  
factors such as range size and neighbourhood size im-  
pact seed quality and quantity and extent of admixture  
between provenances. As part of a collaboration with  
Greening Australia and other research groups across  
Australia, we aim to undertake research with practical  
application to improve outcomes for native seed. The  
overall objective of this project is to develop a Quality  
Assurance (QA)/Quality Control (QC) framework for  
SPAs based on genetic diversity and quality of seed pro-  
duced. This postdoc will contribute to basic research  
problems in a comparative framework across species.  
Using population genomic analyses in SPAs and native  
populations to understand the demographic and evolu-  
tionary history of each species, and eco-evol models of

genetic rescue, paternity analyses and GEA of provide  
practical solutions to SPA design. Opportunities for  
supervisory experience (working with a PhD position  
on this project) and teaching in the department.

The broader group works on a range of plant systems  
(e.g. snapdragons, kangaroo paws, Eucalypts) and re-  
search questions related to speciation, adaptation, ge-  
netic rescue and conservation of threatened species and  
plant-pollinator interactions. We utilise an integrated  
approach using bioinformatics, population and evolution-  
ary genetics, field ecology and glasshouse experiments,  
molecular biology, biochemistry and mathematical mod-  
elling.

Macquarie University is situated in the northern part of  
Sydney. The city is a diverse and vibrant place to live, a  
beautiful harbour city with vast entertainment options  
and outdoor activities on your doorstep. Gold sandy  
beaches and vast National Parks circle the city (e.g.  
Blue Mountains, Ku-ring-gai Chase national parks) situ-  
ated in a global biodiversity hotspot are easily accessible  
by train.

For more details on selection criteria see the link below.

Enquiries: A/Professor David Field,  
david.field[@]mq.edu.au To Apply: [https://-  
www.seek.com.au/job/73819857](https://www.seek.com.au/job/73819857) Closing Date: 31st  
March 2024

David Field <david.field@mq.edu.au>

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ing@mcmaster.ca)

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## Marseille Anthropobiology

Post Doc Position :

We are looking for a motivated and independent post-  
doctoral researcher with experience in ancient DNA  
and evolutionary genomics, who enjoys working in an  
interdisciplinary research environment.

About the project

Our project is part of a multidisciplinary and inno-  
vative framework focused on contrasting the genomic  
evolutionary histories of a pathogen, *Yersinia pestis*,  
and its human host. *Yersinia pestis* was responsible  
for the most-deadly epidemics in Eurasia in Medieval  
history, killing up approximately half of the European  
population by the mid-14th century. It was also the

key pathogenic agent of the epidemics that raged in Provence between 1720 and 1722, which is not only well-documented by extensive historical archives, but also by a considerable number of human skeletons, uncovered through archaeological excavations. Combined, these archives offer a unique window into the genomic makeup of the pathogen and their victims, promising to gain unprecedented insights into the biological and social factors underlying virulence, disease susceptibility and resistance, potentially revealing biological inequalities amongst the population exposed.

This project is a stepping stone to a larger joint project between UMR ADES and the Centre for Anthropobiology and Genomic of Toulouse (CAGT, France). The selected Postdoctoral researcher will join the French A\*midex project entitled “MPMH: memory of plagues, memory of humans”, led by Dr Caroline Costedoat.

#### Missions

The ideal candidate will show first-hand experience in ancient DNA research, including for generating and analyzing next-generation DNA sequencing data. S/he and will have an established record of research achievements and publications and will be able to work in a highly international and multidisciplinary research environment. The postdoctoral researcher selected will dedicate 100% of his/her time to the project and will be in charge of its daily implementation. S/he will have the capacity to communicate his/her research progress to a team of experts in ancient DNA research and evolutionary genomics, as well as archeo-anthropologists and historian experts of the second plague pandemics.

#### When and Where : Administrative information

The postdoctoral position corresponds to a two-year appointments, starting no later than July 2024. The candidate will be recruited by Aix Marseille University and will take up his/her post in Marseille. However, he/she will be required to move to the Centre for Anthropobiology and Genomics of Toulouse for the remainder of the project mainly under the supervision of Dr Ludovic Orlando.

To apply please send to Caroline Costedoat (caroline.costedoat@univ-amu.fr) and Ludovic Orlando (ludovic.orlando@univ-tlse3.fr): your CV, the names and contact details of three references, and a cover letter describing your research and training backgrounds, and your main strengths for making this collaboration a success. Those applicants showing the best profiles will be invited for an online interview.

COSTEDOAT Caroline <caroline.costedoat@univ-amu.fr>

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## Marseille Toulouse Paleogenomics

### Postdoctoral Researcher

We are looking for a motivated and independent post-doctoral researcher with experience in ancient DNA and evolutionary genomics, who enjoys working in an interdisciplinary research environment.

### About the project

Our project is part of a multidisciplinary and innovative framework focused on contrasting the genomic evolutionary histories of a pathogen, *Yersinia pestis*, and its human host. *Yersinia pestis* was responsible for the most-deadly epidemics in Eurasia in Medieval history, killing up approximately half of the European population by the mid-14th century. It was also the key pathogenic agent of the epidemics that raged in Provence between 1720 and 1722, which is not only well-documented by extensive historical archives, but also by a considerable number of human skeletons, uncovered through archaeological excavations. Combined, these archives offer a unique window into the genomic makeup of the pathogen and their victims, promising to gain unprecedented insights into the biological and social factors underlying virulence, disease susceptibility and resistance, potentially revealing biological inequalities amongst the population exposed.

This project is a stepping stone to a larger joint project between UMR ADES and the Centre for Anthropobiology and Genomic of Toulouse (CAGT, France). The selected Postdoctoral researcher will join the French A\*midex project entitled “MPMH: memory of plagues, memory of humans”, led by Dr Caroline Costedoat.

### Missions

The ideal candidate will show first-hand experience in ancient DNA research, including for generating and analyzing next-generation DNA sequencing data. S/he and will have an established record of research achievements and publications and will be able to work in a highly international and multidisciplinary research environment. The postdoctoral researcher selected will dedicate 100% of his/her time to the project and will be in charge of its daily implementation. S/he will have the capacity to communicate his/her research progress to a team of experts in ancient DNA research and evo-

lutionary genomics, as well as archeo-anthropologists and historian experts of the second plague pandemics.

#### Administrative information

The postdoctoral position corresponds to a two-year appointments, starting no later than 1st July 2024. The candidate will be recruited by Aix Marseille University and will take up his/her post in Marseille. However, he/she will be required to move to the Centre for Anthropobiology and Genomics of Toulouse for the remainder of the project mainly under the supervision of Dr Ludovic Orlando. To apply please send to Caroline Costedoat ([caroline.costedoat@univ-amu.fr](mailto:caroline.costedoat@univ-amu.fr)) and Ludovic Orlando ([ludovic.orlando@univ-tlse3.fr](mailto:ludovic.orlando@univ-tlse3.fr)): your CV, the names and contact details of three references, and a cover letter describing your research and training backgrounds, and your main strengths for making this collaboration a success. Those applicants showing the best profiles will be invited for an online interview.

COSTEDOAT Caroline <[caroline.costedoat@univ-amu.fr](mailto:caroline.costedoat@univ-amu.fr)>

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ing a multi-scale approach with a wide array of techniques including in vitro electrophysiology, molecular biology, confocal and lightsheet imaging, optogenetic and chemogenetics, in vivofiber photometry recordings, mouse fMRI and behaviour assays.

The prospective postdoc would combine functional genetic analysis (using RNAi interference, CRISPR, or Cre-conditional knockout strategies among other genetic approaches) to examine variation in sociability and its neurobiological basis using fruit flies and mice as model systems. Qualified candidates will possess a PhD in biology, neuroscience or another relevant field.

Please send a cover letter, current CV, and a list of 3 references to Drs Katrina Choe or Reuven Dukas at [choek@mcmaster.ca](mailto:choek@mcmaster.ca) or [dukas@mcmaster.ca](mailto:dukas@mcmaster.ca).

We will notify applicants before contacting any references.

“Dukas, Reuven” <[dukas@mcmaster.ca](mailto:dukas@mcmaster.ca)>

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## McMasterU SociabilityNaturalVariation

Postdoctoral Fellowship- neurogenetics of natural variation in sociability

The Choe and Dukas labs, McMaster University Hamilton, Ontario, Canada

The Choe and Dukas labs at the Department of Psychology, Neuroscience & Behaviour, McMaster University are looking for a postdoc for a collaborative ongoing project deciphering the genetic basis of natural variation in sociability.

The Dukas and Dworkin labs have artificially selected low and high sociability fruit fly lineages (<https://academic.oup.com/evolut/article/76/3/541/6728481>) and identified promising candidate sociability genes. We have begun the process of quantifying the effects of these genes on sociability in fruit flies and wish to expand our work to examining the role of the verified genes in mammalian sociability using mice as a model system.

The Choe Lab (<http://choelab.ca>) investigates neurobiological mechanisms underlying social behaviour us-

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## Montpellier MetabarcodingBioinformatics

Job: Post-doc on metabarcoding bioinformatics and community analyses in Spain and France

Interested in bioinformatics and eDNA? Holding a PhD in Biology, Data Science or related fields? We offer a two-year post-doctoral position in the framework of the European Project BiOcean5D (<https://www.biocean5d.org/>).

Our final goal is to characterize new indicators of ecosystem health using as model port-related gradients of impact, with a special focus on marine non-indigenous and invasive species. The candidate is expected to contribute through the analysis of eDNA metabarcoding data collected in European ports during the TARA-EUROPA expedition, all the way from raw sequences, data analyses to publication. For selected OTUs, metabarcoding data will be mined for intra-OTU level population analyses.

The candidate should have a background in community ecology or population genetics/molecular ecology, and skills in bioinformatics applied to species and community diversity analyses ((s)he should ideally be knowledgeable of current metabarcoding pipelines). Experiences



the field of marine ecology or biological invasions are not required but would be an asset. If skills exist in other bioinformatic fields, we can help make a smooth transition.

Knowledge of Unix environments and programming is mandatory.

Our team is a collaboration between the Spanish Research Council (CSIC) and two research laboratories in Montpellier (France). The first year the candidate will be hired by the CSIC and will work at the Centre of Advanced Studies of Blanes (CEAB) in the “Molecular Ecology of the Marine Benthos” group led by Xavier Turon. The second year, the candidate will be hired by CNRS (National Center for Scientific Research) and based at the Institute of Evolutionary Science of Montpellier (ISEM) on the Montpellier University campus, working under the supervision of Frédérique Viard. Over the two-years, the work will be done in collaboration with Sophie Arnaud-Haond (Marine Biodiversity Exploitation and Conservation, MARBEC).

Beyond background and skills mentioned above, we value the maintenance of a positive and friendly atmosphere of work, so we look for open-minded candidate eager to collaborate and participate in the activities of the groups, optionally including mentoring of Master students.

Estimated net salary (prior to income taxes) per year will be of ca. 35-42 K euro depending on the experience of the candidate.

The contract is expected to start in September 2024 at the latest.

Interested people, please contact us: Frederique Viard [frederique.viard@umontpellier.fr](mailto:frederique.viard@umontpellier.fr) Sophie Arnaud-Haond [sophie.arnaud-haond@umontpellier.fr](mailto:sophie.arnaud-haond@umontpellier.fr) Xavier Turon [xturon@ceab.csic.es](mailto:xturon@ceab.csic.es)

Xavier Turon Dept. of Marine Ecology Center for Advanced Studies of Blanes Accés Cala Sant Francesc, 14 17300 Blanes (Girona)

Xavier Turon <[xturon@ceab.csic.es](mailto:xturon@ceab.csic.es)>

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## MuensterU EvolNicheConstruction

Postdoctoral Research Associate

Evolution under niche construction in the red flour beetle *Tribolium castaneum*

The Institute for Evolution and Biodiversity at the University of Muenster, Germany, is seeking to fill the position of a Postdoctoral Research Associate (salary level TV-L E 13, 100%) from the earliest possible date. The position is within the externally funded project SFB/TRR 212. We are offering a fixed-term full-time position until 31 December 2025 corresponding to the duration of the project. The position can also be filled as a part time position.

Your tasks: The position is part of the Collaborative Research Centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3), by the German Research Foundation (DFG).

This project focuses on individualised niches in the red flour beetle *Tribolium castaneum*, an upcoming and genetically tractable insect model species. Flour beetles modify the microbial community of their environment (the flour), which is mediated by chemical secretions from the beetles. The successful candidate will be involved in an ongoing project that aims to experimentally study, if and how the processes of niche construction and evolutionary capacitance facilitate evolutionary adaptation. It involves testing the hypotheses that (1) chemical communication via CHC profiles provides the basis for the transfer of individual experience into a group of beetles; (2) epigenetic processes contribute to the rapid adaptation facilitated by niche construction and evolutionary capacitance; and (3) rapid adaptation to new temporal niches is facilitated by evolutionary capacitance. The successful candidate will draw on an ongoing experimental evolution study and existing beetle lines to identify the genetic and epigenetic underpinnings of evolved phenotypes, and study the chemical ecology of beetle communication and biological rhythms of beetles in relation to cryptic genetic variation that may facilitate temporal niche adaptation.

Our expectations: The successful candidate will be a highly motivated scientist, interested in interdisciplinary work. They will have a doctoral degree (or a comparable

qualification) in biology, preferentially with a focus on evolution, behaviour, ecology, genomics or related fields. They will also have a background, and ideally some postdoctoral experience, in at least one of the following areas: practical insect work, molecular skills, genomics and bioinformatics, as well as a good understanding of statistics. They will also have excellent communication skills and be able to work both independently and as part of a multidisciplinary team. The working language of the Institute and the lab is English, and good proficiency in spoken and written English is a requirement. German language skills are not a requirement, but a willingness to learn is desirable. Advantages for you:

The Institute for Evolution and Biodiversity provides a stimulating research environment with a number of scientific groups researching diverse topics centred on different aspects of evolution. As a part of the Collaborative Research Centre SFB/TRR 212 ([https://www.uni-bielefeld.de/fakultaeten/biologie/-forschung/verbuende/sfb\\_nc3/](https://www.uni-bielefeld.de/fakultaeten/biologie/-forschung/verbuende/sfb_nc3/)), the project will involve intensive collaboration with consortium partners at the Universities of Muenster and Bielefeld. The University of Muenster: 45,000 students and 8,000 employees in teaching, research and administration, all working together to shape perspectives for the future. Embedded in the vibrant atmosphere of Muenster with its high standard of living, the University's diverse research profile and attractive study programmes draw students and researchers throughout Germany and from around the world.

The University of Muenster strongly supports equal opportunity and diversity. We welcome all applicants regardless of sex, nationality, ethnic or social background, religion or worldview, disability, age, sexual orientation or gender identity. We are committed to creating family-friendly working conditions. Part-time options are generally available.

We actively encourage applications by women. Women with equivalent qualifications and academic achievements will be preferentially considered unless these are outweighed by reasons which necessitate the selection of another candidate.

Are you interested? Then we look forward to receiving your application, written in English, in one single pdf file, by 15 April 2024. Applications should be sent to Prof Joachim Kurtz at: [Joachim.Kurtz@uni-muenster.de](mailto:Joachim.Kurtz@uni-muenster.de). Please note that we cannot consider other file formats. Applications should include 1) a cover letter with a statement of research interests and motivation (max. 1 page), 2) a CV including details about research experience and publications, and 3)

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## Okinawa IST Evolutionary Ichthyology

Okinawa Institute of Science and Technology Postdoctoral Scholar or Staff Scientist in Ichthyology

A postdoctoral scholar (PhD 5 years) or staff scientist position (PhD 5 years) is available in the Macroevolution Unit at OIST. We seek a highly motivated, expert researcher with a deep knowledge of fish biodiversity, including but not limited to systematics, taxonomy, ecology, and the fossil record. The researcher will pursue groundbreaking projects on ichthyological topics, such as the origins of the Indo-Pacific biodiversity hotspot, the origins and diversification of fish groups, description and characterization of species and communities, and/or the influence of environmental and ecological factors on fish biodiversity. Exact projects will be developed through discussions with PI Sallan based on the skills, interests, and ideas of the selected researcher.

Responsibilities:

Develop and lead innovative projects related to the ichthyological interests of the Macroevolution Unit. Publish results in high-quality journals. Present at national and international conferences.

Qualifications:

(Required)

PhD in Ecology and Evolutionary Biology, Marine Biology, Paleontology, Organismal Biology or related field with dissertation focused on fishes. Experience and interest in fish biodiversity. Willingness to develop knowledge about areas and clades of interest to the unit if outside of past experience (e.g. fishes). Willingness to learn new methods as needed. Willingness to travel to museum collections or collect specimens as needed. Willingness to collaborate with other relevant labs at OIST and outside. Good spoken and written English skills, including for scientific terms and concepts.

(Preferred)

Experience in either fish morphology, fish phylogenetics, marine field work and collections, or work with live fishes, depending on area of expertise.

Start Date: Negotiable from April 2024 (if in Japan already) through mid-2025. Promising senior graduate students and postdocs with time remaining in their current positions are encouraged to apply.

Term & Working hours: Full-time. A postdoctoral position (PhD5 years) is initially for one year and can be renewed to 2 more years based on performance and mutual agreement. A staff scientist position (PhD5 years) is initially for one year and can be extended further based on performance and mutual agreement.

Working hours:

Discretionary working hours

Compensation & Benefits: Compensation in accordance with the OIST Employee Compensation Regulations

Benefits:

Relocation, housing and commuting allowances Annual paid leave and summer holidays Health insurance (Private School Mutual Aid <http://www.shigakukyosai.jp/>) Welfare pension insurance (kousei-nenkin) Worker's accident compensation insurance (roudousha-saigai-hoshou-hoken)

Application Due Date:

Applications will continue to be screened until the position is filled.

Submission Documents:

Cover letter including statement of research interests

CV including the publication list

Contact information for 3 recommendation letters (will be contacted after first pass)

Apply At:

<https://www.oist.jp/careers/postdoctoral-scholar-or-staff-scientist-ichthyology-macroevolution-unit> Lauren Sallan <Lauren.Sallan@oist.jp>

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## Okinawa IST Two ModelbasedEvolutionaryGenomics

Join the Model-Based Evolutionary Genomics Unit (<https://www.oist.jp/research/research-units/-modevolgenom/>) for a postdoc and a senior postdoc (staff scientist) at the intersection of computational

and evolutionary biology. Our unit works to decode the complex patterns and processes that underpin the evolution of life across its myriad forms with a significant focus on reconstructing the Tree of Life and modeling the dependency between different levels of organization in biological systems. By employing probabilistic models and leveraging the power of machine learning, we aim to unravel the co-evolutionary dynamics that have shaped the Tree of Life, from the enigmatic origins of early life forms to the sophisticated structures of modern biological systems.

Current topics include:

- applying and developing phylogenetically-aware models of horizontal gene transfer in order to reconstruct eukaryogenesis and better understand gene transfer in eukaryotes;
- applying and developing molecular dating methods that use novel sources of timing information from transfers and correlations between phenotypes and ancient environments;
- reconstructing ancient phenotypes from genome-scale data using machine learning;
- adapting protein language models to reconstruct fitness landscapes and ancestral sequences;
- understanding somatic evolution in hierarchically organized tissues and across the Tree of Life from a theoretical standpoint (e.g., To what extent has tissue organization evolved to minimize somatic evolution in humans? Why do both plants and animals have stem cells?)

This postdoctoral position offers the freedom to pursue your own research ideas and provides a platform for innovation and discovery in a unit that thrives on intellectual curiosity and interdisciplinary collaboration. The position includes funding, provided by the budget of the Model-based Evolutionary Genomics Unit, to travel to international conferences as well as extended research visits to international collaborators, including Tom Williams at the University of Bristol, Anja Spang at NIOZ in the Netherlands, Phil Hugenholtz at the University of Queensland, and others.

Some recent papers of ours:

“A rooted phylogeny resolves early bacterial evolution” Coleman, Davin, Mahendrarajah, Szánthó, Spang, Hugenholtz\*, Szöllősi\*, Williams\* *Science* 2021 <https://science.sciencemag.org/content/372/-6542/eabe0511.abstract> “Divergent genomic trajectories predate the origin of animals and fungi” Ocaña-Pallarès, Williams, . . . , Baptiste, Tikhonenkov, Keeling, Szöllősi, Ruiz-Trillo *Nature* 2022 <https://->

[www.nature.com/articles/s41586-022-05110-4](https://www.nature.com/articles/s41586-022-05110-4) “Trade-off between reducing mutational accumulation and increasing commitment to differentiation determines tissue organization” Demeter, Derényi, Szöllősi Nature Communications 2022 <https://www.nature.com/articles/s41467-022-29004-1> “Compositionally Constrained Sites Drive Long-Branch Attraction” Szánthó, Lartillot, Szöllősi\*, Schrepf\* Systematic Biology 2023 <https://doi.org/10.1093/sysbio/syad013> “AleRax: A tool for gene and species tree co-estimation and reconciliation under a probabilistic model of gene duplication, transfer, and loss” Morel, Williams, Stamatakis, Szöllősi Bioinformatics 2024 (to appear) <https://doi.org/10.1101/2023.10.06.561091> Okinawa Institute of Science and Technology

The Okinawa Institute of Science and Technology Graduate University (OIST; see [www.oist.jp](http://www.oist.jp)) is a dynamic new graduate university of science and technology in Okinawa Prefecture, Japan. The university is located on 85 hectares of protected forestland overlooking beautiful shoreline and coral reefs. The campus is striking architecturally, and the facilities are outstanding (OIST campus video tour). There are no academic departments, which facilitates multidisciplinary research. Outstanding resources and equipment are provided and managed to encourage easy access and collaboration. English is the official language of the University, and the university research community is fully international, with more than 50 countries represented. OIST is rapidly gaining recognition in the worldwide academic community as a model for excellence in education and research.

Responsibilities:

Devise and carry out state-of-the-art interdisciplinary research in Evolutionary Biology, and have fun doing it!  
Collaborate with team members

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## OklahomaStateU BehavioralEvolution

Job Description: The Reichert lab in the Department of Integrative Biology at Oklahoma State University is seeking a postdoctoral researcher to work on an NSF

funded project on the energetic drivers of individual variation in animal communication behavior. The project focuses on the relationship between metabolic rate and acoustic signaling behavior in gray treefrogs and will involve field recordings of acoustic signals, playback experiments to assess behavioral plasticity, measurement of metabolic rate using respirometry and investigations of the genetic basis of metabolic and behavioral phenotypes. The postdoc will be expected to lead the data collection on project experiments, develop new projects in line with their interests and the aims of the grant, communicate project results through scientific publications and presentations and contribute to student mentorship. The Reichert lab is dedicated to the professional development of all lab members and there will be opportunities to develop skills in teaching, mentorship and outreach. The lab is also dedicated to a research environment that is supportive of all members. The position can start as early as April 15, 2024, but the start date can be adjusted based on the selected candidate's availability.

Requirements: The candidate should have earned a Ph.D. in ecology, evolution, behavior or a related field by the time they are hired, and should be experienced in working on large-scale research projects. In addition, the candidate will have experience working with data curation, analysis and scientific publication, and have the ability to work collaboratively with the PI and others on the project in both field and lab settings. Candidates with experience in any of the following are especially encouraged to apply: bioacoustics, behavioral energetics, behavioral genetics, individual behavioral variation, advanced mixed modeling techniques. Duration: 12 months, with the possibility to extend up to 03/31/2029 contingent upon performance and available funding.

Oklahoma State University, as an equal opportunity employer, complies with all applicable federal and state laws regarding non-discrimination and affirmative action. Oklahoma State University is committed to a policy of equal opportunity for all individuals and does not discriminate based on race, religion, age, sex, color, national origin, marital status, sexual orientation, gender identity/expression, disability, or veteran status with regard to employment, educational programs and activities, and/or admissions. For more information, visit <https://eeo.okstate.edu> To apply please submit a cover letter describing interest in the project and previous research experience, and a current CV to <http://apply.interfolio.com/143528>. Two letters of reference should be also be submitted by the applicant's academic referees to the Interfolio platform. Applications will be evaluated until the position is filed, but review of applications will begin April 5, 2024 and the aim is to have the

position filled prior to summer fieldwork if possible. For further information about the position, please contact Michael Reichert: (michael.reichert@okstate.edu).

michael.reichert@okstate.edu

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## PennsylvaniaStateU ForestGenomics

The Hamilton Lab (<http://jillahamilton.com/index.html>) at Pennsylvania State University in State College, Pennsylvania is seeking to hire a Postdoctoral Scholar to contribute to an USDA funded research program aimed at leveraging genotype-phenotype-environment associations to assist projections needed to make assisted population migration projections, ultimately laying a foundation for climate-smart forestry. The project includes a collaboration with Dr. Laura Leites and Dr. Kim Steiner leveraging mature black walnut provenance trials and associated genomic and phenotypic data. The researcher will analyze reduced representation sequencing datasets alongside phenotypic data (annual growth tree rings, phenology, and more), and climatic data from black walnut provenances planted in a common gardens established at The Pennsylvania State University. The post-doctoral position is highly interdisciplinary, combining phenotypic data with genomic data to associate genomic variation with environment of origin (GEA) and phenotypic variation (GPA) expressed in the common garden environment. A major goal will be to build upon new methods of prediction in genotype-phenotypic and genotype-environment associations that will be directly applicable to delineation of assisted migration population strategies and climate-adjusted seed source provenancing, critical tools of climate-smart forestry. In addition to specific project objectives, there is ample opportunity to collaborate on existing projects and develop new lines of research in genomic prediction broadly related to climate-smart forestry.

The postdoctoral scholar will be expected to analyze genomic, phenotypic, and climatic datasets, lead preparation and publication of peer-reviewed manuscripts, 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, building upon rich provenance datasets and existing

genomic data available through the Schatz Center for Tree Molecular Genetics.

This is a limited-term position funded for one year from date of hire with an excellent possibility of renewal 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, ecological genetics, 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 Ph.D. prior to the effective date of hire. Familiarity with analyzing reduced representation sequencing datasets and expertise in genomic prediction relating genomic data to phenotypic or environmental data are required.

Application Information:

Interested applicants should submit a cover letter describing research interests and experience, a curriculum vitae, and contact information for three professional references to the application link below on <https://hr.psu.edu/careers>. Review of applications will begin immediately and continue until the position is filled. Informal inquiries are welcome - contact Jill Hamilton (jvh6349@psu.edu).

< [https://psu.wd1.myworkdayjobs.com/en-US/-PSU\\_Academic/job/Climate-Smart-Forest-Genomics-Postdoctoral-Scholar\\_REQ\\_0000054149-1](https://psu.wd1.myworkdayjobs.com/en-US/-PSU_Academic/job/Climate-Smart-Forest-Genomics-Postdoctoral-Scholar_REQ_0000054149-1) > Climate Smart Forest Genomics Postdoctoral Scholar 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)

“Hamilton, Jill” <jvh6349@psu.edu>

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## QueenMaryU London BayesianPhylogenetics

Postdoc position in Bayesian Phylogenetics

School of Biological and Behavioural Sciences Queen Mary University of London, London, UK

Salary: £37,182 to £44,722 per annum

Deadline: 29th April 2024

Apply: <https://qmul-jobs.tal.net/vx/candidate/apply/-1807> Applications are invited for a Postdoctoral Research Assistant (PDRA) to work at the School of Biological and Behavioural Sciences (SBBS) in the research group of Dr. Mario dos Reis, as part of a BB-SRC project on development of Bayesian methods to analyse large genomic datasets. We seek a highly motivated individual with relevant background in statistics/physics/computational biology. The successful candidate will contribute to real data analyses and to the development of Bayesian MCMC algorithms in the MCMCtree software and associated R packages. We are interested in Hamiltonian Monte Carlo and covariance-informed MCMC samplers. The project is a collaboration with Prof. Ziheng Yang (UCL) and Prof. Philip C. J. Donoghue (Bristol University).

A PhD in a subject relevant to the project is essential. This is an integrative project and relevant subject areas include computational biology, bioinformatics, physics, statistics, computer science and related. Experience of code development in a major programming language (such as C, C++ or Java) is essential. Experience of phylogenetics software development, use of high-performance computing facilities, evolutionary biology, MCMC sampling algorithms, and genome data analysis are desirable but not essential. You should have excellent communication skills, with the ability to present your research findings both orally and in writing. You must have excellent time management skills, and the ability to complete large tasks on a schedule. The project is highly collaborative, and you are expected to work well within a team, and have the ability to deliver production-ready software for use by other team members.

As a member of the dos Reis group (<https://dosreislab.github.io>) you will be part of a dynamic research community at SBBS (<https://www.qmul.ac.uk/sbbs/>). The school employs circa 120 academics working

in evolutionary biology, genomics, cell biology, ecology, and experimental psychology.

Mario dos Reis

Reader in Statistical Phylogenetics Queen Mary University of London <https://dosreislab.github.io> Mario dos Reis <mariosdosreis@gmail.com>

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## Shanghai BacterialEvolution

Two postdoctoral positions are available in the group of Daniel Falush, Shanghai Institute of Immunity and Infection, Chinese Academy of Sciences, exploring complex adaptation within bacterial populations, The first postdoc will do bacterial evolutionary genomics, for example identifying complex adaptations and elucidating their evolutionary history, The second postdoc will perform laboratory experiments, to elucidate the the ecological function of the complex adaptations.

Genomics position: [http://english.siii.cas.cn/join/-pf/202402/t20240227\\_657733.html](http://english.siii.cas.cn/join/-pf/202402/t20240227_657733.html) Molecular genetics position: [http://english.siii.cas.cn/join/pf/202402/-t20240227\\_657734.html](http://english.siii.cas.cn/join/pf/202402/-t20240227_657734.html) Shanghai is a liveable and safe city and a gateway to explore Asia.

[danielfalush@gmail.com](mailto:danielfalush@gmail.com)

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## SouthAfrica EvolutionaryGenetics

The Conservation and Population Genetics Group in the Department of Genetics at the University of the Free State, and the Centre for Ecological Genomics and Wildlife Conservation at the University of Johannesburg, invite expressions of interest for a joint postdoctoral fellowship to the value of R250 000 (~US\$ 13,400) per annum. The fellowship is awarded over a period of 2 years, during which the applicant will spend 1 year at the one university and 1 year at the other.

Candidates should have substantial experience in the analysis of genetic and/or genomic data by means of

unix-based applications, including high performance computing. The successful applicant will work on existing or new projects in a wide variety of fields, which may include population genetics/genomics, phylogenetics/genomics and eDNA metabarcoding. Projects typically focus on eukaryote species of conservation concern, or document biodiversity.

This is an excellent opportunity for young researchers (with a PhD awarded within the past 5 years) to boost the number of research outputs on their CV. They will also gain experience in student supervision by being officially registered co-supervisors of postgraduate students (MSc and PhD level).

Interested candidates should send the following documents to Prof. Paul Grobler (Grobler.JP@ufs.ac.za) and Prof. Peter Teske (pteske101@gmail.com); the review of applications will commence immediately:

\* A motivation letter not exceeding 1 page in which the applicant briefly summarises skills and interests (with a particular focus on experience in unix-based analyses and other skills relevant to this position) \* A short CV (1-2 pages) that includes key publications; do not include predatory journals (<https://beallslist.net/standalone-journals/>) \* Proof of having completed a PhD no earlier than 2019 (e.g. a scan of the PhD certificate or academic record) \* PDF of at least one published (or in press) scientific paper that is relevant to this position (at least one first authorship is a prerequisite) \* Contact details of three references

The most suitable candidate will be selected by March 20, and is then expected to work with the hosts on a project proposal that needs to be submitted online by March 24. The actual commencement of the position is flexible, but should be no later than 3 months after the outcome of the application has been announced.

Please see the following website for details on this position: <https://www.uj.ac.za/postgraduate-school/postdoctoral-research-fellows/funding-opportunities/> Peter Teske <pteske101@gmail.com>

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## Southwest Fisheries Center Two Genomics

Dear colleagues,

My apologies to anyone who receives this announcement multiple times, but we are trying to spread the word far and wide about two postdoc positions we'd like to fill as soon as possible. Please share the announcement below with anyone you think might be interested.

Cheers, Eric

\*The Opportunities:\* The Marine Mammal and Turtle Division (MMTD) and Fisheries Resources Division (FRD) at the Southwest Fisheries Science Center (NOAA/NMFS) seek highly motivated candidates for two Postdoctoral Research Associate positions. Both research divisions have several funded projects focused on developing and using genomic tools to investigate the ecology, evolution, and population dynamics of various marine mammal, sea turtle, and fish species to contribute to their conservation and management. Both postdocs will participate in a larger network of bioinformatics specialists across NOAA genetics labs.

One postdoc will lead a project within the Marine Mammal Genetics Program (MMGP) designed to generate the data sets and code needed to develop large SNP panels for multiple marine mammal species that are of high management concern. The data generated in the core project will provide exciting opportunities to pursue projects on comparative genomics, population structure, and demography.

The second postdoc will lead a project to develop and enhance workflows to examine spatial and temporal variability of marine mammals, sea turtles, fishes, and abalone from eDNA samples collected from the Southern California Bight from multiple platforms.

These are 3-year, full-time positions offering comprehensive benefits packages, including moving expenses. The positions are based in La Jolla, CA, open to everyone, regardless of citizenship.

\*Qualifications:\* Candidates must have bioinformatics experience, including managing and analyzing large genetic datasets, producing workflows for genomic data analysis, and familiarity with using GitHub for version control and collaborative coding. In addition, the candidate should be proficient with programming in R and

bash, and with working in the LINUX command line environment. Laboratory experience with next generation sequencing protocols, such as ddRAD or low-coverage whole genome sequencing, is beneficial but not required. Applicants must have earned a Ph.D., Sc.D., M.D., D.V.M., or academically equivalent research doctorate no more than five years prior to applying.

Anyone interested in applying should contact Karen Martien ( Karen.Martien@noaa.gov), Eric Archer (Eric.Archer@noaa.gov), or Aimee Lang ( Aimee.Lang@noaa.gov). Additional information regarding benefits and the application process can be found at <https://www.nationalacademies.org/our-work/rap/for-applicants> . –

\*Eric Archer, Ph.D. \*(he/him/his < <https://www.glsen.org/activity/pronouns-guide-glsen> >) Leader, Marine Mammal Genetics Program < <https://www.fisheries.noaa.gov/west-coast/science-data/marine-mammal-genetics-research> > Southwest Fisheries Science Center (NMFS/NOAA) 8901 La Jolla Shores Drive La Jolla, CA 92037 USA 619-837-3170

Adjunct Professor, Marine Biology < <http://profiles.ucsd.edu/frederick.archer> > Scripps Institution of Oceanography University of California, San Diego

GitHub: [github.com/ericarcher](https://github.com/ericarcher) ORCID: <https://orcid.org/0000-0002-3179-4769> “\*The universe doesn’t care what you believe. The wonderful thing about science is that it doesn’t ask for your faith, it just asks for your eyes.\*” - Randall Munroe

“\*Lighthouses are more helpful than churches.\*” - Benjamin Franklin

“\*...but I’ll take a GPS over either one.\*” - John C. “Craig” George

Eric Archer - NOAA Federal <eric.archer@noaa.gov>

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## StellenboschU eDNAMetabarcodingInAfrica

Postdoctoral fellowship in eDNA metabarcoding of freshwater and marine aquatic biodiversity in southern Africa  
Applications are open for a full-time, two-year postdoctoral position to be hosted by the von der Heyden lab at the Department of Botany and Zoology at Stellenbosch

University, South Africa. The successful fellow will take on a leading role projects that makes use of eDNA metabarcoding and species distribution modelling of fish and invertebrate communities in southern Africa and investigate the use of metabarcoding data for various ecological questions. This is a unique opportunity for someone interested in the application of eDNA surveys for conservation and management of biodiversity, whilst seeing southern Africa and supporting the establishment of eDNA surveys for biomonitoring in the region. The primary focus of our research projects is to use environmental DNA metabarcoding to characterise community diversity in a variety of marine (South African coastline) and freshwater ecosystems (Okavango Delta), to not only allow comparison between sites, but to assess this methodology as a tool for monitoring ecosystems changes. Our lab has built significant expertise in developing and carrying out eDNA based research in marine and freshwater ecosystems in the region. The project is based in the research group of Prof. Sophie von der Heyden and has collaborators in Botswana, Switzerland and Namibia. The starting data for this position is flexible, but ideally no later than May/June 2024.

Qualifications and experience: Applicants will require a PhD (obtained within the last four years), with preference given to applicants with a strong background in at least one, but ideally two, of the following fields: eDNA metabarcoding, molecular ecology, species distribution modelling, biological statistics, coastal ecology or freshwater biology. Applicants should have at least three peer-reviewed outputs in an international peer-reviewed journal; the outputs need to demonstrate senior/lead authorship with a strong focus on eDNA metabarcoding in aquatic environments. A valid driver’s license is a requirement due to the extensive field work along the South African coastline. Applicants should be motivated, independent, and willing to engage and mentor postgraduate students at several levels (ranging from Honours to PhD), as well as be willing to work in remote environments. There is a fieldwork component in Botswana and along the South African coastline.

Responsibilities: Applicants will be required to collaborate with all collaborators and students, with the fellow be able to plan and lead field trips, as well as analyse data, writing and publication of peer-reviewed articles, presentations at national and international conferences, and science communication initiatives. Mentorship and some teaching opportunities will be possible for the successful fellow depending on level of experience.

Duration: This is a two year position ideally starting no later than May/June 2024.

Value: The position carries a value of R350 000 per year



(tax free), which comfortably covers needs of living in Stellenbosch and is available for two years. Relocation costs (flights) can be covered.

Background: The postdoctoral fellow will be based at the von der Heyden Lab at Stellenbosch University, one of Africa's leading aquatic (marine, estuarine and freshwater) research groups specializing in the use of molecular tools to understand patterns and processes driving southern Africa's rich marine biodiversity. We are a dynamic lab, with a strong emphasis on research excellence as well as student training and support. Our work spans population genetics and phylogeography, fisheries management/stock identification, historical biogeography and the impacts of historical and contemporary climate change on species distributions. To do this, we utilise a wide range of tools including genomics and environmental DNA, with our overarching goal of promoting the integration of molecular tools into conservation and sustainable utilization of southern African marine species and resources. You can find out more about the von der Heyden lab and marine research at Stellenbosch University here: [www.vonderheydenlab.com](http://www.vonderheydenlab.com), via Facebook: [www.facebook.com/vonderheydenlab](https://www.facebook.com/vonderheydenlab). The vdH lab is housed in the Department of Botany and Zoology at the University of Stellenbosch. This university is one of the top-ranked in the southern Hemisphere, with strong undergraduate and postgraduate training and research. Stellenbosch is a historical, safe and vibrant community surrounded by magnificent mountains, close to the sea and ideal for nature (and wine) enthusiasts. Find out more at [www.sun.ac.za](http://www.sun.ac.za). Queries and applications: Please direct all enquiries to Prof. Sophie von der Heyden ([svdh@sun.ac.za](mailto:svdh@sun.ac.za)). In order to apply, please submit (1)

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## UArkansas NeuroEvoDevo

An NSF-funded postdoctoral fellow position is available in the Nakanishi lab (<https://wordpressua.uark.edu/~nakanishi-lab/>) at the Department of Biological Sciences, University of Arkansas. The primary field of the lab's research is cnidarian evolutionary developmental biology. In particular, this NSF-funded project will investigate

the mechanism of life cycle transition, focusing on elucidating how neuropeptides control this process using the sea anemone *Nematostella vectensis*.

We are seeking a highly motivated and independent scientist with strong interests in advancing our understanding of the mechanism of cnidarian life cycle transition. The specific focus of the project will include 1) identification of neuropeptide receptors that are involved in metamorphosis regulation, and 2) characterization of the identity and function of transcription factors that are regulated by neuropeptidergic signaling at metamorphosis. In addition, the postdoc will be encouraged to develop an independent line of research that is broadly related to the NSF project theme and research interests of the lab. Moreover, the postdoc will have opportunities to mentor diverse students at the high school, undergraduate and graduate levels.

This is a full time, 40 hour per week position. The salary is commensurate with experience and education and includes full benefits. This is a one-year appointment, with the possibility to extend up to two additional years renewable based on the need for the position, availability of funding, and continued satisfactory level of performance in the role.

For a complete position announcement and information regarding how to apply, [https://uasys.wd5.myworkdayjobs.com/en-US/UASYS/job/Postdoctoral-Fellow-in-Biology\\_R0053001?locations=-17a66cdad98201f7890cfb48ca00e249](https://uasys.wd5.myworkdayjobs.com/en-US/UASYS/job/Postdoctoral-Fellow-in-Biology_R0053001?locations=-17a66cdad98201f7890cfb48ca00e249). Applicants must submit a curriculum vitae, a cover letter/letter of application, and a list of three professional references (name, title, email address, and contact number). For more information, please contact Nagayasu Nakanishi, Associate Professor in Biological Sciences, at [nnakanis@uark.edu](mailto:nnakanis@uark.edu).

The University of Arkansas is an equal opportunity, affirmative action institution. The university welcomes applications without regard to race/color, sex, gender, pregnancy, age, national origin, disability, religion, marital or parental status, protected veteran or military status, genetic information, sexual orientation, gender identity or any other characteristic protected under applicable federal or state law. Persons must have proof of legal authority to work in the United States on the first day of employment. All applicant information is subject to public disclosure under the Arkansas Freedom of Information Act.

Nagayasu Nakanishi, Ph.D Associate Professor Department of Biological Sciences University of Arkansas Fayetteville, AR 72701 479-575-2031 (office) 479-575-7393 (lab) [nnakanis@uark.edu](mailto:nnakanis@uark.edu) <https://wordpressua.uark.edu/~nakanishi-lab/> nagayasu nakan-

ishi <nagayasul@gmail.com>

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## UArkansas TraitEvolution

A postdoctoral research associate position is available in the Zhuang Lab in the Department of Biological Sciences, University of Arkansas. We are looking for highly motivated researchers who are willing to tackle fundamental questions in both basic evolution and biomedical research. Research interests in the Zhuang Lab include understanding the genetic basis of complex trait variation and novel trait evolution, involving the genetic architecture of complex diseases, the origination of genetic novelty and diversity, and the underlying molecular mechanisms. Employing molecular evolution, quantitative genetics, genomics, and bioinformatics, the research group conducts studies on both model organisms, such as fruit flies, and non-model organisms, such as polar fishes.

### Qualifications

\* Ph.D. in Quantitative Genetics, Evolutionary Genetics, Statistical Genetics, or related fields; \* Proficiency in R and Python or other programming languages; \* Experience analyzing omic data sets (e.g. genome, transcriptome, metabolome, etc.); \* Good understanding of evolution and genetics theory and methodology; \* Strong written and oral communication skills, and ability to work independently and in collaboration with others.

### Responsibilities

The postdoc fellow will lead a NIH funded project to investigate cryptic genetic variation and gene-environment interaction underlying complex disease traits related to metabolism using *Drosophila* models. The primary responsibilities of this position are developing and implementing computational pipelines to carry out genetic mapping analysis, and genome/transcriptome/metabolome wide association studies, interpreting and organizing results into publishable papers and grant proposals. Other responsibilities include data management, mentoring students, and providing bioinformatics support for the lab.

### Application Instructions

Please email Dr. Zhuang (xz036@uark.edu) the follow-

ing materials:

- (1) CV (includes publications and pre-prints),
- (2) a cover letter outlining previous research experience and future plans, specifically how they are related to the research focus in our lab,
- (3) contact information for two references.

### About the University

Founded in 1871, the University of Arkansas is a land grant institution, classified by the Carnegie Foundation among the nation's top 2 percent of universities with the highest level of research activity (R1 University). The University of Arkansas campus is located in Fayetteville, a welcoming community ranked as one of the best places to live in the U.S. The growing region surrounding Fayetteville is home to numerous Fortune 500 companies and one of the nation's strongest economies. Northwest Arkansas is also quickly gaining a national reputation for its focus on the arts and overall quality of life. Arkansas is a natural wonder of forests, mountains and lakes framed by picturesque rivers and streams. Some of the best outdoor amenities and most spectacular hiking trails are a short drive from campus.

xz036@uark.edu

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## UCalifornia Berkeley EvolutionaryGenomics

### Postdoc in Evolutionary Genomics, UC Berkeley

1-2 NIH-funded postdoctoral positions are available in Doris Bachtrog's group at UC Berkeley. The details of the project are flexible, but should fall within the general interests of the lab. Current research focuses on using cutting-edge genomic and molecular techniques to study sex chromosomes, heterochromatin, transposable elements, meiotic drive, aging and speciation in insects. For more information on current research, see: <https://bachtroglabberkeley.wordpress.com/> Candidates must have a background in either *Drosophila* molecular genetics and genomics (including transgenics) or must have solid programming and bioinformatics skills. Our group shares newly renovated office space with the groups of Rasmus Nielsen, Monty Slatkin and John Huelsenbeck, and strong intellectual ties, including weekly meetings, with other research groups at the

Center for Theoretical Evolutionary Genomics at UC Berkeley (cteg.berkeley.edu/).

Potential projects in the lab include

1 Toxic Y chromosomes: Y chromosomes of many organisms contain large numbers of transposable elements (TEs) that are transcriptionally constrained by repressive chromatin marks. When relieved of these epigenetic modifications, many TEs can readily move from one genomic location to another (toxic Y chromosomes). What are the phenotypic and evolutionary consequences of toxic Y's?

2 Sex chromosome drive and amplified genes: Sex chromosome drive may be common in nature but short-lived due to the quick invasion of suppressor alleles. Can we identify cryptic sex chromosome drive systems by scanning sex chromosomes in *Drosophila* for the footprints associated with known meiotic drive elements, and rigorously validate and characterize them using functional genomic, transgenic and cell biology approaches?

3 Sex chromosome evolution in insects. The evolution of differentiated sex chromosomes (e.g., X and Y or Z and W) from ordinary autosomes has occurred many times in animals and plants. Can we establish general principles underlying the evolution of sex chromosomes and the molecular mechanisms across the most speciose group of animals on earth?

UC Berkeley has a world-class community of evolutionary biologists using genomic approaches spanning the Department of Integrative Biology, the Museum of Vertebrate Zoology, the Department of Molecular and Cell Biology, the Center for Theoretical Evolutionary Genomics, the Center for Computational Biology, the Integrative Genomics Institute, and more. The city of Berkeley and the surrounding San Francisco Bay Area is known for its progressive values, vibrant social and cultural scene, and beautiful surrounding environment.

Interested candidates should submit a cover letter detailing their interest in the position and relevant experience along with their CV and contact information for three references to Doris Bachtrog (dbachtrog@berkeley.edu)

This position is open until filled, but applications will be reviewed starting two weeks after this posting. Please feel free to contact me with any questions.

Doris Bachtrog UC Berkeley <https://bachtroglabberkeley.wordpress.com/> Doris Bachtrog <dbachtrog@berkeley.edu>

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## UCalifornia Berkeley PupfishEvolution

Postdoctoral position on the evolution, genomics, and development of trophic specialization and novel craniofacial morphology in Caribbean pupfishes

The Martin Fish Speciation Lab at the University of California, Berkeley in the Department of Integrative Biology and Museum of Vertebrate Zoology seeks a post-doctoral scholar for genomic, phenotypic, functional, and/or developmental studies of adaptive phenotypes in a radiation of trophic specialist pupfishes. Pupfishes present a rare opportunity to investigate the rare origins of adaptive radiation and the evolution of novel niches (e.g. scale-eating) localized to only two locations, San Salvador Island in the Bahamas and Laguna Chichancanab in Mexico, despite thousands of similar Caribbean environments. This position includes opportunities for fieldwork with collaborators in Mexico, but no previous field experience is necessary and participation is not required.

We are seeking postdoctoral applicants with expertise or interest in \*genomics, phenomics, functional morphology, genetics, or craniofacial development\*.

Multi-year positions are available (initial 24-month appointment with the possibility of renewal for three more years). This research is funded by NIH NIDCR R01 and NSF CAREER grants. Start date is flexible. Salary is based on the recently negotiated rates for the UC system, commensurate with experience, approximately \$67,000 per year with annual raises.

Potential projects in the lab include:

- 1) Characterization of adaptive morphology within San Salvador Island or Chichancanab pupfishes using micro-CT scans, GWAS, QTL mapping, and analyses of selective sweeps and introgression.
- 2) Validation of candidate adaptive variants using HCR in situ hybridization, reporter assays, CRISPR-Cas9 knockouts, chemical inhibition, or other developmental approaches in the pupfish system.
- 3) Connecting specific phenotypes to performance through behavioral assays and kinematic studies of feeding success.

Required qualifications:

Ph.D. or equivalent degree in biology, evolution, genetics, development, bioinformatics, or related field. Publication of work based on dissertation.

Preferred qualifications:

Strong background in either genomics, phylogenetic comparative methods, microCT analysis, or evolutionary developmental biology.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sexual orientation, gender identity, national origin, disability, age, or protected veteran status.

UC Berkeley has a world-class community of integrative biologists studying adaptive radiation spanning the Department of Integrative Biology, the Museum of Vertebrate Zoology, the Department of Environmental Science, Policy, and Management, the Department of Molecular and Cell Biology, the Center for Theoretical Evolutionary Genomics, and more. The City of Berkeley and the surrounding San Francisco Bay Area is known for its progressive values, vibrant social and cultural scene, and beautiful surrounding environment.

Interested candidates should submit a cover letter detailing their interest in the position and relevant experience along with their CV to Chris Martin at [chmartin@berkeley.edu](mailto:chmartin@berkeley.edu)

This position is open until filled, but applications will be reviewed immediately after this posting. Please feel free to contact me at the below email address with any questions.

Christopher Martin

Associate Professor and Curator of Ichthyology Department of Integrative Biology and Museum of Vertebrate Zoology University of California, Berkeley

[chmartin@berkeley.edu](mailto:chmartin@berkeley.edu)

<https://ib.berkeley.edu/labs/martin/> @fishspeciation.bsky.social

[chmartin@berkeley.edu](mailto:chmartin@berkeley.edu)

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## UCalifornia Davis PlantBugPhylogenomics

The Bond Lab at the University of California, Davis and the Forthman Lab at the California Department of Food and Agriculture welcome applications for a postdoctoral researcher to focus on a collaborative phylogenomic project of the megadiverse plant bugs (Miridae).

**PROJECT POSITION:** The successful candidate will work with a multi-institutional team of researchers, involving the Bond and Forthman Labs, as well as the Weirauch Lab at the University of California, Riverside (lead project institution). The candidate will work closely with Ph.D. students and undergraduate interns to complete projects sponsored by a recent NSF award. Opportunities to develop complementary research questions and proposals with the project team will be encouraged. Considerable field collecting within the western US and in South Africa will take place throughout the position. The candidate will also participate in scientific outreach programs at CDFA and UCD to promote scientific discovery, agriculture, and biodiversity for public audiences of all ages. Note that this position will primarily take place at the California Department of Food and Agriculture Plant Pest Diagnostics Center (PPDC) in Sacramento, California. We are seeking a candidate with previous leadership and collaborative experiences, excellent communication and organization skills, a positive attitude, and motivation for learning new skills and knowledge. Prior research experience in systematics, evolution, phylogenetics, biodiversity, and/or entomology is also important.

**PROJECT DESCRIPTION:** This collaborative project will focus on the evolution of Miridae, a megadiverse and understudied insect family known as plant bugs. While most plant bugs are phytophagous with a limited host plant range, the group also includes predatory, mycetophagous, and zoophytophagous lineages, making this group economically important as crop pests and beneficial predatory insects. Plant bugs are extremely speciose in Mediterranean-type regions, including the California Floristic Province (CA-FP) biodiversity hotspot. Despite a substantial biodiversity dataset generated for plant bugs through past NSF-funding, its current utility is hindered by the absence of robustly supported phylogenetic hypotheses, limiting exploration of biogeographic history and host plant evolution. In this project,

we will:

1. Generate a worldwide phylogeny of plant bugs based on ultraconserved element (UCE) data to reconstruct robust tribal and subtribal-level relationships and investigate the temporal and diet evolution of the group.
2. Investigate the biogeographic history and host plant evolution of Nearctic Miridae, focusing on 12 well-documented clades, and determine the origin of taxa in the CA-FP.
3. Test if phylogenetic diversity of Miridae in the CA-FP shows similar patterns to those documented for plants and vertebrates.

The postdoc will lead sequence capture and processing for all three aims, and phylogenomic analyses including manuscript preparation for Aims 1 and 2 (in part). Postdoc mentoring will balance research, publications, presentations, grantsmanship, teaching, and outreach. The successful candidate will gain field experience, expertise in mirid systematics, including identifications, NGS and bioinformatics skills, and expertise with phylogenetic and downstream analyses (e.g., divergence dating, biogeography, phylogenetic diversity). The candidate will be involved in teaching a course-based undergraduate research experience class and a True Bug Short Course, as well as co-mentor undergraduate students.

#### QUALIFICATIONS:

- \* Hold a Ph.D. in evolutionary biology, entomology, or a related field
- \* Have demonstrated background in systematics with preference for insect systematics
- \* Have demonstrated skills in phylogenomic approaches from wet-lab procedures to bioinformatics
- \* Show skills in data analysis and scientific writing
- \* Show strong leadership qualities and excellent communication skills
- \* Work well in a team setting across multiple laboratories
- \* Have experience with mentoring students and interest in outreach activities

Preferred (not required) qualifications:

- \* Experience generating and analyzing UCE datasets
- \* Experience conducting field work

For additional details regarding the project, application materials, and application submission, see <https://recruit.ucdavis.edu/JPF06359>. Questions can be directed to Dr. Michael Forthman ([michael.forthman@cdfa.ca.gov](mailto:michael.forthman@cdfa.ca.gov)) and/or Dr. Jason Bond ([jbond@ucdavis.edu](mailto:jbond@ucdavis.edu)).

“Forthman, Michael@CDFA”  
<[Michael.Forthman@cdfa.ca.gov](mailto:Michael.Forthman@cdfa.ca.gov)>

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## UKansas DissectingComplexTraits

A postdoc position is available in my lab at KU to work on any of a number of quantitative/evolutionary genomics projects that use flies to understand and dissect complex trait variation. Projects emphasize the *Drosophila* Synthetic Population Resource (DSPR) that my group continues to develop. The formal job announcement, and links to the institutional employment website are provided below.

Feel free to email me with any questions about the position; I'm happy to talk more about possible projects. I'll also be at TAGC 2024 next week if anyone would like to chat.

Stuart Macdonald ([sjmac@ku.edu](mailto:sjmac@ku.edu))

Position Overview: The Macdonald group (<https://molecularbiosciences.ku.edu/people/stuart-j-macdonald>) uses a range of genetic, genomic and molecular technologies to dissect the genetic basis of complex phenotypic variation using *Drosophila* as a model system. We are also leading the development of the *Drosophila* Synthetic Population Resource (DSPR, <https://pubmed.ncbi.nlm.nih.gov/22496517>) in collaboration with Tony Long's group at UC Irvine. As part of the ongoing DSPR project (<https://reporter.nih.gov/project-details/10564298>) we aim to expand the utility of the resource for the fly community, explore novel powerful methods for QTL mapping (<https://pubmed.ncbi.nlm.nih.gov/35100395>), and examine the genetic basis of regulatory variation over time, focusing on the response to infection. The breadth of the project, and depth of the data we are collecting, allows for a range of questions to be addressed, providing the opportunity for the successful candidate to position themselves as an independent investigator. The position is funded through a multi-year NIH grant and has an anticipated start date of 10 June 2024 (although this is very flexible).

Job Description: 50% - Carry out primary research to understand the genetic basis of complex trait variation in *Drosophila*. A range of projects are possible using an array of approaches, from those that are heavily focused on the quantitative genetics of trait variation (e.g., identifying QTL for various traits of interest), to those that focus on genomics approaches and are more computational in scope (e.g., RNAseq-based response eQTL mapping).

20% - Present research results in scientific journals and at conferences/symposia.

15% - Work with other members of the research group to develop and execute collaborative projects.

10% - Help mentor and train junior researchers (graduate students, undergraduates).

5% - Pursue non-research professional development activities to advance your career goals.

Required Qualifications: (1) A PhD in evolution, genetics, genomics, or a related field. (2) A first-author publication/preprint that demonstrates experience initiating and executing a research project. (3) Experience with molecular/population/quantitative genetics, as evidenced by application materials and/or publications. (4) Previous experience with coding/scripting (e.g., R, Python) as evidenced by application materials.

Preferred Qualifications: (1) Prior experience with *Drosophila* as an experimental system. (2) Experience working with genomic datasets resulting from next-generation sequencing applications (e.g., whole genome sequencing, RNAseq). (3) Experience working with undergraduates or other researchers in a team setting.

Application:

For a complete announcement and to apply online, go to [employment.ku.edu/staff/27307BR](http://employment.ku.edu/staff/27307BR)

A complete application includes the following: (1) A cover letter outlining relevant experience and interest in the position, (2) a CV/resume highlighting pertinent experience relative to the required and preferred qualifications, and (3) contact information for three professional references.

Only complete applications will be considered. Informal queries about the position are welcome, and can be directed to Dr. Stuart Macdonald ([sjmac@ku.edu](mailto:sjmac@ku.edu), 785-864-5362).

Review of applications will begin on April 1, 2024 and will continue until the position is filled.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the university's programs and activities. Retaliation is also prohibited by university policy. The following persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Director of the Office of Civil Rights & Title IX, [civilrights@ku.edu](mailto:civilrights@ku.edu), Room 1082, Dole Human Development Center, 1000

Sunnyside Avenue, Lawrence, KS 66045,

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## ULausanne EvolutionaryDynamics

Introduction UNIL is a leading international teaching and research institution, with over 5,000 employees and 17,000 students split between its Dorigny campus, CHUV and Epalinges. As an employer, UNIL encourages excellence, individual recognition and responsibility.

Presentation The Group of Prof. Charles Mullon is proposing a Postdoctoral (Premier Assistant) position in Theoretical Evolutionary Ecology or Biology at the Department of Ecology and Evolution, University of Lausanne, Switzerland. The postdoc will join a dynamic team working mainly on developing and analyzing mathematical models to understand the evolutionary dynamics of traits that mediate interactions among individuals and with the environment. Interests include, but are not limited to, the evolution of sexual traits, genetic architecture, ecological interactions, niche construction, and social behaviour. For more information on the lab, visit <https://lab-mullon.github.io/>. Job information Expected start date in position : 01.07.2024 or to be agreed (up to 01.01.2025) Contract length : 1 year, renewable depending on funding availability Activity rate : 100% Workplace : Lausanne-Dorigny Annual gross salary : CHF 82'664.-

Your responsibilities The research project will be defined together with the group leader based on the Postdoc interests and competences in the field of theoretical evolutionary ecology. Most of her/his/their time will be dedicated to research, but a contribution to teaching is expected, including the possibility of supervising master students. The job description stipulates: 70% Personal research 25% Participation to teaching activities and master student supervision 5% Maintenance of lab equipment or other institutional tasks.

Your qualifications We are seeking to recruit someone with a strong interest and a PhD degree in evolutionary biology or ecology, with skills in mathematical or computational modelling.

## Interpersonal skills

- Good cooperative skills with other researchers and team members
- Good communication skills, ability to keep an open mind and to communicate your ideas
- Be motivated and be able to motivate others

What the position offers you We offer an outstanding working place in a multicultural, diverse and dynamic academic environment. Opportunities for professional training, a lot of activities and other benefits to discover. The Department of Ecology and Evolution in Lausanne University hosts research groups working on a broad range of topics, producing a rich intellectual and social life. Although French is the common language in Lausanne region, the department research activities and seminars are conducted in English. The campus is located on the shore of the Geneva Lake, with the view on the Alps.

Contact for further information For further information please contact Prof. Charles Mullon: [charles.mullon@unil.ch](mailto:charles.mullon@unil.ch)

Your application Deadline :12.04.2024 Formal applications should include: - a cover letter detailing your research interests, experience and motivation for applying (max. 2 pages);

- your CV;
- a copy of your PhD certificate; if you haven't yet finished your PhD indicate the scheduled or expected date. A contract as Postdoc/1er assistant can't be issued before the completion of the thesis. The applicant must have received his/her PhD in the last 2 years or be about to obtain a PhD very soon;
- the names of two or three referees;
- PhD thesis summary (approx. one page).

To receive full consideration, application documents should be uploaded online through the University of Lausanne recruitment platform: <https://bit.ly/3Vf7and> Review of applications will begin immediately.

Additional information UNIL is committed to equal opportunities and diversity. We actively encourage applications from individuals of diverse backgrounds, including but not limited to race, ethnicity, gender, sexual orientation, disability, and age. [www.unil.ch/egalite](http://www.unil.ch/egalite) UNIL supports early career researchers. [www.unil.ch/graduatecampus](http://www.unil.ch/graduatecampus) Charles Mullon <[charles.mullon@unil.ch](mailto:charles.mullon@unil.ch)>

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## UManchester Two AntibioticResistance PhageTherapy

Job reference: BMH-024933 Salary: pounds 30,487- pounds 34,980 depending on relevant experience (Pro rata) Faculty/Organisational Unit: Biology, Medicine Health Location: Oxford Road Employment type: Fixed Term Division/Team: Division of Evolution, Infection & Genomics Hours Per Week: 0.8fte Closing date: 18/03/2024 Contract Duration: From 1 April 2024 for 24 months School/Directorate: School of Biological Sciences

Opportunity to join a diverse research group studying microbial evolution. The successful candidate will work as part of an interdisciplinary team of researchers based at four UK universities to investigate the evolution of antibiotic resistance in bacterial human airway infections using a combination of genomics and experimental evolution. This project is funded by a Wellcome Trust Collaborative Award.

The main duties of this role include performing microbiology and molecular biology experiments, conducting high-throughput assays for phenotyping experimentally evolved and clinical bacterial isolates, and long-term experimental evolution. The postholder will collaborate closely with project researchers both at Manchester and the other collaborating universities. In addition, the successful candidate will be responsible for management of the laboratories at Manchester, including managing research budgets and resources, and overseeing compliance with relevant regulations.

The candidate will have a BSc (Hons) in biology or microbiology, experience of evolutionary microbiology research, and possess technical skills in microbiology and molecular biology. Candidates with training in molecular or medical microbiology are strongly encouraged to apply.

What you will get in return: - Fantastic market leading Pension scheme - Excellent employee health and wellbeing services including an Employee Assistance Programme - Exceptional starting annual leave entitlement, plus bank holidays - Additional paid closure over the Christmas period - Local and national discounts at a range of major retailers

As an equal opportunity employer we welcome applicants from all sections of the community regardless of age, sex,

gender (or gender identity), ethnicity, disability, sexual orientation and transgender status. All appointments are made on merit.

Our University is positive about flexible working ' you can find out more here Hybrid working arrangements may be considered.

Please note that we are unable to respond to enquiries, accept CVs or applications from Recruitment Agencies.

Any recruitment enquiries from recruitment agencies should be directed to People.Recruitment@manchester.ac.uk.

Any CV's submitted by a recruitment agency will be considered a gift.

Enquiries about the vacancy, shortlisting and interviews: Name: michael.brockhurst@manchester.ac.uk  
 General enquiries: Email: People.recruitment@manchester.ac.uk  
 Technical support: <https://jobseekersupport.jobtrain.co.uk/support/-home>  
 This vacancy will close for applications at midnight on the closing date. Please see the link below for the Further Particulars document which contains the person specification criteria. [https://www.jobs.manchester.ac.uk/-Job/JobDetail?JobId\(383\)](https://www.jobs.manchester.ac.uk/-Job/JobDetail?JobId(383))  
 Michael Brockhurst <michael.brockhurst@manchester.ac.uk>

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Job reference: BMH-025111 Salary: 36,024 - 39,347 per annum depending on relevant experience  
 Faculty/Organisational Unit: Biology, Medicine Health  
 Location: Oxford Road Employment type: Fixed Term  
 Division/Team: Division of Evolution, Infection & Genomics  
 Hours Per Week: Full Time (1 FTE) Closing date: 22/03/2024  
 Contract Duration: Until 13 February 2026  
 School/Directorate: School of Biological Sciences

We are seeking a postdoctoral research associate in microbial evolution as part of an interdisciplinary consortium developing synthetic phage technologies for use in phage therapy.

Phage therapy is a promising alternative to antibiotics and is likely to be an important part of the response to the global antimicrobial resistance crisis. Synthetic phages offer huge potential to deliver bespoke therapeutics. This project will develop synthetic phage technologies and this role will investigate their effectiveness as therapeutics and their eco-evolutionary biology.

This position provides an excellent opportunity for ambitious researchers interested in applying ecological and

evolutionary approaches to develop synthetic phage therapeutics to combat antibiotic resistance as part of an interdisciplinary team. The postholder will be embedded in a large community of microbial ecology and evolution researchers in Manchester, and will be encouraged to develop new lines of research and collaborations within the consortium.

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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>

## UMichigan DiversificationDynamics

### Postdoc positions

The Knowles lab at the University of Michigan is seeking to hire two postdocs to work on a collaborative NSF funded project. The work entails population level sampling across hundreds of species to test hypotheses about the controls on diversification in a spectacularly diverse genus of grasshoppers. More specifically, we are examining how opportunities for speciation as related to population splitting rates and the biogeographic context of divergence may contribute to difference in species diversity across North American grasshoppers. As a complement to this work, we are also characterizing rates of morphological divergence in male genitalia across species as a proxy for selectively driven divergence in traits related to the evolution of reproductive isolation.

We would like to hire two postdocs with complementary skill sets. For one postdoc line, experience in RAD-seq library construction and bioinformatic processing is required. Someone with an interest (and preferably experience) in population demographic modeling is also required. For the other postdoc position experience with geometric morphometrics and using phylogenetic frameworks to quantify rates of morphological evolution is required. Neither postdoc requires experience working with insects.

As a collaborative project, we are especially interested in people who enjoys working as part of team, mentoring undergraduate and graduate students, and participating in outreach activities. For both positions there are opportunities to develop side projects tailored to your



specific interests as it relates to biogeography, speciation, phylogeography, species distributional modeling, morphological evolution, phylogenetics, museum collections, and species delimitation. If you are interested and would like to discuss the positions in more detail, please contact L. Lacey Knowles; knowlesl@umich.edu. A PhD is required upon the start date of the position.

Postdoctoral Fellow positions are one-year term-limited positions, renewable annually based on performance, work authorization, and funding availability.

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

The University of Michigan conducts background checks on all job candidates upon acceptance of a contingent offer and may use a third-party administrator to conduct background checks. Background checks are performed in compliance with the Fair Credit Reporting Act.

L. Lacey Knowles Robert B. Payne Collegiate Professor Dept. of Ecology and Evolutionary Biology Curator of Insects, Museum of Zoology University of Michigan Ann Arbor MI 48109-1085

L Knowles <knowlesl@umich.edu>

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## UOtago HymenopteranGeneDrive

DEPARTMENT OF BIOCHEMISTRY SCHOOL OF BIOMEDICAL SCIENCES

About us/Mô mâtou

The Biochemistry Department is a large research and teaching department housed in a well-equipped building. It is part of the University of Otago and located in Dunedin, a culturally vibrant and diverse university city.

The role/Te mahi

This Postdoctoral Fellow position is funded by an MBIE Programme Grant located with Professor Peter Dearden in the Department of Biochemistry. In this role, you will be required to work within a nationally distributed team, including close interactions with project members based at Lincoln University and Victoria University of Wellington Te Herenga Waka.

We are seeking an enthusiastic and driven Postdoctoral Fellow to join a team working on developing genetic

solutions to the control of invasive eusocial wasps. You will join a large laboratory working on many aspects of animal development, genomics and evolution.

This project provides an exciting opportunity to generate new ideas on how to control pest insects, deploy genetic technology for the control of significant pest species and understand the biology and population genomics of invasive species. The outcomes of this project will be new knowledge and tools to control invasive social wasps.

Your skills and experience/Kâ pĀ>>keka me kâ wheako

Applicants must have a PhD in genetics, genomics, developmental biology, bioinformatics, population genetics, insect sciences, or evolution and development, as well as experience with: - Relevant programming language(s) (e.g., R, Python, C/C++, Java). - Genome assembly and annotation. - Insect rearing and biology. - Molecular biology. - CRISPR/cas9 gene editing - Large data analysis. - Reproducible Research concepts and tools.

Preference will be given to applicants with skills in developmental biology and genetic transformation techniques.

Further details/PĀ>>roko

This is a full-time (1FTE), fixed term (4.5 years to 31 August 2028) position, located in Dunedin. The successful applicant will be expected to take up the position before June 2024.

The salary for a Postdoctoral Fellow is \$86,210 per annum.

Enquiries should be directed to Professor Peter Dearden, via the contact details below.

Application/Tono

To submit your application (including CV and cover letter), please click the apply button. Applications quoting reference number 2400558 will close on Wednesday, 3 April 2024.

Sent on behalf of Dr. Peter Dearden

Joseph Guhlin <joseph.guhlin@gmail.com>

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## USevilla Spain MacroevolutionPlantDispersal

Dear colleagues,

We are looking for a postdoctoral researcher with experience in phylogenetic comparative analyses and plant macroevolution to study the evolution of plant dispersal modes. More details here: <https://computacionalecology.github.io/posts/-2024-postdoc-plant-macroevolution/>. We would be grateful if you could distribute this offer among potentially interested candidates.

Best wishes,

Francisco

Dr Francisco Rodríguez-Sánchez University of Sevilla (Spain) <https://frodriquezsanchez.net> Francisco Rodriguez Sanchez <f.rodriguez.sanc@gmail.com>

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## UZurich AntibodyEvolution

Postdoctoral Position: Evolution of Antibody Responses and Computational HIV Vaccinology (University of Zurich)

We are seeking a highly motivated Postdoc with a robust quantitative background to contribute to a cutting-edge project at the intersection of bioinformatics, evolutionary biology, virology, and HIV immunology.

The project leverages unique immunological and clinical datasets from the Swiss HIV Cohort Study ([www.shcs.ch](http://www.shcs.ch)), the Zurich Primary HIV Study (<http://www.viralinfectiousdiseases.uzh.ch/ZPHI.html>), and an upcoming HIV vaccine trial scheduled for 2024. The primary goal of the three-year project is to identify the determinants that influence the induction of broadly neutralizing antibodies against HIV by studying the immune response to a lead HIV immunogen.

This interdisciplinary and translational initiative involves intensive experimental work and data analy-

ses, fostering close collaboration between the group of Alexandra Trkola (Institute of Medical Virology, University of Zurich and the groups of Roger Kouyos and Huldrych Günthard at the Department of Infectious Diseases, University Hospital Zurich and international partners.

This position offers: A dynamic and interdisciplinary research environment with connections to both clinical practice and fundamental science.

Engagements with leading experimental and theoretical research groups.

Access to unique immunological and clinical data, providing the opportunity to shape subsequent experimental analyses on a pivotal question in HIV vaccinology.

Given the complexity of the data, the successful applicant must employ mathematical and bioinformatics approaches beyond conventional statistics. Thus, candidates should possess robust quantitative/computational skills and hold a Ph.D. in a discipline relevant to the project, such as Bioinformatics, Bio-Statistics, Bio-Mathematics, or Life Sciences with a substantial quantitative or computational component.

Interested applicants are invited to submit a cover letter, a comprehensive CV, a list of publications, and contact details for two or three academic references to: [roger.kouyos@uzh.ch](mailto:roger.kouyos@uzh.ch).

Roger Kouyos <[roger.kouyos@uzh.ch](mailto:roger.kouyos@uzh.ch)>

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## ViennaU PopulationGenomics

Postdoc Position in Population Genomics, University of Vienna, Austria (f/m/d)

THE POSITION: One-year Austrian Science Fund (FWF) funded Postdoc position with possibility of extension is available at a genomic research group led by Elmira Mohandesan, PhD at University of Vienna, Austria. In this project we aim to use New Zealand feral horse population as a natural, on-going laboratory to investigate the effects of founder events and conservation strategies on genetic diversity and inbreeding in natural and managed populations. To this end, it is planned to whole genome shotgun sequence a large number of feral horses from the Kaimanawa ranges. The obtained data will be analysed using state-of-the-art population

genetic approaches.

**YOUR TASKS:** \* Basic wet-lab experiments (DNA extraction, Illumina library preparation, Quality Control, etc.). \* Population genetic analysis, to examine signature of selection, candidate genes selection, mutational loads, and conservation management modeling. \* Documentation of data generation, and analysis procedure. \* Administration, and organisation of the generated data according to the Research Data Management (RDM) policy at the University of Vienna (<https://rdm.univie.ac.at/>). \* Active participation in lab meetings, seminars, and journal clubs.

**YOUR PROFILE:** \* Background in evolutionary genetics, molecular biology, population genetics, and/or bioinformatics. \* Bioinformatics skills (e.g., Unix, R, Python) and expertise in NGS data is required. \* Proficiency in written and spoken English is required. \* Ability to work independently, and efficiently within a multi-disciplinary research environment. \* Proactive and self-motivated personality.

**WE OFFER:** \* A one-year funded Postdoc position remunerated according to the FWF personnel costs (gross salary 4.752,30 ?? per month. \* A diverse and supportive team in an inspiring, and international setting at the Department of Evolutionary Anthropology (<https://www.anthropology.at/>). \* In-person scientific seminars by the invited renowned scientists around the world organized through the HEAS platform (<https://www.heas.at/>). \* Access to cutting-edge scientific infrastructure and computational resources through CUBE platform (<https://cube.univie.ac.at/>). \* Living in Austria??s capital city Vienna, located in the heart of Europe and ranks as one of the most attractive cities worldwide.

**HOW TO APPLY:** Please send your application (CV, motivation letter), and names/contact information of two potential referees to Elmira Mohandesan, PhD (Email: [elmira.mohandesan@univie.ac.at](mailto:elmira.mohandesan@univie.ac.at)) by April 15th 2024. Preferred starting date June 2024.

Elmira

Elmira Mohandesan, PhD Principal Investigator  
University of Vienna  
Djerassiplatz 1, Room 5.1221030  
Vienna Austria 1030  
Vienna Austria  
Phone: 0043-1-4277-54716  
Email: [elmira.mohandesan@univie.ac.at](mailto:elmira.mohandesan@univie.ac.at)

Elmira Mohandesan <[elmira.mohandesan@gmail.com](mailto:elmira.mohandesan@gmail.com)>

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## WoodsHole USA

### EvolutionMaternalAgeEffects

Postdoctoral Scientist

Maternal age effects: mitochondrial and epigenetic mechanisms

Marine Biological Laboratory Woods Hole, MA Excellent salary and benefits, commensurate with experience and qualifications

Description:

A postdoctoral research position is available to study the cellular, genetic, and epigenetic mechanisms of maternal age effects on offspring health and lifespan. The project will focus on the role of mitochondrial dynamics and metabolism in maternal age effects, using molecular, bioinformatic, biochemical, and imaging techniques.

This is an NIH-funded project in the laboratory of Dr. Kristin Gribble at the Marine Biological Laboratory, Woods Hole, MA. The lab researches the biology of aging, with a focus on maternal age effects on offspring health and lifespan. We use rotifers as a model system for our work. For more information about the lab??s research, see [gribblebiolab.org](http://gribblebiolab.org).

Qualifications:

Applicants should possess a Ph.D. in molecular biology, cell biology, biochemistry, genetics, bioinformatics, or a related field. The ideal candidate will have a record of scientific rigor, productivity, and creativity. Excellent oral and written communication skills are required. Knowledge of rotifer biology is not required; highly motivated individuals with experience in other model systems and with a background in bioinformatics, cell biology, biochemistry, epigenetics, and/or imaging are encouraged to apply.

Required Documents:

Please submit (1) a cover letter with a brief description of your research experience and how you will contribute to research on the mechanisms of maternal age effects on offspring, (2) a CV, and (3) contact information for at least three references.

Apply Here: <https://tinyurl.com/yp2rdv52> Kristin Gribble <[kgribble@mbl.edu](mailto:kgribble@mbl.edu)>

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### Bordeaux Summer School Philosophy In Evolutionary Biology Jun3-7

(Please circulate this announcement in your department) Bordeaux Summer School - Philosophy in biology and medicine \*June 3rd - June 7th, 2024 in Bordeaux, France \*

\*Deadline: March 31st, 2024\*

\*Organized by the PhilInBioMed network < <https://www.philinbiomed.org/> > and the Conceptual Biology and Medicine Team < <https://immunoconcept.cnrs.fr/-conceptual-biology-medicine/> > in Bordeaux.\*

\*Course leaders:\*

Serge Ahmed (neuroscience): University of Bordeaux - CNRS, France

Carl Craver (philosophy of biology, philosophy of neuroscience): Washington University, USA

Fridolin Gross (philosophy of biology, philosophy of computational biology): University of Bordeaux, France

Matt Haber (philosophy of biology, philosophy of evolution): University of Utah, USA

Hannah Kaminski (medicine, immunology): University of Bordeaux, France

Jan Pieter Kohnsman (neuroscience, philosophy of neuroscience): University of Bordeaux - CNRS, France

Mai Lemoine (philosophy of medicine, philosophy of aging): University of Bordeaux, France

Sören Paludan (immunology): Aarhus University, Denmark

Thomas Pradeu (philosophy of biology, philosophy of immunology): University of Bordeaux - CNRS, France

Jonathan Sholl (philosophy of medicine, philosophy of nutrition): University of Bordeaux, France

Marie Vasse (evolutionary biology and ecology): MIVEGEC, CNRS Montpellier, France

\*Information and application: \* <https://bss-philinbiomed.u-bordeaux.fr/en/abstracts> \*Deadline for application: \* March 31st, 2024

PhilInBioMed < <https://www.philinbiomed.org/> > is both an interdisciplinary institute located at the University of Bordeaux < <https://www.u-bordeaux.fr/en> > and an international network < <https://www.philinbiomed.org/> > connecting groups and people working at the interface between philosophy, biology, and medicine, with the shared conviction that conceptual and philosophical approaches can make a critical contribution to science and medicine.

Between June 3rd and 7th 2024, PhilInBioMed is organising an interdisciplinary summer school dedicated to "Philosophy in biology and medicine". For this, 20 young scholars (Master students, PhD students and post-docs) from the fields of philosophy of science, the life sciences, and medicine will come together and learn to use interdisciplinary methods to address conceptual issues in scientific research.

Course leaders will be present to highlight practical

examples of interdisciplinary partnerships from their career, and to advise and interact with participants throughout the week. The programme will also include different formats such as group work, and individual discussions, designed to further interactions between participants and course leaders.

This summer school is a unique opportunity for young researchers to develop new interdisciplinary approaches that will benefit them throughout their career. Participants will not only learn about specific concepts and scientific advances, but they will also learn to take a new look at their own subject of research.

Sincerely,

Thomas Pradeu CNRS Research Director in Philosophy of Science Immunology Unit ImmunoConcEpT, UMR5164, CNRS & University of Bordeaux Presidential Fellow, Chapman University, CA, USA Team Leader Conceptual Biology and Medicine Team < <https://immunoconcept.cnrs.fr/conceptual-biology-medicine/> > Coordinator of the Philosophy in Biology and Medicine Network < <https://www.philinbiomed.org/> > (PhilInBioMed) Université de Bordeaux Bâtiment Bordeaux Biologie Santé, 3ème étage 2, rue Docteur Hoffman Martinot 33076 Bordeaux, France & Institute for the History and Philosophy of Science and Technology < <https://www.ihpst.cnrs.fr/en> > Pantheon-Sorbonne University 13 rue du Four, 75006 Paris, France

Thomas Pradeu <thomas.pradeu.list@gmail.com>

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## Como Italy Bayesian Phylogenetics 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/> If you are interested in the school but unwilling to register for the moment, please send an email to [abs24@mi.imati.cnr.it](mailto:abs24@mi.imati.cnr.it) and we will send you updates and reminders.

As in the past (since 2004), there will be a combination of theoretical and practical sessions, along with presentations by participants about their work (past, current and future) related to the topic of the school.

OUTLINE: The aim of this course is to explore the core challenges of Bayesian inference of stochastic processes in modern biology in terms of data-scale, model-dimensionality and compute-complexity. Challenging and emerging statistical solutions will be illustrated through the analysis of biological sequences, such as genes and genomes. Molecular phylogenetics has become an essential analytical tool for understanding the complex patterns in which rapidly evolving pathogens propagate across and between countries, owing to the complex travel and transportation patterns evinced by modern economies, along with growing political factors such as increased global population and urbanisation. As an accessible course for all, a brief introduction of the underlying biology (for statistical researchers) and of modern Bayesian inference (for practicing biologists) will be also provided.

Topics will cover probabilistic modeling techniques using both discrete- and continuous-valued stochastic processes including continuous-time Markov chains and Gaussian processes; large-scale data-integration approaches incorporating factors like human mobility and climate measurements; recursive computing and other mathematical tricks to evaluate seemingly intractable likelihoods; state-of-the-art sampling methods for high-dimensional models including Hamiltonian Monte Carlo and its more recent non-reversible extensions; delivering timely inference on advancing computing hardware like graphics processing units and (maybe even) quantum devices.

We hope you will be interested in the school and we would like to meet you in Como next year.

We invite you also to share the information with people potentially interested.

Best regards

Elisa Varini and Fabrizio Ruggeri Executive Director and Director of ABS24

Marc Suchard <[msuchard@ucla.edu](mailto:msuchard@ucla.edu)>

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

## Czechia Wildlife Malaria Network Sep1-7

Call now open: funding for Wildlife Malaria Network (WIMANET) 1st Summer Training School

The Wildlife Malaria Network 1st Summer Training School will take place from 1st - 7th September 2024 in Field station Mohelno, Mohelno, Czechia. The training school will consist of five days of lectures and practical activities (2nd - 6th September) designed to introduce students to a broad range of research activities and skills related to working with Wildlife Malaria Parasites. Topics will include sample collection and storage, analysis of haematological parameters and an introduction to parasite identification, analysis of genetic sequence data, collection and identification of vector species, and methods to analyse community-level data. Specific topics will be tailored to the requirements of the selected students.

Geographical restrictions on funded places apply according to COST funding rules, and more information on eligibility can be found in the Annotated Rules for COST Actions (<https://www.cost.eu/uploads/2023/11/COST-094-21-Annotated-Rules-for-COST-Actions-Level-C-V1.4-Final-.pdf>). All teaching materials will be available through the WIMANET website (<https://wimanet-science.github.io/web/>) after the course has concluded.

Applications are open to anyone interested in learning techniques to work with wildlife malaria parasites, but applicants must have an eCOST profile and have applied to be a member of WIMANET in order for their application to be approved. You can apply to join WIMANET here: <https://www.cost.eu/actions/-CA22108>, and more information about the network can be found here: <https://wimanet-science.github.io/web/> The call for applications for the Wildlife Malaria Network 1st Summer Training School will close on 31st March. Applications must be e-mailed to the Grant Awarding Co-ordinator, Dr Alexandra Corduneanu (alexandra.corduneanu@usamvcluj.ro), and to the WIMANET account (wimanet.science@gmail.com). The application consists of the following documents:

- a motivation letter detailing the benefits for the applicant and relevance of the training school to current

research,

- Anticipated travel budget in Euros (costs of transport to Vaclav Havel Airport Prague, and travel insurance)

- a support letter from the Home Institution,

- a CV, including a list of academic publications if applicable.

The applications will be ranked by the Core Group based on: - benefits to the applicant in terms of career progression - benefit and contribution to the development of the COST Action

The selection will follow the COST policies on inclusiveness (gender, age, geography).

The final ranking will be approved by the Action Chair and Co-Chair. All researchers who applied to the call will be informed of the outcome of their application by 19th April.

The selected researchers should wait for the official invitation from the Grant Holder before booking any travel arrangements.

Please direct any questions to [wimanet.science@gmail.com](mailto:wimanet.science@gmail.com), and please alert any students who may be interested and not on the evolDir mailing list to this opportunity.

Best wishes,

Jenny

Dr Jenny Dunn (she/her)

Senior Lecturer in Animal Health and Disease, Postgraduate Research co-Lead, Chair, Wildlife Malaria Network COST Action, School of Life and Environmental Sciences, University of Lincoln, Joseph Banks Laboratories, Lincoln, LN6 7DL, UK

Twitter: @jennycdunn

Google Scholar: <https://scholar.google.co.uk/citations?user=0GP7Tv0AAAAJ&hl=en> Wildlife Malaria Network: <https://www.cost.eu/actions/-CA22108/> I may have sent this email outside office hours, but I do not expect a response outside of yours

[University of Lincoln] < <https://www.lincoln.ac.uk> >

Situated in the heart of a historic city, the University of Lincoln is committed to transforming lives and communities through our teaching and research. We are listed in the world's top 150 universities in the Times Higher Education's (THE) Young University Rankings 2023 and hold a five-star score overall in the QS Stars rating system of global universities. We are one of a select group of universities to achieve the top Gold rating overall and in both aspect ratings for student experience and

student outcomes in the national Teaching Excellence Framework (TEF) 2023. We were awarded the Queen's Anniversary Prize for Further and Higher Education in 2023.

The information in this e-mail and any attachments may be confidential. If you have received this email in error please notify the sender immediately

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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/evodir.html>

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## Online Adaptation Genomics Jun24-28

Dear all,

We are thrilled to announce our upcoming online course on Adaptation Genomics, taking place from June 24th to June 28th, 2024.

Course website: ( <https://www.physalia-courses.org/courses-workshops/courseadaptationgenomics/> )

This course offers an introduction to the study of the genomic basis of adaptation through population genomics approaches. Participants will explore the analysis of both sequence and structural genetic variation, covering everything from raw genomic data handling to advanced methods for detecting candidate genomic regions involved in local adaptation. Hands-on exercises will impart essential bioinformatics skills and provide practical experience in manipulating, visualizing, and interpreting genomic data patterns.

Participants will gain proficiency in handling genomic data, calculating population genetic statistics, visualizing genetic population structure, and detecting genomic regions linked to adaptive divergence or local adaptation. They will also learn to identify signatures of selection in the genome, detect putative structural variants of adaptive significance, and understand the potential and limitations of different methods for studying the genomic basis of adaptation.

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

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
info@physalia-courses.org mobile: +49 17645230846

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

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## Online Advanced Multivariate Analysis In R Jun10-13

Dear all,

registrations are now open for our online course on GLLVMS: Advanced Multivariate Analysis of Ecological Communities in R

Dates: 10-13 June 2024

Course website: ( <https://www.physalia-courses.org/courses-workshops/gllvm/> )

The course will focus on Generalized Linear Latent Variable Models (GLLVMs) as a unified framework for analyzing multivariate data in ecological communities. Participants will learn how to fit GLLVMs using the gllvm R-package, choose appropriate distributions for their data, formulate GLLVMs to address research questions, assess model fit through residual diagnostics, visualize and interpret results, and effectively communicate findings.

The course is aimed at PhD candidates, postdoctoral researchers and researchers with basic statistical knowledge, that have multivariate data (which can be experimental or observational) and want to learn how to analyse it in a statistically appropriate manner.

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

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
info@physalia-courses.org mobile: +49 17645230846

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## Online AdvancedPython Apr15-26

Advanced Python for Biologists

Date - 15 - 26 April 2024 Times - Half days - Mornings  
 Venue - Remote course using Zoom and Slack Trainer -  
 Martin Jones

Description

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at people who already have a basic knowledge of Python and are interested in using the language to tackle larger problems. We will focus on three main themes:

learning about advanced language features (recursion, complex data structures, comprehensions, exceptions) that are relevant to bioinformatics work learning about development tools (benchmarking, profiling, unit testing) that can make it easier for us to write code that is both fast and correct learning about different programming styles and concepts (object-oriented programming, functional programming) that are suitable for different kinds of problems The workshop will use examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) take advantage of the advanced language features in their own programs and (2) use appropriate tools when developing software programs. They will also have a deeper understanding of how Python works internally, which will be invaluable when making sense of existing code and packages.

Feedback from recent attendees

“Fantastic course– excellent organisation and course content. Martin is a great teacher. Learnt a lot, especially coming from a programming-naïve background.”

“This course exceeded all my expectations. Martin was a great instructor, who clearly knows how to frame any programming topic into a biology question. Now I feel very confident to keep improving my Python skills (after a couple of failed attempts with other courses in the past).”

Course fee

500

Cancellation policy

A refund will be issued if a booking is cancelled more than one week prior to the workshop.

Who is the workshop for

This course is designed for people who already know some Python and who are interested in tackling more ambitious programs, particularly ones that will deal with large or complex datasets and will therefore need to work efficiently. Students should have a basic biological background (or be prepared to ask a lot of questions!) as the examples and exercises assume some knowledge of what DNA is, what is meant by gene expression, how to read a phylogenetic tree, etc.

The course is **not** suitable for complete beginners to Python as we will assume quite a lot of knowledge of the basic syntax of the language. The material covered in the Introduction to Python for Biologists

About the trainer

Martin started his programming career by learning Perl during the course of his PhD in evolutionary biology, and started teaching other people to program soon after. Since then he has taught introductory programming to hundreds of biologists, from undergraduates to PIs, and has maintained a philosophy that programming courses must be friendly, approachable, and practical. In his academic career, Martin mixed research and teaching at the University of Edinburgh, culminating in a two year stint as Lecturer in Bioinformatics. He now runs programming courses for biological researchers as a full time freelancer.

Logistics

We will deliver the course over ten days, from Monday 15 April - Friday 26 April 2024. Training will consist of lectures, demonstrations and practical exercises, with the trainer on hand to assist and offer 1-1 support. Slack will be used to share important updates and for asking questions. Lectures/input will be recorded and made available to participants as soon as possible for anyone who needs to catch up. You will need to have an account for Zoom and Slack. We recommend that you download the clients for these rather than using the browser version. Martin will post links to the software and material for the course on the Slack workspace the week before the course starts.

Detailed Syllabus

Session 1 : Recursion and trees

In this session we will cover two very closely related concepts: trees (i.e. the various ways that we can store hierarchical data) and recursive functions (the best way to operate on treelike data). As recursion is inherently confusing, we'll start with a gentle introduction using



biological examples before moving on to consider a number of core tree algorithms concerning parents, children, and common ancestors. In the practical session we'll look in detail at one particular way of identifying the last common ancestor of a group of nodes, which will give us an opportunity to explore the role of recursion. Core concepts introduced: nested lists, storing hierarchical data, recursive functions, relationship between recursion and iteration.

Session 2 : Complex data structures

In this session we will briefly recap Python's basic data structures,

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

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## Online Genome Assembly Annotation Mar18-22

Dear all,

I wanted to bring to your attention our upcoming course on Genome Assembly and Annotation, available at: (<https://www.physalia-courses.org/courses-workshops/course20/>) (only 3 remaining seats available)

Dates: Online, March 18th-22nd

This course offers a unique opportunity for biologists and bioinformaticians to delve into the intricacies of de novo genome assembly and annotation. Through a combination of theoretical discussions and practical examples, participants will gain valuable insights into generating high-quality annotated and curated reference genomes.

Designed for researchers at all levels of expertise, from beginners to advanced users, the course covers fundamental concepts, algorithms, and workflows. We will explore various aspects of genome assembly and annotation, drawing from the Vertebrate Genomes Project assembly pipeline as a model. Hands-on exercises, utilizing both graphical interfaces and basic command line tools, will reinforce learning and skill development.

For more information on this and other courses and workshops we offer, please visit: (<https://www.physalia-courses.org/courses-workshops/course20/>)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
info@physalia-courses.org mobile: +49 17645230846

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## Online GenomicsDataAnalysis Aug26-Sep4

Dear all, Registration is now open for the 15th edition of our course/workshop below.

Genomics Data Analysis Course and Workshop: "ConGen-2024" Online

Theme: Applications of Next Gen Sequencing Data to Understand Population Structure, Adaptive Evolution, and Environmental Influences on Genomic Variation.

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 Linux command line & R)

Where: Online via Zoom.

For details on ConGen-2024: see <https://www.umt.edu/-/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. 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, Ne, GWAS, RoH, landscape genomics & selection detection, assignment tests with low-coverage-WGseq data, and more (see past course contents). New lectures in 2024 (with hands-on

exercises) will include: DNA 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.

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

“Luikart, Gordon” <gordon.luikart@mso.umt.edu>

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We are happy to announce our upcoming course on “Introduction to Genome-Wide Association Studies (GWAS)”! If you’re looking to enhance your skills and knowledge in GWAS analysis, this course is tailored for you. Whether you are a student, researcher, or professional, this course will provide you with the essential tools to confidently navigate the world of GWAS.

**\*\*Course Dates:\*\*** Online, 24-28 June

Course website: ( <https://www.physalia-courses.org/-courses-workshops/course49/> )

This comprehensive course will guide you through the entire process of GWAS data analysis, ensuring that you not only understand the individual steps but also learn how to create a reproducible and efficient bioinformatics workflow.

Over the span of five days, our course will cover a range of topics through a well-structured module-based approach. Each day will commence with informative lectures, followed by interactive class discussions to solidify key concepts. Subsequently, you will engage in hands-on practical sessions designed to foster your skills. These sessions will include both guided exercises with our experienced instructors and independent tasks to reinforce your learning. After each exercise, you will have the opportunity to interpret and discuss results within a group setting.

A background in biology, particularly genetics, is recommended. While a basic familiarity with R programming and Unix will be helpful, our course will provide ample support for learners at varying levels of experience.

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

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
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## Online GWAS Jun24-28

Dear all,

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## Online IntroPalaeogenomics May9-15

Dear colleagues,

Registration is open for the second edition of the course “Introduction to Palaeogenomics”.

Date and schedule: Online live sessions on the 9th, 10th, 13th, 14th, and 15th of May, from 16:00 to 20:30 (Madrid time zone).

Course Overview:

Ancient DNA (aDNA) research, defined as the retrieval and analysis of DNA sequences from various degraded biological materials, has been evolving as a research field for four decades. Through advances in DNA isolation and amplification techniques, sequencing technologies and data analysis pipelines, the field has revolutionized and transitioned to what we now know as palaeogenomics. DNA extracted from archaeological samples, and museum specimens has proven useful to study species and life on earth from the genomic perspective. It has made it possible to measure changes in genetic diversity through time, test hypotheses about the association of environmental phenomena and genetic changes in natural populations, and to resolve long-standing questions about the evolutionary relationships between species.

In a combination of interactive lectures and hands-on practical sessions, this course will provide a theoretical overview of molecular biology laboratory techniques for the retrieval of aDNA from ancient samples from different species and an introduction to the bioinformatic pipelines for the analysis of palaeogenomic data. Students will be introduced to the standard bioinformatic methods often used in palaeogenomic projects for the analysis of aDNA data from human and non-human samples. We will also review the history and developments of the field to understand how it came to be what it is today, and consider and discuss the practical problems of ancient DNA recovery, the theoretical problems associated with the interpretation of palaeogenomic data, and the ethical implications embedded in this type of research.

At the end of the course, students will have gained a general understanding of common key methods and tools used in palaeogenomics projects: from the basics in the field to the interpretation of the results, as well

as ethical and responsibility aspects and implications of aDNA research.

For more information and registration: <https://www.transmittingscience.com/courses/genetics-and-genomics/introduction-to-palaeogenomics-concepts-methods-and-applications-of-ancient-dna-data/> or write to [courses@transmittingscience.com](mailto:courses@transmittingscience.com)

With best regards

Sole

Soledad De Esteban-Trivigno, PhD Transmitting Science [www.transmittingscience.com](http://www.transmittingscience.com) Twitter [@SoleDeEsteban](https://twitter.com/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](mailto: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](http://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.

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## Online IntroSpatialEcoPhylogenetics Mar19-22

ONLINE COURSE - An Introduction to Spatial Eco-Phylogenetics and Comparative Methods (SECM01)

We still have a few places available.

<https://www.prstats.org/course/an-introduction-to-spatial-eco-phylogenetics-and-comparative-methods-secm01/> 19th - 22nd March 2024

Please feel free to share!

**COURSE OVERVIEW** - In this course we introduce phylogenetic analyses in a spatial context. Phylogenetic analyses often imply a high number of species for which phylogenetic information is unavailable, hence we begin by providing an overview on modern techniques to incorporate phylogenetic uncertainty in the analyses (day 1). We then cover the most popular analyses in the spatial phylogenetics discipline (day 2), with particular focus on the canonical analysis of neo- and paleo-endemism (CANAPE). The second part of the course will be devoted to integrating phylogenetic information into models of geographic distribution of species (day 3), followed by an overview of recent advances to improve ecological forecasts using phylogenetic mixed models in a Bayesian framework (day 4).

By the end of the course, participants should:

Know how to expand incomplete phylogenies based on taxonomic information and customizing simulation parameters for optimal expansion. Understand the metrics and concepts used in spatial phylogenetics (i.e. phylogenetic alpha and beta diversity, phylogenetic endemism), interpret them critically, and assess pros and cons of analytical techniques. Calculate phylogenetic predictors that can be included as covariates in Species Distribution or Niche Models. Understand and implement the phylogenetic mixed model (PMM) and translate its predictions into a spatial context.

Day 1 - Expansion of molecular trees using taxonomic information and fundamental metrics of phylogenetic structure

Software for tree expansion exercises; randtip, Phy-

loMaker An overview of the fundamental metrics of phylogenetic structure. Null models.

Day 2 - Spatial Phylogenetics

Canonical analysis of neo- and paleo- endemism. Metrics, rationale, workflow, and implementation.

Day 3 - Phylogenetic Species Distribution Models

Putting phylogenies in the geography: the imprints of evolutionary relationships in distribution models. Combining phylogenies with co-occurrence to infer spatial phylogenetic predictors. Fitting, evaluating and interpreting Phylogenetic-SDMs.

Day 4 - Beyond PGLS - Bayes and more

Most common phylogenetic modelling approaches: PGLS PGLMM The phylogenetic mixed model (PMM) in a Bayesian framework Please email oliverhooker@prstatiatics.com with any questions.

Oliver Hooker PhD. PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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## Online MappingTraitEvolution May20-31

Dear colleagues,

Transmitting Science is offering a new edition of the course "Mapping Trait Evolution" - 7th edition. This course will be held live online (synchronous). Max 18 participants.

Dates: Online live sessions on the 20th, 23rd, 27th, 29th, and 31st of May, from 14:00 to 18:00 (Madrid time zone).

Instructor: Jeroen B. Smaers (Stony Brook University, USA).

**COURSE OVERVIEW** The course provides a comprehensive overview of the state-of-the-art methods in mapping phenotypic trait evolution and will provide participants with a springboard to using these methods to answering their own research questions. We focus on analyses that use a phylogenetic tree and observed trait information from tip taxa (extant and/or extinct) to describe how traits have changed along the branches of a

phylogeny. The course covers methods that estimate and test patterns related to changes in mean, covariation, and rate. Applications for continuous and categorical, and univariate and multivariate research designs are discussed. At the end of this course, participants will have developed an understanding of: (1) Brownian motion and Ornstein-Uhlenbeck models of evolution. (2) How these models can be applied to estimate and test patterns of trait evolution. (3) What the advantages and disadvantages are of different models/methods. (4) How to recognize which model/method is most appropriate given a particular dataset and research question. We provide several data sets that will be used to exemplify the application of these methods. We do, however, encourage participants to work with their own data so as to get direct experience with analysing precisely what they expect to analyse. Methods from the following R packages will be discussed: ape, geiger, phytools, evomap, l1ou, bayou, surface, OUwie, mvMORPH, geomorph (this list may change as new packages become available).

Important note: Please bear in mind that this course is not about reconstructing (building) phylogenetic trees, the methods we cover in this course assume that a phylogeny is known.

You can find more information here: <https://www.transmittingscience.com/courses/-evolution/mapping-trait-evolution/> or writing [courses@transmittingscience.com](mailto:courses@transmittingscience.com)

Full list of upcoming Transmitting Science courses: <https://www.transmittingscience.com/courses/> Best regards

Sole

Soledad De Esteban-Trivigno, PhD Transmitting Science [www.transmittingscience.com](http://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](mailto: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](http://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.

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## Online NetworkAnalysisInSystemsBiology Jun3-6

Dear all,

We are excited to announce our upcoming course on Network Analysis in Systems Biology with R/Bioconductor (2nd edition), scheduled for June 3-6, 2024.

Course website: <https://www.physalia-courses.org/-courses-workshops/network-in-systems-biology/> In this course, participants will delve into the inference and analysis of biological networks from RNA-seq data using R and Bioconductor packages. Topics covered include data structures for quantitative data and graphs, statistical methods for network inference, functional analyses of biological networks, and network comparison. By the end of the course, attendees will be proficient in inferring and analyzing gene coexpression networks (GCNs) and gene regulatory networks (GRNs), comparing networks, and integrating GCNs with genetic markers to prioritize

candidate genes associated with traits.

This course is designed for researchers and students interested in utilizing R and Bioconductor for systems biology projects. While familiarity with RNA-seq and core Bioconductor data structures (e.g., SummarizedExperiment and GRanges) is beneficial, it is not essential, as these will be covered during the sessions. Participants should have a working knowledge of R, including R syntax, commonly used functions, and basic data structures such as data frames, vectors, and matrices, along with their manipulation.

For the full list of our courses and workshops, please visit <https://www.physalia-courses.org/courses-workshops/> For any questions, feel free to send an email to us at [info@physalia-courses.org](mailto:info@physalia-courses.org)

Best regards,

Carlo

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## Online Pangenomics Apr15-17

Dear all,

We wanted to inform you that there are only a few seats remaining for our upcoming online course on the Analysis of Prokaryotic Pangenomes, scheduled for April 15-17.

Course website: ( <https://www.physalia-courses.org/courses-workshops/prokaritotic-pangenomes/> )

In this course, you will gain valuable insights into pangenome analysis and its implications in biological research. Through a series of lectures and hands-on practical sessions, you will learn how to annotate genomes, construct pangenomes, analyse gene relationships, visualize networks, and more.

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

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR

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## Online RADseqAnalysis Mar18-21

The UConn Computational Biology Core is hosting a Virtual Workshop: RADseq Data Analysis

March 18-21, 2024 ~ 9:00 AM - 12:00 PM EST

COST: \$400 (UConn affiliates), \$500 (External participants)

Live sessions on zoom, recordings distributed, No prior bioinformatics experience needed!

Visit <https://bioinformatics.uconn.edu/cbc-workshops/> to register

\* Learn Linux basics and how to navigate High Performance Computing (HPC).

\* Learn High Throughput Sequencing (HTS) platforms and best practices for variant detection.

\* Learn informatic approaches to filter and summarize genotype calls for downstream analysis.

\* Learn basic analyses of population structure.

\* Learn about commonly used tools (Stacks, Freebayes,R), standard file formats, and common analysis pitfalls.

Questions? E-mail [cbcsupport@helpspotmail.com](mailto:cbcsupport@helpspotmail.com)

“Nahom, Mia” <[mia.nahom@uconn.edu](mailto:mia.nahom@uconn.edu)>

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

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## Online ReproducibilityInBioinformatics Apr15-17

Dear all,

there are only a few seats left for the 3rd edition of the online course on “Reproducibility in Bioinformatics,”

scheduled from April 15-17.

Course website: ( <https://www.physalia-courses.org/courses-workshops/bioinformatics-reproducibility/> )

This course is designed to raise awareness and introduce effective strategies for improving reproducibility in bioinformatic analyses. Through a blend of theoretical sessions and hands-on exercises, our experienced instructors will guide participants in developing skills to enhance the reproducibility of bioinformatic analyses and workflows using containers, versioning, and virtual environments.

#### LEARNING OUTCOMES

- Basic concepts and techniques for modern reproducible bioinformatics data analyses - Data organization, documentation and software versioning - Setting up and working in virtual software environments - Software containerization strategies and caveats - how to use and build containers - Knowledge of how to use common workflow management systems

For the full list of our courses and workshops, please have a look at: ( <https://www.physalia-courses.org/courses-workshops/bioinformatics-reproducibility/> )

Best regards, Carlo

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## Online TimeSeriesForecastingInR May27-31

Dear colleagues,

registrations are open for the 2nd edition of the online course on Ecological Time Series Analysis and Forecasting in R, scheduled from May 27th to 31st, 2024. Classes will be held from 9 AM to 12 PM Berlin time, with additional self-guided practical sessions using annotated R scripts.

Course website: <https://www.physalia-courses.org/courses-workshops/time-series-in-r/> In this course, we will delve into dynamic processes using Bayesian modeling software, Stan, along with packages like {mvgam}

and {brms} to build ecologically appropriate models. You will learn to wrangle, visualize, and explore ecological time series data, enabling you to produce accurate forecasts.

By the end of this course, you will: 1. Understand dynamic GLMs and GAMs for capturing nonlinear effects and temporal dependence. 2. Fit dynamic models using {mvgam} and {brms} packages in R. 3. Critically evaluate and compare fitted dynamic models. 4. Produce accurate forecasts and assess their performance using probabilistic scoring rules.

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 TransposableElements Jun3-7

Dear all,

registrations are now open for the next edition of the course “Bioinformatic analysis of Transposable Elements”.

Dates: 3rd-7th June 2024 Format: Online Course website: <https://www.physalia-courses.org/courses-workshops/course24/> his course tackles Transposable Elements analysis complexities, covering TE biology, computational analyses (genome annotation, TE classification), transcriptomics, and manual curation.

The course is aimed at biologists at any career stage who are new to TE analyses and/or de-novo annotation of the repetitive fraction of non-model genomes.

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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courses.org>

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## Oxapampa Peru PopGenomicsRADSeq Jun20-30

The Gen-Pob.org workshop will take place in Oxapampa, Peru from 20 to 30 June 2024, at the Jardim Botânico de Missouri ([www.jbimperu.org.pe/](http://www.jbimperu.org.pe/)) in collaboration with the Universidad Nacional Agraria La Molina ([www.lamolina.edu.pe/](http://www.lamolina.edu.pe/)). This workshop includes 8 days of instruction in population genomic theory and bioinformatics exercises related to the analysis of genomic data generated using RAD-Seq. The workshop will also include an optional two-day field trip to explore some of the incredible biodiversity that Peru offers. Instructors this year include Kevin McCracken from the University of Miami, Jeff Peters from Wright State University, and Phil Lavretsky from the University of Texas El Paso.

Details about the workshop can be accessed at: [www.gen-pob.org](http://www.gen-pob.org) There is no cost to the workshop, but registration is required by 15 April.

To apply please register using this google form:

<https://forms.gle/rsuFaA3aXEYiVakJ7> Only about 25 positions are available.

Kevin McCracken Jeff Peters Phil Lavretsky Rocio Rojas Thomas Valqui

Kevin G. McCracken Department of Biology, College of Arts & Sciences Marine Biology & Ecology, Rosenstiel School of Marine & Atmospheric Sciences Human Genetics & Genomics University of Miami Coral Gables, FL 33146 U.S.A.

Office & Lab: 188 Cox (Biology) <http://www.duckdna.org> email: kevin.g.mccracken@gmail.com  
<http://gen-pob.org> Kevin McCracken  
<kevin.g.mccracken@gmail.com>

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TRAINING AND RESEARCH WORKSHOP IN “EVOLUTIONARY GENOMICS FOR PLANT MODELS AND CROPS”

May 13-17, 2024 | CIBIO-InBIO, Vairao, Portugal

We are pleased to announce that the third edition of the Training and Research Workshop in “Evolutionary genomics for plant models and crops” will take place at CIBIO-InBIO/BIOPOLIS, Campus de Vairao, University of Porto, Portugal, from 13 to 17 May 2024.

For those who attended previous editions, please note that topics and most of the speakers have changed! This workshop is meant for PhD students but will also be opened to Master students and post-docs.

It will present major on-going research topics in plant evolutionary genomics, covering both methodological and biological questions, fundamental and applied perspectives, model plants and crops.

Each theme (day) will be covered by 2 talks given by international specialists and a round table with both speakers moderated by an in-house researcher from the field. Talks will be 1h30 research-oriented lectures (with 30 min of a general/large scope introduction on the subject).

A lot of interaction is expected during these lectures: questions will be asked during the talks and at the round table.

The workshop is also meant to be a platform for connecting students and labs in this field, internationally.

Registration deadline :April 10, 2024

All applicants will be notified about whether they are accepted until April 15, 2024.

The program, practical information and registration platform can be found [HERE](#)

Participation is free of charge for BIODIV and Univ. of Montpellier students.

If you have any questions you may contact us by mail at: [post.graduation@cibio.up.pt](mailto:post.graduation@cibio.up.pt)

Best regards,

Raquel Tavares

Raquel Tavares <[raquel.tavares@cibio.up.pt](mailto:raquel.tavares@cibio.up.pt)>

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## Portugal PlantEvolutionaryGenomics May13-17



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## Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email [evoldir@evol.biology.McMaster.CA](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be send to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA) and processed later. In either case, please do not expect an instant response.

## Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L<sup>A</sup>T<sub>E</sub>X do not try to embed L<sup>A</sup>T<sub>E</sub>X or T<sub>E</sub>X in your message (or other formats) since my program will strip these from the message.