
E v o l D i r

May 1, 2024

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

Foreword

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

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

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



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Conferences

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Bialowieza Poland ForestEvolution Sep15-20

Call for Abstracts: Submit Your Research to the Białowieża Ecology Conference 2024

Dear Sirs,

We are pleased to announce that we have extended the deadline for accepting abstracts for the first edition of the Bialowieza Ecology Conference (BEC).

The conference is entitled “Temperate Forests in the Anthropocene: Disturbances, Species, Humans, and Ecosystem Functioning” and will take place from September 15th to 20th 2024 in the pristine natural beauty of Europe’s last primeval forest in Białowieża, Poland.

<https://bpn.com.pl/index.php?lang=en> Key dates:

Abstract Submissions Open: March 6th, 2024

Submission Deadline: April 30th, 2024

Notification to Authors: May 26th, 2024

Authors’ Acceptance and early bird registration deadline: June 09th, 2024

Registration deadline: June 30th, 2024

Conference Theme and Scope- The Białowieża Ecology Conference (BEC) is a series of international sci-

entific conferences that aim to gather a better understanding of temperate forest ecosystems it takes place in the heart of Europe’s last primeval lowland forest, Białowieża, Poland. This year, 2024 marks the first edition, entitled “Temperate Forests in the Anthropocene: disturbances, species, humans and ecosystem functioning”. The goal of the conference is to exchange and summarize knowledge in the fields of forest ecology and conservation biology, connect researchers working in a variety of scientific fields, and discuss practical solutions for more sustainable forest management and biodiversity conservation in a context of global change. A multitude of research topics are included in this conference to cross-fertilize approaches that yield a better understanding of temperate forests in socio-ecological contexts.

For a more detailed description, please visit our website.

We welcome submissions on topics including, but not limited to:

Human-Forest Interactions

Human-Wildlife Interactions

Invasive Species

Physical Barriers in Forests

Climate Change and Disturbance Regimes

Conservation Biology and Ecosystem Functioning

Submission guidelines: Abstracts should be prepared in English and include the following sections: Aim of the Study, Methods, Results/Findings, and Conclu-

sions/Implications. The word limit for the body of the abstract is 300 words. For detailed submission guidelines and to submit your abstract, please visit the call for abstract page on our website. .

Why participate?

Interesting workshops.

Visit to the BiaÅ³owieÅa Primeval Forest with experienced guides.

Post-conference trip to Biebrza National Park.

Share your research with an international audience of peers.

Engage with key stakeholders in forest ecology, conservation, and management.

Participate in a range of workshops, seminars, and excursions designed to enhance your knowledge and skills.

Contribute to shaping the future of temperate forest research and policy.

We encourage you to submit your abstract and join us in BiaÅ³owieÅa for what promises to be an enlightening and inspiring event.

For any inquiries regarding the call for abstracts or the conference in general, please do not hesitate to contact us at info@bialowiezaecologyconference.org or bec_conference@ibs.bialowieza.pl.

For any updates you can follow our Twitter (X) account@BEco_conf.

We are looking forward to your submissions and welcoming you to BEC 2024.

Best regards, Ewa Komar, PhD, on behalf of the BiaÅ³owieÅa Ecology Conference (BEC) 2024 Organizing Committee

María Losada

Mammal Research Institute, Polish Academy of Sciences Population Ecology Research Unit, Stoczek 1, 17-230 BiaÅ³owieÅa (Poland) Phone: (85) 682 77 50 ext. 114

Maria Losada <m.losada@ibs.bialowieza.pl>

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Bristol UK GenomeScience Jul16-18

Hi everyone,

We would like to welcome you to attend Genome Science UK 2024, Bristol, 16-18th July 2024.

Join us at Genome Science UK 2024, the premier gathering for genomics researchers, clinicians, and industry leaders in the UK. Taking place in the vibrant city of Bristol, July 16th-18th, this three-day conference offers a unique opportunity to hear from world-renowned leaders in the field such Richard Durbin (University of Cambridge), Matt Brown(Chief Scientific Officer, Genomics England), and Peter Holland (University of Oxford).

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

Genome Science UK 2024 promises to be an unforgettable event. Register now at <https://bristol.genomescience.org.uk/register> Limited early-bird registration discounts are available until 30th April. Students early bird registration $\pounds\frac{1}{2}225$, delegates early bird $\pounds\frac{1}{2}260$, industry attendees $\pounds\frac{1}{2}400$.

Sion and Jordi

School of Biological Sciences University of Bristol Life Sciences Building 24 Tyndall Avenue Bristol, BS8 1TQ

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

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Heraklion Crete BiologyAndBiomedicine Jul20-22

Dear Author

You are invited to submit an article in the 4th International Conference on Biology and Biomedicine -

BIOMEDICINE 2024 Heraklion, Crete Island, Greece. July 20-22, 2024. <http://www.wseas.com/bio> Accepted and Presented papers will appear in a Springer Verlag Volume Computational Problems in Science and Engineering III Editors: Nikos E. Mastorakis, Imre J. Rudas, Yuriy S. Shmaliy See our previous volume <https://link.springer.com/book/10.1007/978-3-319-15765-8> Best Papers will be published in the following 3 Journals

Molecular Biomedicine (Indexed in ISI Web of Science, Scopus etc) Best papers from the conference will appear in this Journal: <https://www.springer.com/journal/43556> Editor-in-Chief Yu-quan Wei, PhD, MD, State Key Laboratory of Biotherapy, West China Hospital, Sichuan University, China

Biomedical Journal (Indexed in ISI Web of Science, Scopus etc) Best papers from the conference will appear in this Journal: <https://www.sciencedirect.com/journal/biomedical-journal> Editor-in-Chief Prof. Ming-Ling Kuo, Chang Gung University, Taoyuan, Taiwan

WSEAS Transactions on Biology and Biomedicine (Indexed in Scopus etc) Best papers from the conference will appear in this Journal: <https://wseas.com/journals/bab/> Editor-in-Chief Prof. Nicholas Tritos, Harvard Medical School, Boston, MA, USA

Many Thanks

Kostas Chiotopoulos

“4th International Conference on Biology and Biomedicine - BIOMEDICINE 2024.”
<kostas.chiotopoulos@mail4.engw.org>

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Heraklion Greece Malacology Sep15-20

Dear colleagues,

Registrations and submission of abstracts have started for EUROMAL 2024 <<http://euromal2024.gr/>>, the 10th European Congress of Malacological Societies.

The congress, organized by the Hellenic Malacological Society <<https://www.heme.gr/>>, and the Natural History Museum of Crete <<https://www.nhmc.uoc.gr/en/>>, will take place at the Cultural Conference Centre of Heraklio <<https://www.cccc.gr/en>>, Crete, from

15th to 20th September 2024*.

Please, save the date and follow the announcements about the Congress on its website (<https://www.euromal2024.gr/>) or contact us (euromal2024@gmail.com) for any queries you may have.

We are waiting for you all in Crete!

On behalf of the EUROMAL 2024 Organizing Committee

Sinos Giokas

Professor of Evolutionary Ecology Department of Biology, University of Patras GR-26500 Patras, Greece
Tel: +30-2610-969218 E-mail: sinosg@upatras.gr Web Site: <https://evolecol.upatras.gr/> *ΆβίíΆ² ÁέéΆ¼éáΆ²*
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Hinxton UK AncientDNA Jun3-5

Conference Ancient Biomolecules of Plants, Animals and Microbes 3-5 June 2024 Wellcome Genome Campus, UK

Submit your abstract for an opportunity to present a poster and lightning talk at the 2024 Ancient Biomolecules of Plants, Animals, and Microbes conference (3-5 June 2024).

Submission deadline extended to 23 April 2024.

This is an excellent opportunity to join a global community of evolutionary scientists in-person, to share your research discoveries and gain feedback from leaders in the field.

Contribute to the conversation on research into biomolecules retrieved from ancient plants, animals, and microbes.

We welcome submissions on these topics:

* Better methods more resolution * Ancient animals * Ancient microbes * Ancient plants * Conservation and extinction * Ancient proteins * Ancient environmental DNA

We are also keen to receive contributions that have the potential to shape thinking on best practice approaches for data generation and analysis.

Don't miss out on a chance to network face-to-face with multidisciplinary peers, build your professional profile, and make new connections with scientists working across many different aspects of ancient biomolecule research.

Register for your in-person place and submit an abstract by 23 April 2024!

Find out more on the conference webpage <https://coursesandconferences.wellcomeconnectingscience.org/event/ancient-biomolecules-of-plants-animals-and-microbes-20240603/?2> 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> (to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Houston Evolutionary Genetics Genomics Jun7

The Southeast Texas Evolutionary Genetics and Genomics (STEGG) 2024 Symposium will be held on Friday, June 7, 2024 at the University of Houston (TX, USA). The meeting will take place in the Elizabeth D. Rockwell Pavilion in the M.D. Anderson Library on the University of Houston campus.

Registration for STEGG 2024 is FREE of charge, but we ask that you register by Friday, May 17 so that we can ensure sufficient space and amenities for all attendees. If you would like to give a talk at STEGG, please register and submit an abstract by Friday, May 3. If you would like to present a poster, please submit a title prior to the registration deadline of May 17 (no abstract required for posters).

More information, including a link to register, can be found at the STEGG website: <https://uh.edu/nsm/-stegg/> Richard Meisel (he/him/his) Associate Professor Department of Biology and Biochemistry University of Houston

3455 Cullen Blvd Houston, TX 77204-5001

Office: 453F SR2 Lab: 428/433 SR2

rpmeisel@uh.edu bchs.uh.edu/~rpmeisel 1-713-743-3607

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

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Ksiaz Castle Poland Genetics Sep10-13

Hello, on behalf of the organizational and scientific committees I would like to ask you to send an invitation to participants or post information about the international conference organized by our Department on the website. Below I am sending information about the conference and a link to the website. We have invited speakers with very interesting presentation topics.

On behalf of the organizing and scientific committee of the conference, we cordially invite you to participate in the jubilee international conference XXXth Genetic Days. The conference will be held on September 10-13, 2024, at Książ Castle in Poland.

The conference covers a wide range of topics related to animal and plant genetics, including the analysis of polymorphisms and various omics, the use of artificial intelligence in genetic analysis, and the application of genetics in forensics.

Further details can be found on the conference website www.30thgeneticdays.pl Additionally, a show of Silesian horses is planned as part of the conference. The only stud of these horses is located in the Książ Stallion Herd in historic stable buildings. We look forward to meeting you in September at the beautiful Książ Castle.

Thank you very much and best regards Magdalena Zatoń-Dobrowolska

Dr hab. inż. Magdalena Zatoń-Dobrowolska, profesor uczelni Uniwersytet Przyrodniczy we Wrocławiu Katedra Genetyki

Dr Magdalena Zatoń-Dobrowolska

Associate professor

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ORCID0000-0002-3096-4113

Administratorem Państwa danych osobowych w związku z prowadzoną korespondencją jest Uniwersytet Przyrodniczy we Wrocławiu, ul. C. K. Norwida 25, 50-375 Wrocław. Administrator powołał Inspektora Ochrony Danych, z którym można skontaktować się za pomocą e-mail (iod@upwr.edu.pl).

Państwa dane osobowe przetwarzane będą w celu prowadzenia niniejszej korespondencji, udzielenia informacji i przez czas jej trwania. Przysuguje Państwu prawo dostępu do danych, ich sprostowania, ograniczenia przetwarzania, usunięcia, a także sprzeciwu wobec przetwarzania oraz wniesienia skargi do Prezesa Urzędu Ochrony Danych Osobowych. Szczegółowe informacje na temat ochrony danych osobowych dostępne są w Polityce Prywatności.

Magdalena Zatoń-Dobrowolska <magdalena.zaton-dobrowolska@upwr.edu.pl>

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Montreal BioinformaticsOpenSource Jul15-16

BOSC 2024 dates: July 15-16, as part of ISMB 2024 Location: Montréal, Canada, and virtual Website: <https://www.open-bio.org/events/bosc/> Key Dates April 19: Abstract submission deadline (for talks and posters) (11:59 p.m. Any Time Zone) May 13: Talk/poster acceptance notifications May 20: Late poster abstract submission deadline July 12-16: ISMB (BOSC will be the last 2 days)

About BOSC Since 2000, BOSC has provided a forum for sharing ideas and results in open source bioinformatics and open science. Our annual two-day program includes keynote talks, longer and shorter (lightning) talks from submitted abstracts, posters, panel discussion, Birds of a Feather, and more! This year's special theme is open approaches to AI/ML in bioinformatics; we are planning a joint panel with the MLCSB COSI! Our keynote speakers will be Mélanie Courtot and Andrew Su.

We hope you'll join us for our 25th anniversary this July in Montréal (or online)!

BOSC topics include (but are not limited to): Open

Science and Reproducible Research Open Biomedical Data Citizen/Participatory Science Standards and Interoperability Data Science Workflows Translational Bioinformatics Open Science Developer Tools and Libraries Inclusion, Outreach and Training AI/ML: Open Approaches

Submit an abstract! Abstract submission is now open! (<https://www.open-bio.org/events/bosc-2024/-submit>) We encourage you to submit abstracts on any topic relevant to open source bioinformatics or open science. After review, some abstracts will be selected for lightning talks, longer talks, or posters.

Abstract submission is via ISMB's EasyChair (linked from our submission page). Note that ISMB requires a short (< 250 words) text-only abstract for all submissions (talk or poster), plus a "long abstract" (PDF, 2 pages max) if you want to be considered for a talk. Please see our submission page for more information.

New ISMB rule this year: a presenting author may only present ONE talk or poster. If you want to present your work as both a talk and a poster, you have to do a separate poster submission with a different presenting author.

We hope to see you (in person or virtually) at BOSC 2024!

Sincerely,

BOSC 2024 Organizing Committee (Nomi Harris, Karsten Hokamp, Swapnil Sawant, Hervé Ménager, Monica Munoz-Torres, Deepak Unni, Jason Williams, Chris Fields, Jessica Maia)

BOSC Outreach & Social Media: Mailing list (low-traffic, announcements only): <https://groups.google.com/forum/#!forum/bosc-announce> LinkedIn: <https://www.linkedin.com/groups/14344023/> Mastodon: <https://genomic.social/@BOSC> Bluesky: <https://bsky.app/profile/bosc.bsky.social> Slack: https://join.slack.com/t/obf-bosc/-shared_invite/zt-n5ur1gsj-z2C~69.4lYTFPg5tbWA8Ew Monica Munoz-Torres <monimunozto@gmail.com>

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Montreal ChangingWorldEvolution Jul26-30

Dear colleagues,

We are organizing a symposium in the joint Evolution conference in Montreal on 26-30 July 2024 *‘‘Predicting evolutionary responses to a changing world’’* Submission of talks for the symposium is open to anyone attending the conference. You can register here: <https://www.evolutionmeetings.org/registration.html> *Title* Predicting evolutionary responses to a changing world

Organizers Moi Exposito-Alonso, moisesexpositoalonso@gmail.com, (SSE, ESEB) Stephen Keller, srkeller@uvm.edu, (SSE) Katie Lotterhos, k.lotterhos@northeastern.edu, (SSE, ASN) Seth Rudman, seth.rudman@wsu.edu, (SSE)

Abstract Predicting evolution is both a fundamental test of our understanding of evolutionary processes and a management necessity. Forecasting biodiversity loss depends on accurately projecting how novel environments will disrupt existing adaptation and predicting the capacity for new adaptive responses. New theory and empirical data are needed to build, test, and refine these different areas of prediction. This symposium will bring together researchers working across systems and approaches to share the latest theory, case studies, and critical tests needed to evaluate the potential and limitations of predicting evolution. We welcome theoretical models of evolution in changing environments, genomic forecasting, evolve & resequence experiments, and studies of reaction norms or rapid evolution in wild populations responding to environmental change. The aim is to share new findings and ideas to spur integrative research on how, when, and where we can accurately predict evolutionary responses.

Why do we do this symposium? The potential for adaptation to rescue populations facing rapid environmental change has brought renewed focus and urgency to the longstanding goal of predicting adaptation. Massive temporal and spatial genomic datasets combined with growing data streams from high-throughput phenotyping and remote sensing provides promise of major advances, but our tools to mine these data, our conceptual frameworks, and our integration across sub-disciplines are limiting the pace of progress. To encourage integration and spur new solutions we propose to bring together evolutionists focused on predicting adaptation working in disciplines including landscape genetics, experimental evolution, population genomics, and evolutionary theory. This multidisciplinary symposia will provoke a much needed conversation on best practices in the design of studies, the sharing of data and code in global repositories, and key areas for analytical and theoretical advances.

Mois̃i, $\frac{1}{2}$ s Exp̃i, $\frac{1}{2}$ sito Alonso
<moisesexpositoalonso@gmail.com>

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Montreal EvolutionStories Jul28

Subject line: Call for Story Collider Pitches for the 2024 Evolution Meeting in Montreal

SSE, ASN, ESEB, and SSB are teaming up with The Story Collider < <http://storycollider.org/podcast> > for a science storytelling show on July 28th as part of the in-person portion of the 2024 Joint Congress on Evolutionary Biology < <https://www.evolutionmeetings.org/> > (Evolution 2024)! The theme for this event is ‘‘Throughout the Distribution,’’ and will feature 5 stories from 5 different viewpoints that represent the diversity of experiences in evolutionary biology.

Requirements:

The only requirement is that the story must be about you. We’re seeking true stories about your personal experiences with science to be included in the show. These must be stories-not lectures-with a beginning, middle, and end in which you undergo a change.

All you need at this point is the seed of an idea for your story. It can be about almost anything:

* Perseverance and obstacles overcome (whether professional or scientific) * Expectations upended * Finding community, belonging, or acceptance in biology * Adventure and danger * Coming to a very changed perspective from where you started * Being in over your head or a rough day in the field * Conquering fears * Finding work/life balance * Being inspired * Standing up for yourself * An important experiment * Misadventure, love, or loss * How you first fell in love with science * How your work has affected your personal life

The Story Collider producers will help you develop this idea into an eight-to ten-minute-long story. For further inspiration, you can listen to examples of our last Story Collider Event in 2019 on SoundCloud. < <https://soundcloud.com/sse-communications> >

How to apply:

If you’re interested, please email the Story Collider producers at stories@storycollider.org by May 17th, 2024 and include a short (1-2 paragraphs) summary of your story and ‘‘Evolution 2024’’ in the subject line.

Deadline: May 17th, 2024

Primarily, the producers will look for a strong story arc - a change that takes place in the storyteller from beginning to the end. If selected, storytellers will work with our producers to develop their stories in the weeks leading up to the show. The storytellers will perform their stories at the Story Collider event at 7:00 pm on July 28th at the in-person portion of the Evolution 2024 meeting in Montreal.

Anne CHARMANTIER
<anne.charmantier@cefe.cnrs.fr>

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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.

Registration and abstract submission are open now.

Note that 1 May is the deadline for talk submissions

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.

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 <r.k.butlin@sheffield.ac.uk>

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Montreal Two ISMB Jul12-16 Orthologs Jul17-18

Intelligent Systems for Molecular Biology (ISMB 2024) - Evolution and Comparative Genomics (EvolCompGen) track - July 12-16, 2024 - Montreal, QC, Canada.

CALL : abstract submissions for Talks and/or Posters.

SUBMISSION DEADLINE : April 19

Webpage: https://evolcompgen.org/meetings/-ismb_2024 Abstract submission deadline: April 19, 2024 Talk and/or Poster acceptance notifications: May 13, 2024 Late poster submission deadline: May 20, 2024 Late poster acceptance notifications: May 28, 2024

Scope: The goal of the EvolCompGen track is to foster exchange and collaborations between developers and users of computational methods in evolution and comparative genomics. The track will feature a mix of proceedings talks and contributed talks from the submitted abstracts. In addition, there will be a poster session.

The selection will be made by a committee chaired by Edward Braun (University of Florida) and Katharina Jahn (Free University of Berlin, Germany), based on the following criteria: (i) significance and novelty of the contribution; (ii) completeness of the description of methods, data, and analysis; (iii) quality of the presentation. Talks can be on unpublished work or work published after January 1, 2023, and delivered by speakers at any career stage.

Moreover, authors of selected talks/posters will be eligible for grants to cover registration fees. The procedure for application will be communicated to the relevant people in the talk/poster acceptance email.

Further information on abstract submission deadline and guidelines can be found here: <https://www.iscb.org/-ismb2024/submissions/abstracts> PLEASE FORWARD THIS ANNOUNCEMENT!

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

CALL : abstract submissions for Talks and/or Posters.
SUBMISSION DEADLINE : April 26, 2024

Webpage: <https://event.fourwaves.com/qfo8> Talk
and/or Poster Acceptance Notifications: May 17, 2024

Confirmed Invited Speakers : Fiona Brinkman (Simon Fraser University), Elena Kuzmin (Concordia University), Markus Hecker (University of Saskatchewan), Christine Orengo (University College London).

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

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

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

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

Aïda Ouangraoua <Aida.Ouangraoua@USherbrooke.ca>

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

Montreal WithinOrganismConflicts Jul26-30

Dear colleagues,

We invite submissions to the symposium “Within-organism conflicts” to be held at the 3rd Joint Congress on Evolutionary Biology (<https://www.evolutionmeetings.org/>), July 26-30, 2024, in Montreal.

www.evolutionmeetings.org/), July 26-30, 2024, in Montreal.

ABOUT THE SYMPOSIUM Within-organism conflicts arise when the fitness optima of different organismal parts - genes, chromosomes, genomes, cells - do not align. By now, the threat of selfish genetic elements and selfish cell lineages to the integrity of organisms is well-documented, but they have been researched piecemeal and so we lack a common framework for their study. What do different within-organism conflicts have in common? How are they managed so that organisms retain their primacy as the ultimate beneficiaries of adaptation? This symposium will explore both the variety of internal conflicts that exist in nature as well as the variety of ways that organisms cope and adapt in the face of pressure from within. We will bring together empirical researchers studying diverse systems with theorists to stimulate interactions, and we will seek general principles underlying the evolutionary causes and consequences of within-organism conflicts.

Our invited speaker is Pavitra Muralidhar from the University of Chicago.

REGISTRATION Be sure to register for the conference by May 1 and indicate your interest in our symposium. Details here: <https://www.evolutionmeetings.org/-registration.html> Don't hesitate to get in touch if you have any questions!

All the best, Arvid Ågren, agrenj@ccf.org Manus Patten, mmp64@georgetown.edu Martijn Schenkel, m.a.schenkel@rug.nl

Manus Patten <mmp64@georgetown.edu>

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Online ESEB InternalConflictsSTN Apr18

Dear colleagues,

We would like to invite you to the next online seminar for the “Internal Conflicts and Organismal Adaptation” Special Topic Network (STN) funded by the European Society for Evolutionary Biology, which will take place on April 18th at 15:00 UTC. Our speakers for this seminar are:

Hanna Johannesson (Stockholm University): The spore killers: fungal meiotic drive elements. Cody McCoy

(Stanford University): Immunology and disease in human pregnancy.

We also plan to give some updates on some upcoming events and other things we have planned for the STN. We expect the meeting to take approximately 1-1.5 hours.

Meeting details: Link: Zoom < <https://georgetown.zoom.us/j/96080831086> > Date: April 18th, 2024. Time: 15:00 UTC.

If you would like to get on our mailing list and take part in our upcoming events, please sign up HERE < https://docs.google.com/forms/d/e/1FAIpQLSeJkKjGDXh76JYjqxLS035D_Zhpo3IG00HHD8G56w1zaw3Q/viewform?usp=sf_link > or visit our website (<https://internalconflictsstn.wordpress.com/>) for more information.

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

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

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OnlineSeminar ESEB STN Speciation Apr30

Dear colleagues,

The next instalment of the online seminar series organised by the ESEB-funded STN network « Integration Of Speciation research » ([<https://speciation-network.pages.ist.ac.at/>]) will be held on 30 April 2024, 5 pm CET.

The upcoming session addresses the topic of “Spatial patterns of speciation”. We welcome speakers Gideon Bradburd and Lacey Knowles (University of Michigan, USA).

The session will last 1.5 hours, with the first hour dedicated to talks from our speakers followed by questions. The last half-an-hour is dedicated to a more general discussion.

To attend the session live, please use the following

link: <https://gu-se.zoom.us/j/63975939157> Talks (but not the discussion session) are recorded and made available here: https://www.youtube.com/channel/UCIEkDdE_5sDw70SQq78DIAA . The IOS network aims to promote scientific integration and also integration of the community. A main objective on this front is to foster diversity and inclusion across the field. The seminar series and subsequent discussion is open to everyone, from students to established researchers and non-scientists alike. In order to maximise the geographic diversity of attendees, we will alternate between two time slots every other month: 5 pm CET and 9 am CET. Please help us to circulate this email to anyone who may be interested, especially those in countries that are typically underrepresented in scientific discourse.

The programme of the seminar series is announced by email, on Twitter (@Speciation_net) and on the IOS network website. People who wish to automatically receive the programme and other news from the IOS network can sign up to the network mailing list from the IOS website.

We look forward to seeing you there!

The STN IOS organising committee:

Jonna Kulmuni (chair), Chris Cooney, Sean Stankowski, Carole Smadja (co-chairs), Sonal Singhal, Liz Scordato, Joana Meier, Richard Merrill, Konrad Lohse, Nick Barton and Roger Butlin

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

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Online SociallyTransferredMaterials May7

Dear colleagues,

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

The BYOF session will last for one hour, where we will

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

Topic: Bring Your Own Fluid Seminars (7 May) Time: May 7, 2024 12:00 PM Amsterdam, Berlin, Rome, Stockholm, Vienna <https://vu-live.zoom.us/j/94238053625?pwd=-ZGRaZWZ2Qk1bUIwYUpLZGg0V0Z0Zz09> 7
May Programme:

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

Plasticity and evolution in the metabolic division of labour in burying beetle families - Eleanor Bladon (Department of Zoology, Cambridge, UK)

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

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

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

The Social Transfer Network organising committee:

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

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

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Reading UK Systematics Jun19-21

Reading Systematics Association Biennial Conference
19th-21st June 2024

The Systematics Association has planned an exciting programme of talks and activities for this year's meeting, our first in-person conference since 2019. You can find more information on the conference website: <https://systass.org/events/biennial/>. The programme is designed to be especially attractive to students:

Just 150 for three days for student Systematics Association members - including the scientific programme, a choice of workshops, refreshments and lunches, and a free welcome drink at our student networking event
Opportunity for students to present their work to a friendly and supportive, specialist audience

Prize for best presentation

Registration and abstract submission closes 31st May 2024.

Julie Hawkins <j.a.hawkins@reading.ac.uk>

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Switzerland Ornithology Jun21-22

Header: Switzerland_Ornithological.symposium.June21-22

Dear colleagues and bird enthusiasts,

As part of the 100-year celebrations of the Swiss Ornithological Institute (Vogelwarte), it's our pleasure to announce a 2-day Scientific Symposium entitled “100 years of Vogelwarte: celebrating bird science”, which will be held on June 21st and 22nd in Sempach, Switzerland.

The aim of this symposium is to bring together researchers on ornithology to discuss current perspectives covering a wide range of topics, from bird monitoring and population modelling, to migration, evolutionary and ecological research and applied conservation. Each topic will be addressed by invited international experts, followed by presentations from researchers at the Swiss

Ornithological Institute to celebrate the wide range of scientific research and achievements carried out at our Institute. We hope that this symposium will provide an opportunity to identify the important and urgent issues that the scientific community needs to address, and that it will kick-start new collaborations. Our list of invited speakers and the scientific program can be found on our website: <https://www.vogelwarte.ch/en/100-years/-centennial-symposium/> There is no registration fee, but we kindly ask you to register early using our website, since we are limited to 350 participants, and places are going quickly. The deadline for registration is April 30th.

Sempach is located in central Switzerland, around 20 minutes from the beautiful city of Lucerne. Sempach is easily accessible by public transport from Zurich (1h30), Basel (1h50) or Geneva (3h30).

Please, do not hesitate to spread the word to colleagues or students.

On behalf of the organizing committee, we look forward to welcoming you in Sempach,

Barbara Helm, Pierre Bize and Reto Burri

Pierre Bize <pierre.bize@vogelwarte.ch>

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Turkey EcolEvolBiology Jul23-25

We are organising 10th EEBST (Ecology and Evolutionary Biology Symposium) in Canakkale/Turkey. This symposium will take part in 23-25 July 2024. Abstract submission deadline is 15th April. Researchers can access and take more information regarding to symposium at <https://eebst.ekoevo.org/> or mail me directly.

Baran Taylan Fidano>>lu
<barantaylanfidanoglu@gmail.com>

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Turkey EcolEvol Jul23-25

We would like to post a reminder about our symposium:

10th ECOLOGY AND EVOLUTIONARY BIOLOGY SYMPOSIUM

Dates: 23-25 July

Location: Canakkale/ Turkey.

KEYNOTE SPEAKERS:

Eörs Szathmáry : The Parmenides Center for Conceptual Foundations of Science, Parmenides Foundation.

Astrid Vik Stronen: University of Ljubljana, Department of Biology.

Jitka Klimesova: Czech Academy of Sciences, Institute of Botany.

Maria Anisimova: Zurich University of Applied Sciences, Institute of Applied Simulation.

For registration and Abstract Submission: <https://eebst.ekoevo.org> Abstract Submission Deadline: 1st May.

Full program will be announced: 1st of July.

For more information, visit <https://eebst.ekoevo.org> or mail eebst@ekoevo.org directly.

Baran Taylan Fidano>>lu
<barantaylanfidanoglu@gmail.com>

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UMichigan Herpetology Evolution Jun27-30

The Society for the Study of Amphibians and Reptiles (SSAR) will meet June 27-30 on the campus of the University of Michigan, Ann Arbor, Michigan, USA. The SSAR is meeting jointly with Partners in Amphibian and Reptile Conservation (PARC) and the International Society for the History and Bibliography of Herpetology (ISHBH) on the Ann Arbor campus of the University of Michigan.

The conference includes numerous events of interest to evolutionary biologists, including several symposia on functional/evolutionary morphology and reptiles & amphibians as models for evolutionary developmental biology. Plenary speakers include Neil Shubin, Kartik Shanker, & Earyn McGee. Symposium details & speaker lineup are available at:

<https://sites.lsa.umich.edu/ummz-ssar2024/schedule/>
See registration links on SSAR 2024 main page: <https://sites.lsa.umich.edu/ummz-ssar2024/> Key Deadlines at a glance:

**Early registration discount ends: April 22, 2024

** Standard registration: April 23 - May 15

**Abstract submission deadline (talks & posters): April 22, 2024

Conference schedule at a glance: <https://sites.lsa.umich.edu/ummz-ssar2024/schedule/> **
Selected events:

Museums Extravaganza: Flagship dinner and tours at the world-famous Museum of Zoology (UMMZ), largest university-affiliated herpetological collection in the world. Also featuring the U-M Museum of Paleontology and U-M Herbarium.

Toledo Zoo day trip: Less than an hour drive from Ann Arbor, the Toledo Zoo is a world-class zoological park that features one of the most comprehensive live herp collections in the US. One of the only North American zoos with tuatara, plus the largest captive crocodilian in the US (the ever-impressive Baru, at 17 feet long and 1500 pounds) and a special collection of venomous snakes that includes several gorgeous *Protobothrops mangshanensis*. Behind-the-scenes tours with Toledo Zoo staff and researchers. Zoo grounds include the ProMedica Museum of Natural History and its Pleistocene bestiary, plus one of the best aquariums in the midwest. Zoo features 150 species of reptiles and more than 60 species of venomous snakes. Space is limited - register soon!

Local field trips: We are excited to offer two half-day trips to natural sites just a short drive from campus: the Edwin S. George Reserve, and the Matthaei Botanical Gardens. Trips include the potential to see some iconic midwestern herps in the wild, including the massasauga, Blanding's turtle, and Butler's garter snake. The George Reserve is a research property administered by U-M Ecology and Evolutionary Biology and has been the focus of decades upon decades of pioneering herpetological research, including Earl Werner's work on amphibian community ecology and Justin Congdon's long-term studies of turtle demography. The George Re-

serve features rugged topography with numerous kettle holes, a steep and sinuous esker, and numerous other glacial landforms. The reserve is continuous with the most expansive forested area in southern Michigan.

Field trip to the U-M's Matthaei Botanical Gardens, just 10 minutes from U-M's central campus, will visit an extensive outdoor garden complex, plus a Conservatory that features fascinating plants from deserts and rainforests around the world. Super bonus: the Garden grounds are one of the best places to see massasauga rattlesnakes in the wild.

Additional travel and lodging information, including room codes for discounted rates in local hotels, is available on the conference website.

Questions: email ssar-2024@umich.edu

Dan Rabosky <drabosky@umich.edu>

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Urfa Turkey Archaeogenomics Nov4-8

Dear colleagues,

Those of you doing archaeogenomics or ancient biomolecules might be interested joining our symposium at the World Neolithic Congress in Sanliurfa, Turkey, November 4-8 2024.

The description of the session is below and the meeting website is: <https://worldneolithiccongress.org/> The deadline for abstract submissions is Apr 30.

Looking forward to seeing you in Urfa!

Mehmet and Wolfgang

Title: Bioarchaeological Perspectives on the Neolithic Transition (G15)

Description: This session will cover bioarchaeological advances that can or will shed new light on the Neolithic from the perspective of natural sciences, broadly including ancient DNA from animal, plants and humans, stable and dietary isotopes, microbiome, proteomics and residue analyses. The scope of the session is multidisciplinary and covers the many regions of the world that have witnessed a transition from foraging to food producing, sedentary lifestyles, including the domestication

of plants and animals.

Emphasis is placed on comparisons of data from before, during and after the transition, between foraging and farming groups, or between regions, which can identify and characterise modes of change or continuity, but also on patterns of assimilation, exchange and admixture. Cross-regional, comparative analyses of bioarchaeological evidence on Neolithic transitions, i.e., from different parts of the world, would also be highly welcome.

We invite contributions of 20 minutes (incl. discussion time) on any of the four themes, or combinations thereof: 1) The roles of human movement and cultural interaction in processes of sociocultural change during the Neolithic transitions, studied through genetic continuity vs. discontinuity through time 2) Individual mobility, kinship practices and social organization in early sedentary communities 3) The domestication of animals and plants, with particular emphasis on the tempo of domestication processes 4) Evidence from dietary isotopes and residue analyses (e.g. proteomics or lipidomics) that are shedding light on changing lifestyles

Organizers: Wolfgang Haak / Max Planck Institute, Germany Mehmet Somel / Middle East Technical University, Türkiye

Mehmet Somel METU Dept. Biology / ODTÜ Biyoloji Bölümü 06800 Ankara, Turkey Tel: +90-543-9799060; Office: +90-312-2106460 Email: msomel@metu.edu.tr Lab: compevo.bio.metu.edu.tr aDNA Lab: <http://adna.bio.metu.edu.tr/> Eco-Evo Society of Turkey: <https://ekoevo.org> Mehmet Somel <msomel@metu.edu.tr>

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Vienna QuantGenetics Jul22-26 DeadlineMay1

Seventh International Conference of Quantitative Genetics (ICQG7), Vienna, July 22-26 2024.

Abstract deadline closes May 1st!!

Registration deadline without an abstract is in the end

of May, 2024.

Please make sure to register early, we aim for 500-750 participants and places are going quickly!

Register here: <https://icqg2024.ista.ac.at/registration/>
Our list of invited speakers can be found here: <https://icqg2024.ista.ac.at/contributed-talks/> ICQG7 will bring together researchers with a focus on theory and methodological development. We aim to represent the full range of applications of quantitative genetics - from plants, crops and trees to livestock to humans including common disease, to wild populations and laboratory model species. We aim to focus on the presentation and discussion of state-of-the-art results, theoretical developments and new methodologies, and we will prioritise unpublished research.

The conference provides a forum to highlight novel, principled statistical approaches which may be relevant to the problems faced across a range of applications. In the genomics era the integration of quantitative genetics theory across species applications is converging, and new quantitative trait phenotypes such as single cell gene expression are being studied. This represents an exciting time for understanding and translating the contribution of genetic variation of quantitative traits. Make sure you take part!

For more information, please visit our website <https://icqg2024.ista.ac.at> or get in touch with us at icqg7@ista.ac.at, or <https://twitter.com/icqg2024> Conference organising committee:

Matthew Robinson (ISTA) Nicholas Barton (ISTA) Michaela Pavlicev (Vienna University) Wolfram Weckwerth (Vienna University) Christian Schlötterer (VetMed University Vienna) Magnus Nordborg (Gregor Mendel Institute, Vienna) Kelly Swarts (Gregor Mendel Institute, Vienna) Frederic Berger (Gregor Mendel Institute, Vienna)

Matthew R. Robinson Medical Genomics Group|Institute of Science and Technology Austria|Am Campus 1, 3400 Klosterneuburg, Austria

<https://ist.ac.at/en/research/robinson-group/> Tel: +43 2243 9000 2173 Email: matthew.robinson@ist.ac.at

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AngliaRuskinU PlantEvolution

About the Project

Fixed term contract for 3 years, commencing September 2024.

Bursary of 19,237 per annum and a full fee-waiver for UK tuition fees.

Closing date:31 May 2024 Interview date:TBC June 2024 About Anglia Ruskin University: Anglia Ruskin is a vibrant workplace and our university is recognised both nationally and internationally. We have ambitious plans for the future, and we are determined that our students and staff will realise their full potential. Our main campuses in the cities of Cambridge, Chelmsford, London and Peterborough have been transformed with major capital investment. With an annual turnover of over 200m, we are a major force for higher education and one of the largest universities in the East of England.

About the position: Somatic mutations are genetic changes which occur in the cells of organisms during their lifetime. These somatic mutations lead to an increasing 'mosaic' of genetic variation within an organism. They can have profound effects including the development of cancer and they have long been theorised to be a driver of ageing. The principles and consequences of somatic evolution are an emerging field in biology yet remain understudied in plants.

Plants are particularly interesting because mutations that occur in meristematic tissues will be passed on to all descendent cells, and eventually the gametes at branching termini, blurring the distinction between somatic and germline evolution.

This PhD aims to investigate somatic mutation rates and processes in plants using different sequencing technologies in a model organism and in wild populations. Annual Arabidopsis and ancient, long-lived trees such as oaks (*Quercus*) offer two ends of the lifespan scale in plants, providing tractable systems in which to investigate the principles of somatic evolution in plants. In recent years excellent genomic resources have been developed across a wide range of model and non-model plant species - for example the Darwin Tree of Life (DToL) has produced chromosomal-level assemblies for both Arabidopsis and *Quercus robur* (English Oak). Using these systems, and benefitting from open-source data from DToL, we will:

investigate somatic mutational processes across different age classes in Arabidopsis compare sequencing technologies in calling somatic mutations in a long-lived oak tree look across a population of age classes in oak trees to see how somatic mutation rate varies The student will benefit from a very active and interdisciplinary collaborative network across Anglia Ruskin University, the University of Cambridge, and the Wellcome Sanger Institute.

Through established partnerships, the student will have access to DToL project resources. A comprehensive training programme will be provided comprising both specialist scientific training and transferable and professional skills. The student will develop skills in experi-

mental design in both field collection and plant growth experiments and how to produce (this may involve laser-capture microdissection and/or flow sorting of cell populations) and analyse genomic data (duplex and long read sequencing) for somatic evolutionary studies.

About the Studentship: A 3-year studentship is offered, intended to start in September 2024, providing a tax-free stipend of 19,237 per annum plus tuition fees at the UK rate. Due to funding restrictions, this studentship is only available as a full-time position and to UK candidates.

Project location: Cambridge campus. Prospective candidates who would not be Cambridge-based are encouraged to contact the principal supervisor prior to application (contact details below).

Candidates for this PhD Studentship must demonstrate outstanding qualities and be motivated to complete a PhD within 3 years.

Qualifications: Applicants should have a minimum of a 2.1 Honours degree in a relevant discipline and a relevant level 7 (or equivalent) qualification (e.g., Masters degree). An IELTS (Academic) score of 6.5 minimum (or equivalent) is essential for candidates for whom English is not their first language.

In addition to satisfying basic entry criteria, the University will look closely at the qualities, skills, and background of each candidate and what they can bring to their chosen research project in order to ensure successful and timely completion.

A strong interest in experimental work and data analysis is required, along with the ability to communicate scientific work. Experience in bioinformatics, statistics, genetics, and/or genomics is highly desired.

How to apply: To apply, please visit Biology PhD, click 'Apply online' and complete the application form for full-time study with a start date of September 2024. Please ensure the reference 'PhD Studentship: Somatic evolution in plants' is clearly stated on the application form, under the title 'Outline of your proposed research'.

Within this section of the application form, applicants should include

— / —

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>

Berlin AlgalPathogens

REMINDER Application deadline: 22.04.24

Project: PatHogens of Algae for Biocontrol and Biosecurity (PHABB)

Funded by the prestigious HORIZON-MSCA-2022-DN program of the European Commission, PHABB < <https://mcam.mnhn.fr/en/about-phabb-pathogens-algae-biocontrol-and-biosecurity-6679> > unites eight European institutions alongside the University of Aberdeen, thanks to co-funding by UK Research and Innovation. Collaborating with several industry partners, our mission within PHABB is to cultivate the next cohort of researchers and engineers poised to address the intricate biological and evolutionary mechanisms underpinning microbial community dynamics, virulence, and host specificity of pathogens targeting both beneficial and detrimental algae. Our overarching goal is to pioneer novel strategies for disease management in seaweeds and combatting harmful algal blooms. Situated at the Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB) < <https://www.igb-berlin.de/en> > in Berlin, the doctoral project within PHABB aims to unlock the mysteries surrounding harmful algal bloom (HAB) pathogens. Our objectives encompass identifying pivotal factors influencing disease dynamics (including anthropogenic stressors, such as elevated temperature and various pollutants), evaluating adaptation to novel environments through experimental evolution, and exploring the significance of HAB diversity in pathogen resistance. Employing a diverse array of methodologies, including experimental assays, field collections, metabarcoding, and transcriptomics, we aim to illuminate the intricate interplay between algae and their pathogens.

The successful candidate will enroll in a PhD program at the Free University Berlin, benefiting from two planned secondments: at BioPol (Iceland) and at the University of Aberdeen (UK). Your tasks

§ Designing and executing laboratory experiments focusing on various HAB species and their pathogens

§ Analysing field plankton samples, employing microscopy and cutting-edge metabarcoding techniques

§ Isolating and processing RNA/DNA extracted from both HAB species and their respective pathogens

§ Publishing in scientific journals and conference presen-

tations

§Active participation in PHABB Doctoral Network

Your profile

§Master's Degree in Biology or related field

§Demonstrated experience in experimental work

§Experience with molecular/genomic techniques would be advantageous

§Strong statistical or bioinformatic skills

§Collaborative team player

§Effective communication skills in English, including scientific writing

Eligibility To be eligible for this PhD position the applicant should fulfil the trans-national mobility criterion, i.e. not have resided or carried out their main activity (work, studies, etc.) in Germany for more than 12 months in the 36 months immediately before the recruitment date unless as part of a compulsory national service or a procedure for obtaining refugee status under the Geneva Convention. In addition, the applicant has to be at the date of recruitment a doctoral candidate (i.e. not already in possession of a doctoral degree). Researchers who have successfully defended their doctoral thesis but who have not yet formally been awarded the doctoral degree will not be considered eligible.

Our offer We offer an exciting position in an international and dynamic team of researchers, and an attractive scientific working environment including excellent equipment and technical support. We foster flat hierarchies and active participation and offer a variety of training opportunities < <https://www.igb-berlin.de/en/doctoral-education> >. We actively support the reconciliation of work and family life < <https://www.igb-berlin.de/en/equal-opportunities> >. Qualified women are particularly encouraged to apply. The IGB is committed to diversity < <https://www.fv-berlin.de/en/careers/diversity> >. We welcome every application, regardless of gender and gender identity, origin, nationality, religion, belief, health and physical disabilities, age or sexual orientation. Disabled applicants with equal qualification and aptitude will be given preferential consideration. This is a full-time position with 3 years duration and a tentative start date of 01.07.2024 (or shortly thereafter). For the salary of the Marie Skłodowska-Curie PhDs in Germany the European Commission provides a monthly Living Allowance of 3,342.20 euro plus a monthly Mobility Allowance of 600 euro. Researchers who have or acquire family obligations during their employment are

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>

CEBC France AlbatrossNaturalSelection

I have a fully funded PhD position available for a student to study current natural selection in albatross populations.

The student will apply and develop cutting-edge statistical methods to quantify patterns of natural selection acting on series of traits, infer the causal mechanisms of selection, and study the interplay of demography and selection in wild populations. The work will use data from the long-term monitoring of several albatross populations at French sub-antarctic territories. The student will contribute to fieldwork on Kerguelen island and collect original data on nest properties.

The student will be based at CEBC (affiliated La Rochelle Université¹ - CNRS), Chizy¹, France. The research campus is located in the middle of a forest in the countryside, 1h from the Atlantic coast. The expected starting date is October 2024, for a duration of 3 years.

The project description can be found here: <https://timotheenivalis.github.io/Rnotebooks/PhDProjectEnglish.pdf> Apply by sending a CV and cover letter to timothee.bonnet@cebc.cnrs.fr. Interested candidates can contact me informally for extra details.

Timothée¹ Bonnet

Timothée¹ Bonnet, PhD Chargé¹ de recherche / Researcher

Centre d'études Biologiques de Chizy¹ UMR 7372 Université¹ de la Rochelle - CNRS 405 route de Prissé¹ la Charrière¹ 79360 Villiers en Bois France

timothee.bonnet@cebc.cnrs.fr

<https://timotheenivalis.github.io/>

[https://-](https://timotheenivalis.github.io/)

CPG Stockholm PollinatorMuseumics

4-year PhD on pollinator genomics with focus on museum samples (deadline: 30 April 2024)

The Department of Zoology invites applications for a four-year PhD position based at the Centre for Palaeogenetics in Stockholm. The project is aimed at investigating temporal patterns of population structure and genomic diversity in pollinating insect populations. The analyses will use state-of-the-art genomic and palaeogenomic methods with focus on recovering DNA from museum specimens collected throughout the last 200 years. This will be a conservation genomics project part of a research programme funded by the Swedish Research Council and focused on investigating the genomic effects of population decline in insect pollinators. The PhD student will join the research group led by David Díez-del-Molino at the Centre for Palaeogenetics located on the Stockholm University campus.

The following criteria will be used to fill the position: the candidates' documented knowledge in a relevant field of research, written and oral proficiency in English, the capacity for analytical thinking, the ability to collaborate, as well as creativity, initiative, and independence. The assessment will be based on previous experience and grades, the quality of the degree project, references, relevant experience, interviews, and the candidate's written motivation to apply for the position. Experience in population genetics, insect ecology, bioinformatics, and working in a DNA laboratory (ancient/historical/modern) are relevant qualifications.

Check the full requirements and apply here <https://www.su.se/english/about-the-university/work-at-su/available-jobs/phd-student-positions-1.507588?rmpage=job&rmjob=23451&rmlang=UK> More information about the Centre for Palaeogenetics and my research group can be found here <https://palaeogenetics.com> For informal inquiries, contact David Díez-del-Molino (david.diez@zoologi.su.se)

All welcome to apply!

David Díez-del-Molino

Centre for Palaeogenetics Stockholm University Svante Arrhenius väg 20C SE-106 91 Stockholm, Sweden

Mobile: +46(0)739512922 diez.molino@gmail.com @in-

dianadiez

David Díez <diez.molino@gmail.com>

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Finland MicrobiomeThermalAdaptation

Doctoral Researcher, Gut microbiome and thermal adaptations in wild birds

A Doctoral Researcher position is available at the Department of Biological and Environmental Sciences, University of Jyväskylä, Finland, in the group of Dr. Suvi Ruuskanen. The Doctoral Researcher will work in an ERC-funded project where the overarching aim is to understand the significance of the gut microbiome in thermal adaptations in birds within and across generations, and species. Starting date is August 2024 or as mutually agreed.

PROJECT DESCRIPTION

All animals on our planet carry microorganisms in their gut. The gut microbiome has recently been shown to be strongly linked to health in humans and model animals. However, we still have limited knowledge on how the gut microbiome can contribute to host adaptation, particularly in light of climate change. Interestingly, studies in vertebrate and invertebrate model organisms, and our own data in great tits (*Parus major*) suggest that the microbiome changes with temperature, and there is proof-of-concept data that this compositional shift in the microbiome occurs as an adaptive response to cold exposure. In this project the student will study the short-term flexibility of the gut microbiome to environmental (incl thermal) challenges, and its adaptive function in thermoregulation, using great tits as the model species. This will involve conducting novel experiments on wild-caught captive birds (e.g. manipulation of temperature and other stressors as well as microbiome manipulations), combined with physiological measurements in the lab, using a variety of bioinformatic and statistical tools.

DUTIES

The doctoral researcher position will involve conducting experiments with captive birds at the Konnevesi Research station, contribution to laboratory analyses (physiological and molecular), bioinformatic analyses of 16s

rRNA and possibly other sequencing data, manuscript preparation and supervision of students.

QUALIFICATIONS

We are seeking a highly motivated, innovative, productive person, who will be willing to gain experience both in the lab and in the field and contribute intellectually to the project development. Suitable candidates should have a Msc in ecology/evolution, (eco)physiology, molecular biology, microbial ecology or related field by the time of starting the position, and interest in host-microbiome research and bioinformatics. Experience in laboratory analyses or working with (wild) animals will be considered beneficial.

The duties, qualification requirements and language skills of a Doctoral Researcher are stipulated by the University of Jyväskylä Regulations and language skills guidelines. The MSc degree required for the position must have been completed before starting the position. Doctoral Researcher needs to be also enrolled in the doctoral programme which can be applied from the Faculty of Mathematics and Science after selection for the position.

WE OFFER

Funding for 4 years in the doctoral program of the University of Jyväskylä. Supervision in all aspects of the work (from field to lab to computational skills), possibility to join workshops to improve specific skills in e.g. bioinformatics, data analysis. International, enthusiastic working environment (working language is English) in a friendly research group with a large collaborator network. Well-equipped research station (Konnevesi research station), labs and state-of-the-art scientific equipment, software, access to journals and scientific databases. Resources for travel to conferences or workshops abroad.

The Doctoral Researcher will be supervised by Dr. Suvi Ruuskanen, Dr. Charli Davies and Dr. Antoine Stier

At the University of Jyväskylä, you are a recognized member of our community with an ample opportunity to be drawn into international research. You get to participate in our international and multidisciplinary community, where everybody's welfare is essential. You will work in an inspiring and lively campus area and an environment that supports a healthy and active lifestyle.

Finland has a high standard of living with healthcare, free schooling (also in English), affordable childcare, and good family benefits. The city of Jyväskylä is located in central Finland amidst Finnish lakes and has excellent opportunities for different nature, outdoor, and sports activities. It is a major educational center, whose large

student population is responsible for a vibrant cultural scene. To find useful information about the University of Jyväskylä, the City of Jyväskylä, and living in Finland, see the University's Handbook for international staff and visitors.

The initial annual salary will be approximately 30,000 EUR (gross income, including a holiday bonus). With progress of the thesis work, the salary will be revised in accordance with the Collective Agreement of Finnish Universities. The employment starts with a trial period of six months.

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FrenchGuiana PalmsEvolution

Location : Cayenne, French Guiana Ph.D. Start Date: September 1, 2024 Grant Duration: 36 months

ERC-funded PhD in Evolutionary Genomics of Amazonian palms.

As part of the ERC Starting Grant DOPAMICS project, we are offering a PhD position in Evolutionary Genomics of Amazonian palms in Cayenne (French Guiana), under the supervision of Mathieu Chouteau (HDR, CNRS UAR LEEISA) and Louise Brousseau (IRD UMR AMAP, DOPAMICS project coordinator).

DOPAMICS investigates how climatic adaptation and ancient domestication have influenced the microevolutionary history of Amazonian palms and shaped the diversity of forest landscapes in French Guiana. Within WP3, the proposed topic will aim to retrace the microevolutionary history of palms using “omics” approaches, drawing on genomic data acquired through a large-scale exon capture experiment, and on fruit metabolomic data acquired by GC-MS.

We are seeking a candidate with a Master degree in Ecology/Evolution or Bioinformatics and a strong interest in Evolutionary Ecology and Genomics for a recruitment on 01/09/2024.

Detailed information is available here: <https://euraxess.ec.europa.eu/jobs/187422> Applications must be submitted on the “IRD Emploi” website by

26/04/2024: https://emploi-recrutement.ird.fr/offre-de-emploi/emploi-contrat-doctoral-en-genomique-evolutive-des-palmiers-d-amazone-h-f_182.aspx

Mathieu Chouteau and Louise Brousseau

Chargé_i¹/₂ de recherche CNRS USR MIXTE 3456 LEEISA Centre de Recherche de Montabo 275 Route de Montabo 97300 Cayenne CEDEX Guyane Française_i¹/₂aise 0694 40 39 61 (5h de moins que la France Métropolitaine)

Mathieu Chouteau <mathieuchouteau@hotmail.com>

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HeinrichHeineU PlantEvolution

PhD: HHU_PlantEcologicalGenetics_2024

The Institute for Plant Ecology and Evolution at the Faculty of Mathematics and Natural Sciences of Heinrich Heine University (HHU) Duesseldorf, Germany, invites applications for a

PhD (w/m/d) (50 %, EG 13 TV-L, for 3 years): Rapid Evolution to Changing Environments in Brassicaceae: Bridging Ecology and Genetics

To be filled as soon as possible

Our research focuses on the responses of plant populations to climate change and attempts at disentangling the relative contributions of adaptation, phenotypic plasticity, and range shifts. We also aim to identify the drivers of rapid contemporary evolution and to uncover the genetic basis of climate change adaptation. To examine these themes, we combine traditional field- and greenhouse-based studies, as well as the resurrection approach, with quantitative genetics and ecological genomics. Our lab is integrated in the research initiative TRR 341 on Plant Ecological Genetics (<https://trr341.uni-koeln.de/>).

We are looking for a motivated PhD candidate to study the ecological and genetic adaptation to changing environments in the annual *Brassica rapa* and closely related Brassicaceae species. The candidate is also encouraged to develop related projects within the lab's research framework. The position has a teaching requirement of 2 SWS (contact hours per week).

YOUR TASKS: - Use the resurrection approach to study rapid evolution in Californian *Brassica rapa* populations in response to drought and examine potential costs of

adaptation under water and nutrient limitations (i.e., common garden experiment) - Conduct fieldwork for in situ sampling and scoring of local Brassicaceae species and populations and subsequent common garden experiments to identify intraspecific trait and genetic variation underlying ecological diversification and local adaptation - Apply statistical and computational tools for the analysis of trait, environmental, and next-generation sequencing data - Present research results at conferences and publish in peer-reviewed scientific journals - Supervise and mentor students in the lab

YOUR PROFILE: - MSc in the field of plant biology, ecology, botany, evolutionary or population genetics, quantitative biology or related - Strong interest in plant ecological genetics, quantitative and evolutionary biology, contemporary evolution, and field ecology - Experience conducting large multi-factorial plant experiments (i.e., common gardens, reciprocal transplants, etc.) is preferred - Experience in the use of statistical data analysis and programming languages (e.g., R, Java, Python) is preferred - Experience with population genetics, NGS data, SNP calling, genome annotation, standard molecular techniques is preferred - The languages spoken in the group are English and German - demonstrated ability to communicate effectively in English is essential (written and spoken) and German would be preferred - Good interpersonal skills (i.e., communication, cooperation, motivate others, open-minded, etc.) - Lawful ability to work in the EU (i.e., Schengen residence/work permit)

WE OFFER: - A unique, dynamic, and interdisciplinary research network in the field of Plant Ecological Genetics (TRR 341), funded by the DFG, that bundles the expertise of excellent scientists from seven different research institutions - A comprehensive training program with targeted scientific education in the field of Plant Ecological Genetics as well as complementary training supporting your personal and career development (GEcoGen, iGRAD, JUNO, HeRA) - Family-friendly and multicultural working environment

TO APPLY: Qualified candidates should send their application (Cover letter including statement of interest - max. 2 pages, CV including publication list, contact info of two references, BSc and MSc certificates) by e-mail (one single pdf-file) until 30.04.2024 to elena.hamann@hhu.de.

If you have further questions on the project or position, please contact Prof. Elena Hamann and see lab website <https://www.biologie.hhu.de/institute-und-abteilungen/institute-hhu/pflanzenoekologie>. "Hamann, Elena" <Elena.Hamann@hhu.de>

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JGU Mainz GreekPalaeogenetics

Dear all,

We're seeking a PhD student to join our team at the iome (<https://iome.biology.uni-mainz.de/>) at the JGU University in Mainz, Germany, to work on the genomic investigation of inhabitants of the ancient city of Thessaloniki in Greece.

Details about the position and how to apply (including specific instructions for the cover letter) can be found here:

<https://stellenboerse.uni-mainz.de/HPv3.Jobs/jgu/-stellenangebot/36909/Academic-staff-member> THE PROJECT:

Within the framework of a project funded by the European Union, we are investigating the genetic history of the ancient Greek city of Thessaloniki. The primary goal of this doctoral thesis is to reconstruct the historical development of this city based on the genetics of its inhabitants. Through palaeogenetic analyses of archaeological skeletons, we aim to gain insights into social structures, mobility, migration, and kinship relationships. The palaeogenetic research group at JGU is an internationally recognized anthropological research team investigating biological and evolutionary aspects of key events in human history based on genomes. We are seeking applicants with backgrounds in molecular biology, anthropology, or forensics who enjoy laboratory work and collaborating closely with our team in the palaeogenetic laboratories (<https://palaeogenetics-mainz.de/>), subsequently analyzing the generated genomes with a bioinformatics PostDoc on the computer.

YOUR TASKS:

Your responsibilities will include conducting independent research in the subject area with the aim of completing a doctorate. Generating ancient genomic data in the laboratory and conducting computer-assisted data analysis will be key components of your role, as well as regular collaboration with international project partners, publishing research results in scientific publications, and independently preparing and implementing courses for students within the scope of the teaching load.

Applications can be submitted until May 8th, 2024, using the link provided above. For any further questions, please contact Prof. Joachim Burger, at [jburger@uni-](mailto:jburger@uni-mainz.de)

[mainz.de](mailto:jburger@uni-mainz.de).

Best wishes,

Joachim Burger

“Grant, Dr. Viviane” <vgrant@uni-mainz.de>

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LundU EvolutionaryBiology TrinidadianGuppies

We are pleased to announce a PhD position in Evolutionary Biology at Lund University in Sweden. The preferred starting date is between 1 July and 1 September 2024, for a duration of four years.

Project: Ecology and evolution of phenotypic plasticity in Trinidadian guppies

The overall goal of the PhD project is to better understand how the environment affects genetic and phenotypic variation, and how these insights can be used to improve predictions of evolution. Evolutionary change happens constantly all around us. This contemporary evolution can allow populations to adapt and persist, or contribute to their decline and extinction. Which of the two it will be is often unclear because current methods to predict microevolution work poorly in natural populations. Considering the global environmental crisis, this is particularly alarming. A key cause of the predictive inaccuracy is environmental variation.

This PhD project will investigate environmental effects on additive genetic (co)variances, narrow-sense heritabilities, and evolvabilities. Additionally, as resource availability is a crucial aspect of the environment in many species, it will evaluate to what extent including information on individual resource accrual can reduce environmental bias. The project will combine quantitative genetic experiments in a newly established, state-of-the-art fish research laboratory with analyses of long-term field data, using the well-known Trinidadian guppy system. The successful candidate will have a keen interest in evolutionary biology, quantitative genetics, or related fields. A curious mind, a sense of responsibility, and excellent organisational skills are strong additional merits for the position. Note that, while there may be a possibility for conducting fieldwork in Trinidad, the project neither requires nor guarantees it.

The application deadline is 26 April 2024. Further in-

formation and instructions for applying can be found here: <https://lu.varbi.com/en/what:job/jobID:716838/> If you have further questions on the project or position, please contact Dr. Anja Felmy at anja.felmy@biol.lu.se

Anja Felmy <anja.felmy@biol.lu.se>

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StockholmU Two Genomics

PhD student position at Stockholm University

We have an open four-year position for a PhD student in the Swedish Research Council funded project “Convergent evolution and loss of distyly ’ genetic causes and genomic consequences”. The aim of the project is to investigate the genetic basis and genomic consequences of convergent evolution and loss of the floral polymorphism distyly in *Linum* (wild flaxseed species).

The PhD student will use a combination of experiments, functional genomics and genomic analyses to investigate the genetic basis of distyly in *Linum* and to test hypotheses on the genetic basis and genomic consequences of breakdown of distyly. As there have been multiple losses of distyly in *Linum*, this system is ideally suited for characterizing the genomic consequences of this shift in a comparative framework. The project builds on recently published work from our group (Gutiérrez-Valladares et al. 2022. *Current Biology* 32: 4360-4371).

For this position, we are looking for a person with a strong interest in evolutionary genetics, who enjoys both experimental work and genomic analyses.

The complete ad with information on qualification requirements and instructions on how to apply through the Stockholm University system (application link in ad) is available here: <https://shorturl.at/acvFX> The PhD student will join the research group of Dr Tanja Slotte (<http://tanjaslottelab.se>) and will be enrolled in the research subject Ecology and Evolution at the Dept. of Ecology, Environment and Plant Sciences, Stockholm University. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both evolutionary geneticists, plant biologists, and ecologists. The city of Stockholm is known for its beauty, its buildings and architecture and its abundant clean and open water.

For additional questions on the position, please contact Dr Tanja Slotte directly.

Tanja Slotte Professor, Subject head of Ecology and Evolution Department of Ecology, Environment and Plant Sciences (DEEP) Stockholm University 106 91 Stockholm

E-mail: tanja.slotte_AT_su.se

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PhD student position at Stockholm University

We have an open four-year position for a PhD student associated with the project “Unlocking genetic variation for climate adaptation of crops”.

In this project, we will test whether population genetic methods that identify genetic variants associated with environmental variation can efficiently identify adaptive genetic variation for crop improvement in collections of crop wild relatives. The results can potentially contribute to more efficient utilization of crop wild relative collections to unlock wild genetic variation for food security and fibre production in a changing climate.

The project is funded by Formas and will include collaborations with researchers at the Swedish Agricultural University (Uppsala and Alnarp, Sweden), Durham University (United Kingdom), and University of Granada (Spain).

For this position, we are looking for a person with a strong interest in population genetics, who enjoys both experimental work and genomic analyses.

The complete ad with information on qualification requirements and instructions on how to apply through the Stockholm University system (application link in ad) is available here: <https://shorturl.at/orCY6> Application deadline: April 23, 2024

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

For additional questions on the position, please contact Dr Tanja Slotte directly.

Tanja Slotte Professor, Subject Head of Ecology and Evolution Department of Ecology, Environment and Plant Sciences (DEEP) Stockholm University 106 91

Stockholm

E-mail: tanja.slotte_AT_su.se

Tanja Slotte <Tanja.Slotte@scilifelab.se>

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Toulouse PopGenomicsMetagenomics

Dear Colleagues,

We are offering a 3-year PhD position for a project at the interface between population genomics and metagenomics at INRAE Toulouse, France (Southwest France).

The thesis aims to position genomics and metagenomics of hive products as a new tool for both improving traceability of the hive products and $\frac{1}{2}$ monitoring colony health against the varroa mite. More specifically, the PhD student will (i) conduct a metagenomic analysis of samples from hive products, especially honey and wax, (ii) deploy a population genomics approach for bees tailored to the joint analysis of samples with the massive data available in the laboratory (>1200 honeybee genomes), (iii) demonstrate the utility of these approaches for taxonomic placement of honeybees from different samples of honey and wax with known and unknown origins, (iv) investigate the significance of varroa parasite reads for monitoring infestation dynamics, (v) explore the contribution of plant reads in tracing hive products.

The student must have a master's degree in one of the following thematic fields: evolutionary biology, genomics, population genetics or bioinformatics. Experience or knowledge in environmental DNA, including barcoding or metagenomics, would be a plus but is not required. The candidate should have a strong interest in the analysis of large genetic datasets. Students with a strong scientific curiosity, good interpersonal skills, and effective communication abilities are particularly encouraged to apply.

To learn more about the position and/or apply, please send an email to both Thibault Leroy (thibault.leroy@inrae.fr) and Kamila Tabet (kamila.tabet@inrae.fr) before May 15th.

Best regards,

Thibault Leroy

thibault.leroy@inrae.fr

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UAarhus PrimatePopulationGenomics

Population genomics of speciation in primates

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

Title: Population genomics of speciation in primates

Research area and project description: If you have strong skills in data science and are interested in basic evolutionary questions, then there is a PhD position available. The student will be tightly involved with designing specific research projects in the general area discussed below.

How new species form is a basic unsolved question in evolutionary biology. This position will use modelling and large-scale analysis to identify both processes and specific candidate genes responsible for speciation in primates. This is part of a larger ERC funded project that integrates surveys of spermatogenesis and genome analysis to address these questions.

Genomics data from more multiple individuals of more than 300 primate species will be available at the start of the project and a framework called TRAILS (Rivas-Gonzalez et al., 2024, PLOS Genetics) for analysis has recently been published. New models can also be employed to analyse how the different species have split throughout the phylogeny. Specific focus will be on groups that often hybridise such as macaque species, baboon species and gibbon species, but also the speciation process of human and Neanderthal can be investigated.

Primate X chromosomes evolve extraordinarily fast and are also tightly associated with the establishment of reproductive barriers between emerging species and these can be of specific focus. The results of these evolutionary studies will be intersected with analysis of gene expression during spermatogenesis at the single cell level generated in the research group in order to identify potential functional roles of the genes involved with speciation. The results will also be translated to understand better

what causes reduced fertility in men.

Candidates interested in further information should please contact Mikkel Heide Schierup (mheide@birc.au.dk, or +4527782889)

Please upload a project description (\hat{A} $\frac{1}{2}$ -4 pages). This document should describe your ideas and research plans for this specific project. If you wish to, you can indicate an URL where further information can be found.

Qualifications and specific competences: Applicants must have at least one year of a Master's degree in molecular biology, mathematics, statistics, bioinformatics or similar and have an interest in addressing biological problems with large scale data analyses. An interest in evolutionary biology and/or population genetics will be an advantage. The PhD study can be three years (with an MSc) or four years (with one year of an MSc completed at the time of enrollment)

Place of employment and place of work: The place of employment is Aarhus University, and the place of work is Bioinformatics Research Centre, Universitetsbyen, Building 1872, DK 8000 Aarhus C, Denmark.

Contacts: Applicants seeking further information for this project are invited to contact: Professor Mikkel Heide Schierup (mheide@birc.au.dk)

How to apply:

For information about application requirements and mandatory attachments, please see the 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/> (Note, the online application system opens 1 March 2024)

Choose May 2024 Call with deadline 1 May 2024 at 23:59 CEST. You will be directed to the call and must choose the programme "Population genomics of speciation in primates (Pogspp)". In the boxed named "Study": In the dropdown menu, please choose: "Computer Science"

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 and want to make your opportunities transparent. On our website, you can find information on all types of scientific positions, as well as the entry criteria we use when assessing candidates. You can also read more about how we can assist you in your career planning and development.

Aarhus University's ambition is to be an attractive and inspiring workplace for all and to foster a culture in which each individual has opportunities to thrive, achieve and develop. We view equality and diversity as assets, and we welcome all applicants. All interested candidates are encouraged to apply, regardless of their personal background.

Mikkel Heide Schierup Novo Nordisk Distinguished Investigator Bioinformatics Research Centre, Aarhus University, Universitetsbyen 81, building 1872

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UAlberta Landscape Epigenomics

PhD position in Multi-species Landscape Epigenomics (Venney lab)

I am seeking a highly motivated student for a PhD project on multi-species landscape epigenomics. This is a funded PhD position in the Department of Biological Sciences at the University of Alberta (minimum guaranteed salary of \$25,917/year for 5 years). The start date is anticipated to be January or September 2025 but is negotiable. Previous experience with genomic data or bioinformatics (Linux and R) is an asset.

DNA methylation is a potential underlying mechanism for phenotypic plasticity and can respond to environmental fluctuations such as climate change. Due to the potential for epigenetic inheritance, populations living in different environments could accumulate epigenetic differences over many generations. These methylation differences could slowly lead to genetic divergence over long evolutionary periods due to the mutagenic nature of DNA methylation.

We will assess variation in DNA methylation due to climatic variation and its associations with genetic variation. We have performed ~16X coverage whole genome methylation sequencing for 80 lake whitefish (*Coregonus clupeaformis*) and 80 brook charr (*Salvelinus fontinalis*): 10 fish per species from eight sampling locations across a latitudinal climatic gradient in Hudson Bay and James Bay. We will combine these data with environmental data and ~20X whole genome sequencing data for the

same fish to answer diverse questions on interactions among DNA methylation, the genome, and environmental variation in a natural system.

The successful candidate will be co-supervised by Dr. Clare Venney (<https://clarevenney.weebly.com/>) and Dr. Jean-Sébastien Moore (Université Laval, <https://jean-sebastienmoore.weebly.com/>). The successful candidate can also contribute to upcoming fieldwork in the lab as desired (e.g., potential work in and around Banff and Jasper National Park). Interested candidates should send a CV, unofficial transcripts, and one page cover letter detailing their interest in the position to venney@ualberta.ca on or before July 1st, 2024.

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

Clare Venney Incoming Assistant Professor Department of Biological Sciences University of Alberta

Clare Venney <venney@ualberta.ca>

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

UAmsterdam TheoreticalEcoEvo

We are looking for an enthusiastic and highly motivated PhD-candidate who is eager to study the ecological consequences of sexual size dimorphism using mathematical models. You will be embedded in the Theoretical and Computational department, which is part of the Institute for Biodiversity and Ecosystem Dynamics (IBED) at the Faculty of Science at the University of Amsterdam.

In the animal kingdom, we commonly see species where one sex is larger than the other - a phenomenon called sexual size dimorphism. Despite remarkable differences between the sexes, these are not present early in life for most species. Because many differences between the sexes arise during an individual's development, the ecological conditions experienced early in life influence the expression of sexual dimorphism later in life. To understand the ecological consequences of sexual size dimorphism, we need to know how early-life growth and development shape differences between the sexes.

What are you going to do?

In this project, you will develop sex- and size-structured population models to study how plasticity in growth in body size during development affects the ecological

consequences of sexual size dimorphism. You will use numerical continuation techniques and mathematical bifurcation analyses to analyse these models. While this is mainly a theoretical and computational research project, it is possible and highly encouraged to also carry out some experimental lab work at the University of Karlstad (Sweden) to test model predictions with an empirical fruit fly system.

As long as it fits in the general topic of this research position, you will have flexibility in choosing the questions you wish to investigate.

Possible questions that you may address for this project are:

- * How do changes in early life growth rate and the size at first reproduction affect population dynamics and species persistence in sexual size dimorphic species? *
- How does food availability and size-specific mortality shape sexual size dimorphism, and, vice versa, how do differences in size between the sexes affect the feedback on food availability and population dynamics? *
- What is the effect of resource segregation between the sexes or between life-stages on the ecological dynamics of sexual dimorphic populations? *
- How is sexual size dimorphism shaped by evolution, resource availability, and developmental plasticity?

Application deadline: 20 May 2024

For more information please visit <https://-vacatures.uva.nl/UvA/job/PhD-Candidate-in-Theoretical-Ecology/793274302/> Hanna ten Brink <j.a.tenbrink@uva.nl>

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UCopenhagen MarineMammalAncientDNA

PhD fellowship in Ancient DNA and Palaeoecology of Arctic Marine Mammals at the Globe Institute

We are looking for a highly motivated and dynamic researcher for a 3-year PhD fellowship in Ancient DNA and Palaeoecology of Arctic Marine Mammals. The position will commence on 15th August 2024, or as soon as possible hereafter.

Our group and research The successful candidate will be part of the Molecular Ecology and Global Climate Change group, led by Professor Eline Lorenzen, within

the Section for Molecular Ecology & Evolution based at the Globe Institute. In the group, we integrate biomolecular data from past and present populations of mammal species, in combination with ecological modelling, to understand patterns and drivers of eco-evolutionary change. We are an international group of PhD students and post-docs. We are currently six people in the group - from Denmark, France, Germany, New Zealand, South Africa, and the US. Our work is interdisciplinary and highly collaborative, and we work towards fostering an inclusive, supportive, and team oriented work environment.

The Section for Molecular Ecology and Evolution is one of six research sections at Globe Institute. The research of the section is driven by curiosity and shared excitement for scientific collaboration and discovery and we value a diverse and inclusive scientific environment that fosters creativity. Information on the institute can be found at <https://globe.ku.dk> Your job

The PhD project, as part of the Carlsberg Foundation funded project INTERACT, will examine the Holocene history of Arctic marine mammals, by investigating fossil specimens of several species (incl. beluga, bowhead, polar bear) with ancient DNA and stable isotope analysis. Specifically, your research would focus on investigating patterns of demographic change and shifts in foraging ecology. The fossil data will be understood in the context of the genomic diversity and structuring of contemporary populations. The project includes working in a clean lab environment for ancient DNA data generation, and bioinformatic processing and analysis of the data. The PhD student is expected to first-author papers in international peer-reviewed journals. The PhD student will work closely with collaborators in Canada and Greenland during the project, and with the other members of the Molecular Ecology and Global Climate Change group.

Principal supervisor is Professor Eline Lorenzen, Section for Molecular Ecology and Evolution, Globe Institute, University of Copenhagen, elinelorenzen@sund.ku.dk.

Start: 15 August 2024

Duration: 3 years as a PhD fellow

Job description Your key tasks as a PhD fellow at Globe Institute are:

- Carrying through an independent research project under supervision
- Completing PhD courses or other equivalent education corresponding to approximately 30 ECTS points
- Participating in active research environments including conducting a stay at another research institution
- Obtaining experience with teaching or other types of dissemination related to your PhD project
- Writing a PhD thesis on the grounds of your project

Key criteria for the assessment of applicants You must have qualifications corresponding to a master's degree related to the subject area of the project, e.g. ancient DNA, palaeoecology, evolutionary ecology, population genomics, or a related field. Please note that your master's degree must be equivalent to a Danish master's degree (two year duration).

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

Professional qualifications relevant to the PhD project - Documented experience working in a molecular biology lab; experience working in a clean lab environment is a plus - Strong bioinformatic skills - Experience with quantitative analysis of data - A curious mind-set with a strong interest in combining molecular lab work in the natural and cultural history of the Arctic - Proficient communication and interpersonal skills, the ability to work in teams, and an openness to other cultures - Excellent English skills, written and spoken

Place of employment The place of employment is at the Section for Molecular Ecology and Evolution, Globe Institute, Åster Farimagsgade 5A, 1014 Copenhagen K, Denmark.

About Globe Institute The Globe Institute is part of the Faculty of Health and Medical Sciences at the University of Copenhagen. The Institute's main purpose is to address basic scientific questions through interdisciplinary approaches. The institute operates at the intersection of natural and medical sciences and the humanities. Information on the institute can be found at: <http://www.globe.ku.dk/>. The Globe Institute is committed to creating an inclusive and diverse environment where employees and students can belong and thrive. Check this part of our website for

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UHohenheim Germany TheoreticalEvolution

The Department of Eco-Evolutionary Modelling at the University of Hohenheim in Stuttgart (Germany) seeks a PhD student in Theoretical Ecology (m/f/d). Preferred starting date is 1 October 2024, for a duration

of three years. Salary and conditions are according to public service positions in Germany (TV-L E13; 65%; see <https://oeffentlicher-dienst.info/tv-l/allg/>). Availability of this position is subject to a positive funding decision by the German Research Foundation (DFG, decision expected in April 2024).

The PhD student will investigate the role of biotic interactions for eco-evolutionary dynamics of biodiversity and interaction networks. The project is led by Dr. Korinna Allhoff (Theoretical Ecology) and Prof. Dr. Frank Schurr (Landscape Ecology). It is part of the joint research group FLINT that investigates fitness consequences of biotic interactions in various systems from both a theoretical and empirical perspective (see <https://ecology.uni-hohenheim.de/flint> for more information). Students will benefit from the diverse expertise of 12 PIs and from being part of a cohort of 5 PhD students that collaborate within FLINT. Our project focuses on ecological network models, where nodes represent species or individual organisms and links represent biotic interactions between them. The PhD student will address fundamental questions about the link between biotic interactions and biodiversity dynamics. To this end the PhD student will develop a new eco-evolutionary modelling framework, based on fitness landscapes of biotic interactions, that facilitates theory-based synthesis across empirical study systems and interaction types.

Application deadline : 05.05.2024

For more information please visit the job portal of the University of Hohenheim:

Korinna Allhoff <korinna.allhoff@uni-hohenheim.de>

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ULausanne Drosophila Adaptation

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

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

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

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

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

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

For further information about the position please con-

tact Tadeusz Kawecki <tadeusz.kawecki@unil.ch>.

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

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

Review of applications will begin on April 15 and will continue until a suitable candidate is found.

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

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lar, and cellular bases of chimerism. Candidates should have a strong interest in genomics and/or cell biology, ideally with bioinformatics or microscopy experience. The details of the project can be tailored towards the research interest of the candidate. Training in evolutionary biology and experience with ants are advantageous, but not mandatory. This position is supported by the DFG for three years. The PhD student will be able to join the GenEvo graduate program (<https://www.genevo-rtg.de/>), which fosters a supportive community of graduate students and offers comprehensive training in molecular and evolutionary biology. The host department has a dynamic and inclusive environment, welcoming candidates from all backgrounds.

To apply for this PhD position, please submit a motivation letter, including a possible start date, a CV, and the contact details of two referees. Please compile all these documents into a single PDF file and submit it by May 11, 2024, to hdarras@uni-mainz.de.

Hugo Darras - <https://www.blogs.uni-mainz.de/fb10-evolutionary-biology/darras-hugo/> “Darras, Dr. Hugo” <hdarras@uni-mainz.de>

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UMainz AntsGenomics

PhD position to study male chimerism in yellow crazy ants [Mainz, Germany]

We are inviting applications for a PhD position to investigate male chimerism in the yellow crazy ant. This position is immediately available and has secured funding for three years. The successful applicant will conduct their research in the research group of Hugo Darras at the Johannes Gutenberg University Mainz, Germany.

Sexual reproduction is widespread in eukaryotes, but alternative reproductive systems, such as female or male clonality, have evolved repeatedly across various taxa. Our group investigates the proximate and ultimate mechanisms that drive transitions between different reproductive systems in ants. We recently discovered an extraordinary reproductive system in the yellow crazy ant. In this species, males are all chimeras carrying maternal and paternal genomes in different body cells (<https://www.science.org/stoken/author-tokens/-ST-1119/full>). Chimerism occurs when parental nuclei bypass syngamy and divide separately within the same egg.

The PhD student will investigate the genomic, molecu-

UMississippi Treefrog Polyploidization

Ph.D. Position in Endocrinology of Polyploids. The Leary lab in the Department of Biology (biology.olemiss.edu) at the University of Mississippi is looking for a Ph.D. student with strong interests in endocrinology. The candidate will be involved in a funded research project aimed at understanding how polyploidization has impacted neuroendocrine regulation in gray treefrogs. The candidate will learn mechanisms of endocrine control, hormone manipulation procedures, radioimmunoassay, and bioacoustics and will be directly involved in field data collection from populations of frogs across the eastern United States. Background in neuroendocrinology, radioimmunoassay procedures, or experience working with amphibians is highly desirable but not required. Required Qualifications: A strong interest in research involving amphibians and endocrinology. Ability to work long hours in the field at night. This position is for a term of up to three years as a research assistant during the Spring and Summer and will be supplemented with departmental teaching

assistantships during the Fall semester. Please send inquiries to Christopher Leary (cjleary@olemiss.edu). Proposed Start Date: Fall semester 2024 or sooner.

Christopher J Leary <cjleary@olemiss.edu>

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UOttawa Three MolEvolution

Dear All,

I have three PhD positions in my lab. My research areas are roughly split into

- 1) Molecular mechanisms in translation/transcription and RNA processing/genome replication through comparative studies, focusing on how molecular machines carry out their functions by decoding signals, e.g., release factors decoding termination signals, spliceosomes decoding splicing signals, etc., and how these signals and decoders coevolve.
- 2) Microbiology and infectious diseases, with a focus on host-parasite coevolution at the molecular level.
- 3) Molecular evolution/bioinformatics, i.e., how proteins, DNA, and RNA interact with each other and how the interaction partners change over time, leading to functional changes and adaptation at the molecular level.
- 4) Molecular phylogenetics and phylogeography to understand the distribution of life over space and time, with a focus on invasive species and how they evolve in the new environment.

You might first browse the recent articles from my laboratory at: https://scholar.google.ca/citations?hl=en&user=fbAS_FcAAAAJ&view_op=list_works&sortby=pubdate You can then let me know which article is the closest to your interest. We can schedule a zoom meeting to discuss the details.

Best Xuhua Xia University of Ottawa, Canada <http://dambe.bio.uottawa.ca> <https://www.uottawa.ca/faculty-science/professors/xuhua-xia> https://scholar.google.ca/citations?hl=en&user=fbAS_FcAAAAJ&view_op=list_works Xuhua Xia <Xuhua.Xia@uottawa.ca>

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USussex SpeciationGenomics

PROJECT TITLE: Revealing the genomic basis of reproductive mode evolution and speciation in Littorina snails Funding for: UK Students only Funding amount: Home (UK) tuition fees and stipend at standard UKRI rates. Deadline: Open until filled

A fully-funded PhD studentship (3.5 years) is available from September 2024 under the supervision of Dr. Sean Stankowski department of Ecology, Evolution and Behaviour, School of Life Sciences.

We are seeking an enthusiastic and motivated PhD student to study the links between reproductive mode evolution and speciation in intertidal snails from the genus Littorina.

The process of speciation involves the build-up of isolating barriers that restrict gene exchange between populations. Although barriers to gene flow are critical to divergence and species coexistence, we rarely understand the traits and loci that underpin strong isolation.

The aim of this project is to understand how differences in female reproductive mode contribute to strong isolation between closely-related species of intertidal snail. In the UK and Europe, a live-bearing species of periwinkle (*Littorina saxatilis*) coexists with egg-laying species (*Littorina compressa* and *Littorina arcana*). A lack of hybrids between sympatric egg-layers and live-bearers indicates that the barrier to gene flow between them is very strong.

Recent work has revealed many candidate regions of genome that underpin the difference in reproductive mode. In this project, you will use a new reference genomes, new and existing genomic data, and cutting-edge methods to determine if mode-associated loci also act as barriers to gene flow. Specific objectives include: (1) to more precisely determine the number and genomic distribution of loci associated with the difference in reproductive mode; (2) to determine if reproductive mode acts a barrier by (a) identifying barrier loci and (b) testing for overlap with reproductive mode-associated loci; and (3) to reconstruct the demographic history of divergence to reveal help us understand when and how barriers to gene flow evolved. The successful candidate will be encouraged to take the project in directions that excite them most.

You will work in the Speciation Research Group (<https://>

[/www.speciationgroup.org/](http://www.speciationgroup.org/)) led by Dr Sean Stankowski in the Ecology and Evolution department at the University of Sussex, Brighton. There will be ample opportunity to collaborate and share findings with other scientists from the Littorina research community (<https://littorina.sites.sheffield.ac.uk/home>).

Informal enquiries about the project are especially welcome and can be made to Sean Stankowski at s.stankowski@sussex.ac.uk

How to apply:

Please submit a formal application using the online admissions portal attaching a CV, degree transcripts and certificates, personal statement, and two academic referees. A research proposal is not required.

On the application system select Programme of Study - PhD Biology. Please state the project title under funding obtained and the supervisor's name where required.

Ideal candidates will have some bioinformatics skills (coding in bash, Python and or R), experience working with genomic datasets, will have used a HPC, and be excited about the subject area. Candidates should have or expect to obtain a minimum 2:1 undergraduate degree. An MSc degree will be advantageous. Your qualification should be in Biology or a related subject area. You may also be considered for the position if you have other professional qualifications or experience of equivalent standing.

Candidates for whom English is not their first language will require an IELTS score of 6.5 overall, with not less than 6.0 in any section - English language requirements

Applications are particularly welcomed from candidates with protected characteristics - e.g., from Black and other ethnic minorities - who are under-represented in postgraduate research at our institution.

For enquiries about the application process, please email Emma Chorley: lifesci-rec@sussex.ac.uk

Sean Stankowski <S.Stankowski@sussex.ac.uk>

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UZurich Three EvolBiology

1.

PhD thesis in microbial community assembly (computational ecology and evolution)

A Ph.D. studentship in computational biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study the assembly of microbial communities using computational modeling. Traditional mathematical and computational models do not take into account that organisms have a rich internal structure. For example, even the simplest bacterium has a complex metabolism in which hundreds of enzymes determine which foods the bacterium can consume, which defense molecules it produces, and which waste products it excretes. Traits like these determine in which environments an organism survives and which kinds of communities it can form. They can be predicted for many species with the aid of genome-scale metabolic models. The project will use genome-scale metabolic models to predict the assembly, stability, diversity, and composition of microbial communities from first principles of metabolic biology. It may also study how ecological and evolutionary processes interact during community assembly. The kinds of questions it will ask include how the structure of an ecological community depend on its history. Do communities become more resilient to perturbations over time? Why do simple rules fail to predict the stability of complex communities? How does ongoing evolution of a community's organisms influence the structure and stability of the community?

The successful candidate will be expected to shape their own project within this research area. They will have strong mathematical or computational skills, and a background in biology, bioinformatics, computational biology, biochemistry, biophysics, or related subjects. Fluency in a major programming language, such as python is essential. Familiarity with computational models to analyze complex metabolic systems, such as Flux Balance Analysis is a plus. Applications without a demonstrated interest or research history in fundamental ecological or evolutionary questions will not be considered further. We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and can work independently.

Lab members have diverse backgrounds and research projects but are unified by their interests in life's fundamental organizational principles. Ongoing projects cover a broad range of topics in evolution and at the interface of ecology and evolution, such as the dynamics of microbial community assembly, the evolution of multicellularity, and the structure of adaptive landscapes (e.g., Wagner, *Molecular Ecology* 2022; Papkou et al. *Science* 2023).

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with

a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs.wagner@ieu.uzh.ch. CV including publication list, academic transcripts, a statement of research interests not exceeding three pages, and contact information for three academic references. Please include the word “PHD24COMM” in the subject line. Applications will be considered until May 10, 2024. The position is available from Summer 2024.

2.

PhD thesis in machine learning and evolutionary biology

A Ph.D. studentship in computational biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to develop and use machine learning methods to understand the topography of experimentally mapped fitness landscapes. Fitness landscapes are analogues of physical landscapes in which a location corresponds to a genotype and the elevation of that location corresponds to fitness. The topography of such landscapes is crucial to determine how and whether Darwinian evolution enables populations to reach high fitness. For many years, such landscapes

have been studied only theoretically, but experimental techniques such as CRISPR-Cas genome editing have permitted measuring the fitness of thousands of microbial genotypes. Experimentalists in our lab have used this and other techniques to map experimental fitness landscapes, but our ability to predict the structure of such landscapes is rudimentary. For example, we do not know how sparse sampling of fitness data may affect our ability to predict landscape topography. We also cannot predict how landscape topography depends on the environment.

The subject of this project is to develop appropriate machine learning methods to answer this and related questions for experimentally mapped fitness landscapes. The successful candidate will be expected to shape their own project within this research area. They will have strong mathematical or computational skills, and a background in computer science, biology, bioinformatics, biochemistry, biophysics,

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AlbertaGovt TroutConservationGeneticist

The Alberta Government is looking for a conservation geneticist! Reporting to the Provincial Recovery Specialist, the Conservation Geneticist is responsible for the development and application of advanced genetic tools to recover and manage the three native trout species at risk in Alberta, Bull Trout, Athabasca Rainbow Trout and Westslope Cutthroat Trout, through the Native Trout Recovery Program. The Native Trout Recovery program is involved in assessing the genetic characteristics of trout populations, understanding potential risks to current and future genetic integrity and assessing potential management options. Please visit the GoA Job Board for more information: <https://jobpostings.alberta.ca/job/Edmonton-or-Calgary-Conservation-Geneticist/579919717/> Jess

Jessica Reilly <jessica.reilly@gov.ab.ca>

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ArizonaStateU GenomicDiversity

Presidential Postdoctoral Fellowship for One Health, Many Diverse Genomes School of Life Sciences Arizona State University

The Schools of Life Science at Arizona State University (ASU) as part of The College of Liberal Arts and Sciences invite applications for a Presidential Postdoctoral Fellow position researching comparative genomics and One Health. Presidential Postdoctoral Fellowships are intended to support the career development of outstanding Ph.D. or equivalent doctoral recipients with great potential for advancing the ASU Charter through a future tenure-track appointment at ASU. The selected postdoctoral fellow will join a cohort of ~20 other scholars at ASU as part of the Presidential Postdoctoral Fellowship Program.

With the rapid expansion of genomic data, we have an opportunity to make foundational discoveries in biology through the analysis of natural selection in shaping molecular diversity across the tree of life. Natural selection and demographic history pattern the distribution

of genetic variants in each species' genome, which affects their resilience to environmental perturbations and risk of disease. However, genomic sampling of species long stewarded by Indigenous and local communities, and the collection of genomic data from diverse communities and their homelands, has many cultural, ethical, legal, and social implications that increase the responsibilities of the scientific community. Respectful research opportunities can unite communities through biology, data science, stewardship, and sustainable health for all lifeforms.

This Presidential Postdoctoral Fellow, with an anticipated start date in the 2024-2025 academic year, will be appointed to help advance one or more initiatives at ASU including: generation and comparative analysis of genomic information across eukaryotic taxa and species to potentially include flora and fauna of the Sonoran Desert region; the comparative genomics across species in alignment with interests related to evolutionary medicine, and in particular the comparative genomics of cancer resistance across species (in collaboration with the Arizona Cancer Evolution Center); and advancing existing programs at ASU related to computational life sciences programs.

The School of Life Sciences has committed to provide individualized mentorship and career development to ensure the fellow is well prepared to succeed in a future tenure-track appointment at ASU. Career development and community building will also occur through programmatic support at the ASU Graduate College's Postdoctoral Affairs Office, and peer-mentoring with other presidential postdoctoral fellows.

The Presidential Postdoctoral Fellowship program seeks applicants whose professional preparedness, experience, and accomplishments are informed by experiences working with and within groups historically underrepresented. Where pools of qualified applicants are strong, priority will be given to applicants who demonstrate, through prior actions and achievements, intentional and actioned commitment in alignment with the ASU Charter mission of inclusive excellence. Examples of such contributions are research, teaching, mentorship, or community-centered service focused on empowering underserved populations that increases equitable access and inclusion in fields where historically excluded populations are underrepresented.

Expected Job Duties - The Presidential Postdoctoral Fellow will conduct research and ensure that all studies are appropriately conducted following the policies and procedures of Arizona State University - Engage in science communication such as research manuscripts for publication in scientific journals, advocacy documents

and/or presentations - Engage in grant writing activities independently and/or with colleagues - Demonstrate progress, with the assistance of faculty mentors, towards establishing independent research aims/goals/objectives, to begin at the start of a future tenure-track appointment at ASU

About Arizona State University ASU is a large, comprehensive, research university that for two decades has transformed into the “New American University,” one dedicated to the simultaneous pursuit of excellence, broad access to quality education, and meaningful societal impact. By our Charter and Design Aspirations, we center inclusion and success as values that drive the enterprise; adopt inter- and transdisciplinary approaches to teaching and learning as ways to address society’s greatest challenges; and develop innovative partnerships to produce master learners across the lifespan. In 2022, ASU was designated a Hispanic- Serving Institution (HSI) by the U.S. Department of Education, with 26% total undergraduate Hispanic full-time equivalent student enrollment in 2021. To learn more about ASU, visit <http://www.asu.edu> . Qualifications and Characteristics Successful candidates will engage in scholarly research and may be asked

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Barcelona Two BioinformaticsTech

Position 1: BIOINFORMATICS DEVELOPER - BIODIVERSITY CELL ATLAS DATABASE The role The CRG is recruiting a Bioinformatician with experience in genomics pipeline development and database infrastructure. The position will entail developing computational pipelines for the processing of novel and existing single-cell transcriptomic datasets from diverse species across the tree of life, as well as developing a comparative cell atlas database. The candidate will be a part of a highly interdisciplinary team that includes computational, evolutionary, and molecular biologists in different groups at CRG (including the Bioinformatics Unit), and this project will be developed in very close contact with groups at EMBL-EBI (Hinxton, UK) and at the Earlham Institute (Norwich, UK).

About the team Cells are the fundamental units of life - underlying cooperative functions in multicellular organisms and complex temporal life cycles in microbial eukaryotes. In recent years, the rapid advance in single-cell genomics technologies, combined with the growing availability of whole-genome sequences, opened up the opportunity to systematically map cell types in diverse organisms.

The goal of the Biodiversity Cell Atlas is to articulate a community effort to build whole-organism cell atlases across the diversity of life, working in a phylogenetically informed way, supported by high-quality genomes, and using shared standards that make comparisons across diversity possible. This coordinated effort should boost our understanding the evolution and diversity of life at cellular resolution: from gene regulatory programs, through cell type molecular profiles, to biological interactions between species.

At CRG, and together with EBI and the Earlham Institute, we are developing the computational infrastructure to host a multi-species database for the Biodiversity Cell Atlas initiative. This will enable the interactive exploration of cell type molecular maps, gene co-expression profiles across evolution, comparison of cell types across species, and more.

For further information, you can directly email arnau.sebe@crg.eu Link: <https://recruitment.crg.eu/-content/jobs/position/bioinformatics-developer-biodiversity-cell-atlas-database> Position 2: BIOINFORMATICS TEAM LEADER - BIODIVERSITY CELL ATLAS DATABASE The role The CRG is recruiting a Bioinformatics Team Leader with experience in genomics pipeline development and database infrastructure. The position will entail coordinating a small (3-5) team of Bioinformaticians and computer scientists working together to develop computational pipelines to analyse of single-cell transcriptomic data across the tree of life; to curate and integrate these datasets using phylogenetic methods; and to set-up a comparative cell atlas database. The candidate will be a part of a highly interdisciplinary team that includes computational, evolutionary, and molecular biologists in different groups at CRG (including the Bioinformatics Unit), and this project will be developed in very close contact with groups at EMBL-EBI (Hinxton, UK) and at the Earlham Institute (Norwich, UK).

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For further information, you can directly email arnau.sebe@crg.eu Link: <https://recruitment.crg.eu/content/jobs/position/bioinformatics-team-leader-biodiversity-cell-atlas-database> Arnau Sebe Pedros <arnau.sebe@crg.eu>

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BrighamYoungU EvolutionaryBotany

Job Title: Botanist/Plant Ecologist Department/College: Biology/Life Sciences Desired Start Date: Jan 2025 Job Close Date: 6/01/2024 Required Degree: Ph.D.

The Department of Biology seeks to fill a full-time, Continuing Faculty Status (BYU's equivalent to tenure) track position in Botany/Plant Ecology. We seek a colleague whose research addresses basic questions in botany including (but not limited to) ecology, evolution, development and/or systematics. The qualified candidate is required to have a PhD and postdoctoral or comparable experience is preferred.

The Department expects the successful candidate to be a productive, creative, and collaborative scholar with a vision for research, mentoring, and teaching that align with the mission of BYU. The successful applicant will

be expected to establish a research program that demonstrates independence and pursue external funding while mentoring both undergraduate and graduate students. There are many opportunities for collaborative and cross-disciplinary links within the Department (<https://biology.byu.edu/>) and University, including the DNA Sequencing Center, Evolutionary Ecology Laboratories, and Lytle Nature Preserve. The Bean Life Science Museum houses a vast and growing collection of databased plant specimens that supports diverse research, provides opportunities for curation and facilitates community outreach. Undergraduate teaching responsibilities include a course in Plant Diversity and/or Field Botany, a botany-focused upper-level course (e.g., Plant Ecology, Plant Classification, or other course related to the candidate's expertise), and other undergraduate courses in the biology core curriculum. Graduate teaching expectations include course(s) consistent with the applicant's area of specialization. A potential for excellence in teaching is expected in addition to building a botanical emphasis within the Biodiversity and Conservation major. Candidates are expected to cultivate an equitable and diverse scholarly environment in teaching, mentoring, research, life experiences, and service. The Department offers generous start-up packages and reduced teaching loads for new faculty. The anticipated start date is January 2025, but the start date is negotiable.

Applications can be submitted at yjobs.byu.edu by searching for "Botanist/Plant Ecologist Faculty - 130029". Send any questions to Clinton Whipple: whipple@byu.edu

Clinton Whipple <whipple@byu.edu>

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ColoradoStateU RootGeneticsResearch

The McKay lab is looking for a Field Research Manager for Fort Collins, Colorado. The goal of the research is understand the genetics of plant adaptation. Our current NSF funded research focuses on drought adaptation and nitrogen use, with genetic variation in root traits is the key response variables . The candidate will be responsible for planning and carrying out field research. A non-conclusive list of activities includes: Field planning, team management, permit acquisition, collaboration with other researchers and field workers,

data collection, and data analysis.

Applications will be considered until 22 April 2024.

<https://jobs.colostate.edu/postings/141519>.

CSU is an EO/EA/AA employer and conducts background checks on all final candidates.

“McKay, John” <John.McKay@ColoState.EDU>

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ICN UNacional Colombia FiveCurators Systematics

Five full-time research curators/faculty, tenure-track jobs are open at the Natural Sciences Institute (Instituto de Ciencias Naturales - ICN) at the National University of Colombia (UNAL) in Bogotá.

The ICN holds the largest biological collections worldwide of the megadiverse Colombian biota.

The selected faculty will be associated with the biology undergraduate and graduate programs, and will lead the collection-based research in systematics, taxonomy, biogeography / evolutionary biology in their field.

Open positions:

- Fungi (macromycetes) - curator of the fungarium at the National Herbarium of Colombia COL - Amphibian systematics - curator of the ICN frog/salamander/caecilian collections - Arachnida - curator of the ICN arachnology collection - Embryophyte - curator of the ICN collections of the mosses, liverworts, hornworts collections at COL - Magnoliophyta (Angiosperms) - curator of a group of flowering plants (family-level) at COL

Everyone with a PhD and active research in any of these 5 areas are welcome to apply, as long as she/he demonstrates museum-based/curator experience on top of the required teaching experience. The Colombian official language is Spanish (and of the UNAL application process), and we hope for a diverse pool of applicants

UNAL is the largest public university in Colombia, with 9 campuses across country, about 55K students.

Deadline: 30 April 2024

Documents and details: <https://ciencias.bogota.unal.edu.co/equipoDirectivo/-decanatura/concurso.docente> Twitter thread details: <https://twitter.com/ICNUNAL/status/>

1774830235764101532 Formal Contact: concurso_fcbog@unal.edu.co +57 1 3165000 ext. 15646

Informal enquiries can also be directed to Carlos Sarmiento <cesarmientom@unal.edu.co> head of the Natural History Museum at UNAL and ad-hoc ICN director.

Andrés M. Cuervo, Ph.D. Profesor Asociado Director & Curador Colección de Ornitología - ICN Instituto de Ciencias Naturales

Universidad Nacional de Colombia Cra. 30 # 45-03, Ed. 425, Of. 217 Bogotá, Colombia <https://linktr.ee/avesicn> “Andrés M. Cuervo” <amcuervom@unal.edu.co>

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ImperialCollege London GenomicsResAssociate

Imperial College London

Location: London

Salary: GBP 45,593 to 53,630 per annum

Hours: Full Time

Contract Type: Fixed-Term/Contract

Location: Silwood Park Campus

Job Summary

We are actively seeking a passionate and dedicated individual to join our research team in the pivotal role of conducting evolutionary genomic analyses. This position offers a unique opportunity to delve into diverse genomic datasets, focusing on elucidating key insights into stress tolerance mechanisms in coconut palms and unravelling the complexities of sexual behaviour in monkeys.

You will not only spearhead these crucial analyses but will also contribute significantly to our overarching genomic and metagenomic research endeavours within our cutting-edge laboratory, with ample prospects for co-authoring publications in top journals.

This position presents an exhilarating opportunity to immerse oneself in forefront research endeavours and effect tangible advancements in the field.

Lab website: <https://www.imperial.ac.uk/people/>

v.savolainen Duties and responsibilities

- Genomic Analyses: Your primary responsibility will entail conducting comprehensive genomic analyses of a varied array of coconut palm and macaque genomes.
- Team Leadership: In addition to your analytical duties, you will assume a leadership role in supervising a dynamic, multi-disciplinary team comprising both PhD and Masters students. This pivotal position necessitates adept guidance, fostering collaborative synergies, and ensuring the seamless execution of our research objectives.
- Publications: As a valued Research Associate, you will actively contribute to disseminating our groundbreaking research findings by co-authoring publications in high-impact, refereed journals, thereby fostering broader scholarly discourse and advancement in the field.

Essential requirements

You should:

- Hold, or be near completion of, a PhD in evolution, ecology, genetics, or genomics.
- Have a robust background in genomics, molecular biology, or a closely related field.
- Demonstrated proficiency in analytical methodologies and research techniques.
- Proven experience in leadership roles within collaborative research environments.
- Exceptional written and verbal communication skills to effectively convey complex scientific concepts.

Further Information

This is a full time, fixed term position until 31 December 2024, with possibility of extension subject to funding. You will be based at Silwood Park Campus.

Candidates who have not yet been officially awarded their PhD will be appointed as a Research Assistant.

For insights into ongoing projects, please visit <https://www.imperial.ac.uk/people/v.savolainen> or feel free to contact Professor Vincent Savolainen directly at v.savolainen@imperial.ac.uk.

The College is a proud signatory to the San-Francisco Declaration on Research Assessment (DORA), which means that in hiring and promotion decisions, we evaluate applicants on the quality of their work, not the journal impact factor where it is published. For more information, see <https://www.imperial.ac.uk/research-and-innovation/about-imperial-research-research-evaluation/> The College believes that the use of animals in research is vital to improve human

and animal health and welfare. Animals may only be used in research programmes where their use is shown to be necessary for developing new treatments and making medical advances. Imperial is committed to ensuring that, in cases where this research is deemed essential, all animals in the College's care are treated with full respect, and that all staff involved with this work show due consideration at every level. <http://www.imperial.ac.uk/research-and-innovation/about-imperial-research/research-integrity/animal-research/>
Closing Date:02/05/2024

To apply visit

<https://www.jobs.ac.uk/job/DHE988/research-associate-in-genomics> Sent from my iPhone

“Savolainen, Vincent” <v.savolainen@imperial.ac.uk>
(to subscribe/unsubscribe the EvoDir send mail to golding@mcmaster.ca<<mailto:golding@mcmaster.ca>>) golding@mcmaster.ca<<mailto:golding@mcmaster.ca>>)

ISYEB Paris ResearchTech Haplotagging

We offer a 4.5 years (54 months) position, working as Ingénieur·e d'Études (roughly equivalent to a Lead Research Technician position) to manage and implement the EvoGenArch ERC research project, especially aspects related to molecular ecology (molecular and bioinformatics aspects of the haplotagging approach, participating to field work, data management).

The job provides the opportunity to explore a wide area of molecular ecology, from bench work to field work, with support from a lab technician and a bioinformatician for the most technical aspects of the job. The bench work (notably developing the new haplotagging approach in the lab) will compose most of the work load, followed by sequences analysis and data management, while field work will be the lightest part (two months each year).

The candidate will work for the *École Pratique des Hautes Études* (PSL University), joining Pierre de Villemerueil's team, at the Institute for Systematics, Evolution, Biodiversity (ISYEB), located within the Muséum National d'Histoire Naturelle (MNHN) in Paris. This position is funded as part of the EvoGenArch ERC Starting Grant. The position starts on 2024-09-16.

More informations and instructions to apply here:

<https://euraxess.ec.europa.eu/jobs/225940> Pierre de Villemereuil <pierre.devillemereuil@ephe.psl.eu>

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MichiganStateU KBS Tech SwitchgrassEvolution

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

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

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

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Senckenberg Frankfurt ComparativeGenomicsBats

ERC-funded PhD and Postdoc Positions in Comparative Genomics

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

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

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

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

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

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

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

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

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

Senckenberg is committed to diversity. We benefit from the different expertise, perspectives and personalities of our staff and welcome every application from qualified

candidates, irrespective of age, gender, ethnic

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Smithsonian GenomicsBioinformatics

The Center for Conservation Genomics (CCG), Smithsonian National Zoo and Conservation Biology Institute (NZCBI), located in Washington, DC, invites applications for a not to exceed three-year term Data Scientist position (GS-09).

In this position the Data Scientist is responsible for developing, planning, and executing basic and applied research in bioinformatics as applied to biodiversity genomics and conservation biology, and provide bioinformatics and computational expertise and training to CCG/NZCBI scientists.

In this position, you will:

- * Utilize software tools for biodiversity genomics and informatics research to perform analyses, modifications, and implementations to modify workflow. * Enhance programs using modern programming languages, statistical packages, and algorithms for mathematical modeling.
- * Assist management and curation of genomic data produced by the Center. * Train researchers, technicians, student interns, postdoctoral fellows, and permanent staff in bioinformatic analyses. * Advise on selection of appropriate bioinformatic analyses that optimize the application. * Perform research in biodiversity genomics involving the implementation of algorithms, and analysis of new workflows. * Ensure publication of research results in scientific/academic literature.

CCG works to understand and conserve biodiversity through genetic and genomic research. We creatively apply genetic theory and methods to build knowledge about the evolutionary and life histories of animals, to understand the importance of genetic variation to species' survival, and to identify the methods needed to sustain them in captivity and the wild.

To obtain details of the position and to apply, proceed to the USAJOBS website (<https://www.usajobs.gov/GetJob/ViewDetails/782000900>). Information about

CCG and NZCBI can also be found at <https://nationalzoo.si.edu>. This position is open to all U.S. Citizens or U.S. Nationals. The Smithsonian Institution is an Equal Opportunity Employer and Provider.

R. Fleischer

“Fleischer, Robert” <fleischerr@si.edu>

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StateUNewYork Oswego FishGenomics

The SUNY Oswego Biological Sciences Department, in collaboration with the USGS, USFWS Northeast Fishery Center, and Ontario Ministry of Natural Resources, seeks a research scientist to lead the development of a high-throughput genomic monitoring and parentage-based tagging (PBT) panel for Cisco (*Coregonus artedii*) and Bloater (*Coregonus hoyi*). This urgent work directly supports the active restoration of these ecologically and culturally important fish species. To learn more about coregonine research in the Great Lakes, visit <https://www.greatlakesciscoes.org/> to learn more about ongoing efforts.

This project will develop and optimize a novel microhaplotype-based GT-seq panel for genomic monitoring and PBT applications in coregonines (Cisco, Bloater). It will assess the panel’s accuracy in tracking changes in genetic diversity over time, estimating demographic parameters, and reconstructing pedigrees. This panel will generate crucial data to effectively manage coregonine broodstock, hatchery-rearing practices, and stocking strategies.

The successful applicant will work at the forefront of conservation genetics with an exceptional collaborative team. They will gain experience in genomic techniques, data analysis, and the application of science to management problems. A competitive salary and benefits package is offered, and remote work is negotiable.

Qualifications MS. or Ph.D. in ecology, evolutionary biology, genetics, genomics, or a related field (start date)

Demonstrated expertise in molecular biology lab techniques and bioinformatics.

A commitment to collaboration and science communication.

A strong publication record is preferred.

Applications will include 1) A cover letter describing research interests and their alignment with the project’s goals; 2) a CV highlighting relevant coursework, research experience, and publications; 3) A Diversity, Equity, and Inclusion Statement; 4) Contact information for three professional references.

Please submit applications at <https://oswego.interviewexchange.com/jobofferdetails.jsp?JOBID=174292> Nicholas Sard <nicholas.sard@oswego.edu>

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Stockholm DirectorOfBeijerInstitute

DIRECTOR

Of the Beijer Institute of Ecological Economics at the Royal Swedish Academy of Sciences

The Royal Swedish Academy of Sciences invites applications for the position of Director of the Beijer Institute of Ecological Economics, an international research institute for global sustainability. The Director will be employed as Professor at the Academy.

The overall objective of the institute is to foster understanding of major challenges and opportunities for the wellbeing and future of humanity as part of the biosphere, and how to tackle these challenges. With this overall objective, the Beijer Institute of ecological economics advances research frontiers on the interplay of ecological systems and social and economic development in relation to sustainability.

The institute’s major activities are currently research programmes and research projects, synthesis workshops, dissemination of results, and the science-policy interface. There are some 30 members of the staff, including principal investigators, post-docs, PhD students and assistants. Please visit www.beijer.kva.se for more information.

The Institute is one of the Royal Swedish Academy’s research institutes, and a collaborative partner of the Stockholm node of sustainability science centres.

Main duties

The Director will be responsible for further strengthening the institute’s scientific reputation and its role in

connecting science and policy. The Director provides strategic leadership, fosters excellence and is responsible for operational management of the institute. It is imperative that the Director actively contributes towards a good working environment and maintains a close and fruitful relationship to the Academy.

Candidates should possess the ability and motivation to lead one of the most prestigious institutes for sustainability research in the world, and to contribute to the national and international visibility of the institute and the Academy within the sustainability research landscape.

Over the longer term, you will be expected to identify, develop and progress new initiatives and ideas.

Qualifications

The position of the Director requires demonstrated leadership qualities and experience in research management, excellence in scholarship or science, international recognition and networks, and experience in interdisciplinary work. Specifically,

we are looking for someone who has

a strong research record with a focus on the interplay between ecological systems and social and economic development in relation to sustainability

documented experience of interdisciplinary research and international scientific collaboration strong administrative skills, including personnel management and economic responsibility has demonstrated an interest and ability to strategic leadership a documented track record in attracting external funding very good communication and social skills

Job details

This is a full-time position placed at the Royal Swedish Academy of Sciences in Stockholm. Salary will be commensurate with qualifications and experience.

The working language at the institute is English. To be able to efficiently handle administrative matters, the successful candidate - if non-Swedish speaker - is expected to be fluent in Swedish within two years after starting the employment.

The Director reports to the Secretary General of the Academy.

Preferred start date 1 January 2025, but is open to negotiation.

Last Application date

30 June, 2024.

Applications may be considered until the position is filled.

Applications must include

§A letter of application containing a description of your skills and experience as they relate to those called for in the job description

§A vision for future research directions

§A curriculum vitae

§A list of publications, but no attached publications

§Contact details to two references

Please note: Send your application as a PDF file. Material contained within multiple files will not be considered. Applications should be e-mailed to beijerdirector@kva.se

Further information about the position can be obtained from Professor Hans Ellegren, Secretary General of the Royal Swedish Academy of Sciences (hans.ellegren@kva.se), or Professor Carl Folke, currently Director of the institute (Carl.Folke@kva.se).

HANS ELLEGREN, Professor
Ständigsekreterare/Secretary General

E-mail: Hans.Ellegren@kva.se

KUNGL. VETENSKAPSAKADEMIEN THE ROYAL SWEDISH ACADEMY OF SCIENCES Box 50005, SE-104 05 Stockholm, Sweden Besök/Visit Lilla Frescativägen 4 A, SE-114 18 Stockholm, Sweden Web www.kva.se Hans Ellegren <hans.ellegren@kva.se>

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UDenver FieldTech DeerMouseBotflyEvol

Small Mammal Field Technician - Deer mouse-botfly evolutionary ecology

The Velotta Lab in the Department of Biological Sciences at the University of Denver (velottalab.com) is seeking to hire one seasonal field technician to assist with research on the evolutionary ecology of deer mice (*Peromyscus maniculatus*) in Colorado in collaboration with Nathan Senner's lab at the University of Massachusetts Amherst. The project is focused on understanding how deer mouse physiology and population dynamics are influenced by botfly parasites and environmental variation. The field technician will assist with all aspects of fieldwork, with opportunities for learning research skills

throughout the season.

The position will run from approximately May 20, 2024 - October 20, 2024 (5 months). Airfare, shared field housing, food, all necessary equipment, and a stipend of \$18.50/hour will be provided.

Essential Functions

Maintenance of a small mammal trapping grid.

Capture, handling, and tagging of wild deer mice.

Field physiology including respirometry (metabolic rate measurement).

Field behavioral trials.

Working in the plains and mountains in sometimes rugged terrain.

Work collaboratively and effectively to promote teamwork, diversity, equality and inclusiveness.

Knowledge, Skills, and Abilities

Interest in mammalian ecology, field biology, physiology, species interactions, and/or related fields.

Comfortable living and sleeping in close quarters with the team.

Comfortable working at high elevations in sometimes rugged terrain.

Strong work ethic, eagerness to learn fieldwork and research methods, and ability to work well on a team and independently in challenging physical conditions and sometimes stressful scenarios. Applicant must be adaptable, communicative, cooperative, and detail oriented.

For more information and to apply, please visit this website: <https://jobs.du.edu/en-us/job/497191/field-technician-velotta-lab> Jonathan Velotta

Assistant Professor Department of Biological Sciences
University of Denver 2101 E Wesley Ave Denver, CO
80210 Office: SGM 280 Twitter: @JonVelotta velotta-
lab.com he/him

Jonathan Velotta <Jonathan.Velotta@du.edu>

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The Department of Biological Sciences invites applications for a Probationary (Tenure-track) position at the rank of Assistant Professor beginning as early as January 1, 2025, or on a date mutually agreed upon. Salary will be commensurate with experience and qualifications.

The Department seeks an outstanding and visionary early career scholar committed to the study of Quantitative Biology and Ecosystem Resilience. The candidate will hold a PhD degree or equivalent in a relevant discipline. Post-doctoral experience or equivalent is strongly preferred. Diversity at the individual, population, species, and community level all underlie functioning resilient ecosystems. The successful candidate will be expected to develop and sustain a competitively funded research program in one or more of these or any other facets of ecosystem resilience. We particularly encourage applications by researchers at the forefront of the development and/or implementation of modern statistical, simulation, or theoretical approaches to their research questions.

Duties will include meaningful contributions to the research, teaching, and service activities of the Department. The successful candidate will have a track record of high-quality scholarly research leading to peer-assessed publications; will either have, or demonstrate the potential to, establish an independent and innovative externally funded research program; will have demonstrable strength in, or strong potential for, outstanding teaching contributions; and will exhibit evidence of the ability to work in a collaborative environment.

To enhance our Department, we particularly invite applications from those who will increase and support our diversity, including diverse gender and sexual identities, Indigenous peoples, persons with disabilities, racialized persons, underrepresented groups such as 2SLGBTQIA+, and those committed to an inclusive environment. The Department of Biological Sciences is supported by strong research links within the Faculty of Science including; Data Research Alliance of Canada, Data Science Nexus, Mathematical Biology and Statistics; and off campus through IISD-Experimental Lakes area; Fisheries and Oceans Canada's Freshwater Institute; Environment and Climate Change Canada. Strong undergraduate programs in biological sciences, genetics and data science in majors and honours are available for our undergraduate students.

Applications should include a cover letter; curriculum vitae; a two page description of teaching and mentorship philosophy, including application of EDI principles; a single page description of the applicant's previous research strengths and potential research program; a two-three page prospective of their five-year research

UManitoba QuantitativeBiologist

University of Manitoba https://universityaffairs.ca/-search-job/?job_id=64766 Location: Manitoba, Canada

plan; and contact information for three academic references. Applications should be sent in PDF format to: BIOSCIBR@umanitoba.ca. Please specify position number 34681 in the application. For further information, contact the search committee Chair Dr. W. Gary Anderson (gary.anderson@umanitoba.ca).

The closing date for receipt of applications is April 22, 2024.

The University of Manitoba is committed to the principles of equity, diversity & inclusion and to promoting opportunities in hiring, promotion and tenure (where applicable) for systemically marginalized groups who have been excluded from full participation at the University and the larger community including Indigenous Peoples, women, racialized persons, persons with disabilities and those who identify as 2SLGBTQIA+ (Two Spirit, lesbian, gay, bisexual, trans, questioning, intersex, asexual and other diverse sexual identities). All qualified candidates are encouraged to apply; however, Canadian citizens and permanent residents will be given priority.

If you require accommodation supports during the recruitment process, please contact UM.Accommodation@umanitoba.ca or +1-204-474-7195. Please note this contact information is for accommodation reasons only.

Application materials, including letters of reference, will be handled in accordance with the protection of privacy provision of The Freedom of Information and Protection of Privacy Act (Manitoba). Please note that curriculum vitae may be provided to participating members of the search process.

The University of Manitoba is a driving force of innovation, discovery and advancement. Our momentum is propelled by our campus community - UM faculty, staff and students whose determination and curiosity shape our world for the better. Our teaching, learning and work environment is uniquely strengthened and enriched by Indigenous perspectives. With two main campuses in Winnipeg, satellite campuses throughout Manitoba, and world-wide research, UM's impact is global.

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UMichigan Tech PlantAdaptation

A full-time technician position is available in the Baucom lab in the EEB Dept at the University of Michigan in Ann Arbor, MI. General research in the laboratory addresses plant adaptation to environmental stresses. Duties will include working at the University's main campus, in the nearby greenhouses, at nearby field sites, and will include travel for germplasm collections.

The senior research technician will help deploy and coordinate field experiments between five main labs, and will be responsible for growth room and greenhouse plant care and experiments. The start date of the senior research tech would ideally be asap, as we are looking to start field work this summer.

The job listing can be found here with more information about required qualifications: https://careers.umich.edu/job_detail/247672/research-lab-tech-senior-baucom-lab NOTE: This is a one (1) year term limited appointment with a start date of approximately May 15, 2024 through May 31, 2025 with possibility of renewal.

Responsibilities Carry out large greenhouse and field studies (40%) - develop and implement greenhouse experiments to monitor plant adaptation to environmental stress. Monitor and maintain the health and welfare of the lab's Ipomoea lines within the greenhouse. Includes general upkeep of plants in the greenhouse and maintenance of crossing records. Adhere to all University of Michigan policies and procedures for laboratory/greenhouse research.

General lab maintenance (10%) - Clean and maintain equipment. Act as the primary resource for lab safety management. Oversee undergraduate in basic lab maintenance tasks and lab safety. Responsible for ordering research and laboratory supplies.

Molecular genetics work and microscopy (40%) - Perform microscopy experiments, RNA/DNA extraction and basic PCR. Maintain databases of lab Ipomoea seed collections, chemicals, and supplies ordered. Potential trips to collect weed seeds from the field in the fall.

Mentor 1-2 undergraduate students (10%)

I am happy to answer any questions about the position, living in Ann Arbor, or the UMich EEB department.

Regina S Baucom Professor 4034 Biological Sciences Building Dept of EEB University of Michigan Ann Arbor, MI 48109 (734) 647-8490 baucomlab.wordpress.com Google Scholar Zoom [she/her/hers](https://www.zoom.us/j/9198912345)

Regina Baucom <rsbaucom@umich.edu>

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UMissouri LabManager EvolutionaryGenomics

The King Lab at the University of Missouri is planning to hire a research specialist (senior level) to conduct research in evolutionary genomics. This position will include coordinating and carrying out complex laboratory experiments, general lab maintenance and administrative tasks, and data management & analysis. Research in the King Lab addresses fundamental questions in evolutionary genomics, seeking to understand how genomes change when phenotypes evolve. We integrate computational methods with large-scale empirical studies, with a primary focus on understanding the evolution of complex traits, particularly sensory and life history traits, using the fruit fly model system.

The research specialist will be part of a research team working to understand the genetic and physiological mechanisms underlying complex phenotypes using fruit flies as a model system.

Duties will include:

- Carrying out complex laboratory experiments including: fruit fly maintenance and care, DNA and RNA sample preparation, coordinating experimental evolution of fly populations, developing physiological assays. (40%)
- Experiment and data management including: maintaining a detailed lab book, organizing and keeping records about data storage for the lab's projects, collating and organizing protocols, experimental plans, data collection sheets, and collaborative work schedules (15%)
- Management of the research team including: providing assistance and training for incoming trainees, coordination of projects involving collaboration between lab members, participation in lab and research meetings (25%)
- General laboratory tasks including: preparing reagents, ordering and re-stocking supplies, ensuring laboratory

compliance for lab safety (10%)

- Other job duties and tasks as assigned (10%)

- Occasional flexibility in the typical work schedule may be necessary for some experiments (e.g. occasional brief weekend hours, etc.)

Interested applicants should apply here:

https://erecruit.umsystem.edu/-/psp/tamext/COLUM/HRMS/c/-HRS_HRAM_FL.HRS.CG.SEARCH_FL.GBL?Page=-HRS_APP_JBPST_FL&Action=U&SiteId=-6&FOCUS=Applicant&SiteId=6&JobOpeningId=-51377&PostingSeq=1 If you are a current employee of the University of Missouri please use the following link instead: https://myhr.umsystem.edu/-/psp/myhrprd/EMPLOYEE/HRMS/c/-HRS_HRAM_EMP_FL.HRS.CG.SEARCH_FL.GBL?Page=-HRS_APP_JBPST_FL&Action=U&FOCUS=-Employee&JobOpeningId=51377&PostingSeq=-1&SiteId=6

Please email Elizabeth King (kingeg@missouri.edu) with any questions. Review of applications will begin May 6th and the position will remain open until filled.

“King, Elizabeth G.” <kingeg@missouri.edu>

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UNacionalAutonomaDeMexico Botany

Faculty Position. Botany Chamela Field Station Institute of Biology. Universidad Nacional Autonoma de Mexico

<http://www.ib.unam.mx/ibunam/-Convocatoria-Chamela.pdf>

The Universidad Nacional Autonoma de Mexico (UNAM; <https://www.unam.mx>) is Mexico's preeminent public higher-education center that is among the highest-ranking Spanish-speaking and Latin American universities. UNAM's Institute of Biology (IBUNAM) has the mission to develop scientific research on the origin and maintenance, interactions, distribution, composition, sustainable use and conservation of biological richness. The Institute also houses the National Biological Collections of Mexico, including ten zoological collections and the National Herbarium, and contributes substantively towards education and outreach.

The Institute of Biology consists of two academic Departments (Zoology and Botany), a Botanical Garden, and two field research stations. One of these is the Chamela Biological Station (Estacion de Investigacion, Experimentacion y Difusion Chamela) on the coast of Jalisco in western Mexico, which comprises more than 3,300 ha of conserved mostly Seasonally Dry Tropical Forest (SDTF) that maintains high levels of species richness and endemism. The Chamela Biological Station also has a campus in the city of Colima (in the state of Colima), and both facilities have research, laboratory and collections areas. The main goal of the Chamela Biological Station, and its campus in Colima, is the study of the biotic composition of the SDTF, including species discovery, as well as the origin, evolution, relationships and maintenance of its richness.

To fulfill its mission, the Institute of Biology seeks qualified applicants for one tenure-track full-time position as an Associate Research Scientist (Investigador/a Asociado/a de Tiempo Completo) in the field of systematics and evolution of Seasonally Dry Tropical Forest, to work at the Chamela Biological Station and its campus in Colima, under the following specifications:

Candidate's profile. We seek a scientist to conduct research on any group of plants with a significant floristic, evolutionary or ecological role in Mexican SDTFs, who specializes in systematic biology (e.g., species discovery and description, work in biological collections, phylogenetic estimation), extending to the application of innovative theoretical concepts and methodological tools to investigate one or more processes associated with their evolution above the species level (e.g., morphological or functional diversity, species richness, distribution, evolution, coevolution), or the relevance and interaction with local human communities. Their research must be closely and continuously linked with the Chamela Biological Station.

Requirements. - Doctoral degree (Ph.D.) in biological sciences, specializing in the areas of systematics or evolution. - Knowledge and professional experience of at least 3 years in research in phylogenetic systematics and evolution of any group of plants that play a significant floristic, evolutionary or ecological role in Mexican SDTFs. - Field research experience. - Experience using or developing biological collections. - Ability to teach and supervise undergraduate and graduate students from UNAM's undergraduate and graduate programs and/or regional universities, as well as to participate in outreach and institutional activities. - Capacity to develop their own line of independent research, including procurement of funds for research, and interaction and collaboration with other national and international research groups. - Willingness in the short term to inte-

grate with the academic activities of both the Chamela Biological Station and its campus in Colima. - Non-native speakers must be fluent in the Spanish language.

Application and supporting documents. To apply, please send the following documents to the Office of Academic Affairs (Secretaria Academica) of the Institute of Biology at sacademica@ib.unam.mx, with copy (Cc:) to secacad_v1@ib.unam.mx: 1. Curriculum vitae (CV), including academic degrees, publication history and experience in plant systematics. 2. Description of research conducted during at least the past 3 years (2 pages maximum). 3. Research proposal to be developed in the first year of work, in the context of a longer research plan, focused on the systematics and evolution of any group of plants that play a significant floristic, evolutionary or ecological role in Mexican SDTFs (10 pages maximum). 4. Cover letter addressed to the Director, Prof. Susana Magallon, stating the motives and interest in developing an academic career at the Institute of Biology, UNAM (2 pages maximum) 5. Names and contact information of at least three persons who can provide academic references.

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UPuertoRico Two PhylogeneticsNeuroscience

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

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

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

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

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

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

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

Deadline for applications: May 3, 2024

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

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

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

[tgiray2 <tgiray2@yahoo.com>](mailto:tgiray2@yahoo.com)

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Since evolutionary, basic, comparative neuroscience is relevant to Evolutionary biologists, again the announcement would be of interest to EvolDir clients. The an-

nouncement specify basic and also environmental neuroscience as desired research areas. Thanks.

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

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

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

Responsibilities: The new faculty member is expected to develop a strong research program supported with external funds; strengthen the course offering of the Department at the undergraduate and graduate levels, including teaching at all available teaching hours and using diverse technologies; provide mentorship for undergraduate and graduate (M.Sc. and Ph.D.) students; and participate in service activities at the level of the Department, University and beyond. We seek a colleague who has demonstrated a commitment to enhancing and promoting inclusion, equity, and diversity in research, mentoring, teaching, and outreach. The University of Puerto Rico

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USheffield EvolutionaryBiology

The Ecology and Evolutionary Biology research cluster at the University of Sheffield (UK) is keen to support early career researchers in developing applications for independent research fellowships that align with our broad

interests. We are driven by our curiosity to understand how the natural world has evolved and operates. Together we work to answer fundamental questions in ecology, conservation, and evolutionary biology, addressing key global challenges facing biodiversity and humankind. More information about our research interests can be found here <https://www.sheffield.ac.uk/biosciences/research/areas/ecology-and-evolutionary-biology>. As part of the School of Biosciences, and Faculty of Science, we aspire to be a welcoming and inclusive environment for science researchers, and recognise that some researchers - especially women and BAME staff - may not receive the same support as their peers in applying for fellowships and career progression. For this reason, we are especially encouraging members of under-represented groups to apply to hold an independent research fellowship with us.

We offer long-term Independent Research Fellows an academic position after their fellowship and a PhD student during the fellowship. Within EEB, upcoming eligible schemes include NERC Independent Research Fellowships (<https://www.ukri.org/opportunity/nerc-independent-research-fellowship-2023/>), Royal Society Dorothy Hodgkin (<https://royalsociety.org/grants/dorothy-hodgkin-fellowship/>) and University Research Fellowships (<https://royalsociety.org/grants/university-research/>), with closing dates in September/October. We have a strong track-record of supporting IRFs within EEB, and many of our current faculty have come through this route. Due to the support we offer, we have internal selection processes, so please get in touch by the end of April if you want to apply for one of these fellowships with us. Please complete this short, initial expression of interest form, so we can start a conversation with you. <https://forms.gle/jfsVYM3EFVSQcpEt5> For enquiries about any other fellowships, or for future rounds, please get in touch at any time.

Further details on IRFs at the University of Sheffield and what we offer, can be found here <https://www.sheffield.ac.uk/science/research/fellowships>. Informal enquiries can also be directed to Nicola Nadeau (n.nadeau@sheffield.ac.uk, head of the Ecology and Evolutionary Biology research cluster) or Gavin Thomas (gavin.thomas@sheffield.ac.uk, researcher development lead of the Ecology and Evolutionary Biology research cluster).

Nicola Nadeau <n.nadeau@sheffield.ac.uk>

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VanderbiltU ResearchTech ExperimentalEvolution

The Behringer Lab in the Department of Biological Sciences at Vanderbilt University is looking for a Research Technician to oversee long-term experimental culture of various anaerobic and aerobic bacteria, including *Lactobacilli* and *Escherichia coli*. The Behringer lab is a young and vibrant team dedicated to understanding fundamental biological processes in a collaborative environment. Our lab is actively involved with the Vanderbilt Evolutionary Studies Initiative and the Vanderbilt Institute for Infection, Immunology, and Inflammation, making it a wonderful opportunity for recent graduates looking for a two-year position to gain valuable research experience prior to pursuing a graduate degree. The major research focus of this position is understanding how oxygen exposure shapes microbial evolution, which aligns with the global lab interests of how microbes evolve in stressful environments. The Research Technician is a key member of the research team responsible for supporting the research, organization, and day to day operations of the lab. As such, this position requires skills in microbial cell culture, nucleic acid extraction, and project organization. Applicants with experience conducting experimental evolution or anerobic microbial cell culture are strongly preferred. For more information e-mail the PI, Megan Behringer (megan.g.behringer@vanderbilt.edu) with your CV/resume.

“Behringer, Megan” <megan.g.behringer@Vanderbilt.Edu>
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Vienna TechAssistant MolecularGenetics

Dear colleagues,

Our Konrad-Lorenz-Institute of Ethology, Department of Interdisciplinary Life Sciences, University of Veterinary Medicine (Vetmeduni) Vienna, Austria, has an open position for a permanent technical assistant in the Molecular Genetics Laboratory. The application

deadline is 30.04.2024 and we very much look forward to receive your application.

Technical Assistant in the Molecular Genetics Laboratory

Grade: IIIb Level of employment: 40 hours per week Duration of contract: unlimited Deadline for applications: 30.03.2024 Reference number: 2024/0071

Working place: Konrad-Lorenz-Institute of Ethology, Savoyenstraiße 1, 1160 Vienna

Responsibilities and tasks

* Support in the general organization of the laboratory (orders, equipment, calibrations) as well as adherence to good laboratory practice.

* Assistance to scientists in research projects using molecular- genetic techniques. * Execution of experiments and genetic analyses of biological substances (blood, feces, hair, tissue). * Implementation of molecular biology techniques (e.g., various PCR techniques, NGS library preparation). * Development of laboratory protocols, execution and documentation of measurements. * Assistance for data management (e.g., data entry in Excel).

Necessary education, qualifications and knowledge

* Bachelor's degree in the field of natural sciences and relevant experience in biological/genetic research, or matriculation examination and training as a Medical Technical Assistant (MTA), Biological Technical Assistant (BTA), or matriculation examination and comparable qualifications as well as relevant professional experience in the fields of biological/genetic research. * Knowledge in molecular biology. * Excellent computer skills (especially MS Word, Excel). * Good German language skills (B2 level). * Good English language skills (B2 level).

Desirable qualifications and skills

* Experience in the field of molecular-genetic research, particularly DNA and RNA extraction from various biological samples (e.g., tissue, feces, urine, blood), cDNA library preparation, DNA sequencing, PCR, Real-time PCR, ddPCR, Microsatellite and SNP Genotyping, NGS library preparation. * Experience in laboratory organization (database management, ordering of laboratory supplies, etc.). * Experience with bioinformatic analyses (fragment analysis and NGS sequence assembly, gene expression analyses). * Ability to work in a team. * Precision.

We offer

* Top university: the Vetmeduni is one of the leading academic institutions in Europe to offer education in and undertake research on veterinary medicine * Stable employer * Attractive campus * Opportunities for further training, both personal and in connection with your career * Preventive and medical health care * Diversity- and family-friendly culture * Childcare facilities, both in term time and during holidays * Many attractive fringe benefits * Staff events

Minimum salary The minimum salaries at universities are governed by a collective bargaining agreement. At the level given above, the minimum salary amounts to EUR 2.958,90 gross per month (based on full-time employment).

Applications We look forward to receiving your application with the reference number 2024/0071, which you should send via email to bewerbungen@vetmeduni.ac.at. Please make sure to include the reference number, as we will not be able to correctly assign your application otherwise.

The application process is free of charge. Applicants are not entitled to compensation for travel and accommodation expenses incurred in connection with the selection process.

The Vetmeduni proudly holds the “university and family” certificate, and we therefore welcome applications from individuals with family competencies. Applications from individuals with disabilities and chronic illnesses are also encouraged. For any inquiries regarding the reference number: 2024/0071, dated 20.03.24, please feel free to contact our disability liaison officer, Mr. Franz Mitterbauer (franz.mitterbauer@vetmeduni.ac.at).

Further information

Olga Hofer, MBA +43 1 25077-7106 olga.hofer@vetmeduni.ac.at www.vetmeduni.ac.at/klivv
Priv.-Doz. Dr. Pamela Burger

Senior Researcher < <https://www.vetmeduni.ac.at/en/research-institute-of-wildlife-ecology/working-groups-units/genetics/population-genetics-and-conservation-genetics> >

Research Institute of Wildlife Ecology

Vetmeduni



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FieldTech SiberianJayAdaptations

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

Do you want to contribute to understanding how animals are adapting to changing environments?

Are you interested in learning why social interactions matter for this?

Can you work in the field with temperatures down to -10C, and walk up to 15km per day?

Do you have:

*Past experience of field work birds, mist netting and ringing?

*A social mindset, good people skills and want to contribute to our diverse team?

*A valid drivers licence (manual transmission)?

*Are you available from 5 August to 20 October 2024?

If so, please send your application, including a CV, letter of motivation (1 page), and the name of two referees, to Michael Griesser michael.griesser@uni-konstanz.de, preferably in a single PDF.

We are looking for 2 highly motivated, expenses-paid field technicians to join our diverse team (lead by principal investigators Dr. Michael Griesser, University of Konstanz & Dr. Miya Warrington, Oxford Brookes University).

This position is suitable for a person considering further studies (e.g., postgraduate degrees) in wildlife conservation, ornithology and ecology, or those people looking to expand their field skills.

Our study site is located in Northern Sweden. An overview over our past work can be found here: <https://www.youtube.com/watch?v=JaH6wjAYAiE>. Further information can be found here: <https://sites.google.com/view/c-wild-griesser/home> We will cover accommodation, food, and travel expenses to and from the study site (up to 400 euros return).

Review of applications will start 20 May 2024, position will remain open until filled.

Michael Griesser Department of Biology University of Konstanz

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

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JohnInnesCentre UndergraduateStudentship

Funded undergraduate summer studentship - Investigating genetic resistance to insect pests in Oilseed Rape

We are currently advertising a funded eight-week undergraduate summer studentship at the John Innes Centre, Norwich, UK (<https://www.jic.ac.uk/>), through the Royal Society of Biology's Plant Health Undergraduate Studentship (<https://www.rsb.org.uk/get-involved/grants/plant-health-ug-studentships>) programme.

The student will investigate crop-pest interactions between winter Oilseed Rape (*Brassica napus*) and the Cabbage Stem Flea Beetle (*Psylliodes chrysocephala*), to

verify larval development differences across resistant and susceptible Oilseed Rape genotypes, with the goal of understanding the evolution of resistance/susceptibility traits across oilseed rape. The student will gain experience in the following: - Plant and insect husbandry - Experimental design, crop-pest experimentation, and statistical analyses (using R) - Semi-automated image phenotyping - Scientific record keeping and data management

The studentship will take place during the summer of 2024 (ideal start date: 24th June 2024) and is open to students who are registered at a UK institution and in the middle years (i.e. 2/3, 2/4 or 3/4) of their degree. Final year undergraduates intending to continue to study for a Master's or PhD may also be considered. Successful students will receive a stipend of $\frac{1}{2}$ £380 per week.

Interested students can apply at: <https://my.rsb.org.uk/services.php?section=grants&grantid=104> or contact Dr Ryan Brock (ryan.brock@jic.ac.uk) or Dr Rachel Wells (rachel.wells@jic.ac.uk) for more information about the project.

Application deadline: 23:59 on Sunday 21st April 2024.

Dr Ryan Brock Postdoctoral Researcher Department of Crop Genetics (Biffen 111) John Innes Centre Norwich NR4 7UH

“Ryan Brock (JIC)” <Ryan.Brock@jic.ac.uk>

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OhioU SummerREU PlantEvolution

The Schenk Lab at Ohio University is seeking an undergraduate student to conduct research this summer funded by the National Science Foundation's (NSF) Research Experiences for Undergraduates (REU) program. The student will conduct research on the evolution of flowers over the course of 12 weeks starting in May. The position will be in person in Athens, Ohio.

The REU student will conduct an independent research project to answer the question: are re-evolved stamens reproductively viable? The student's project will investigate whether pollen is viable when stamens re-evolve from staminodes (= infertile stamens). We hypothesize that once stamens re-evolved, either (1) pollens are inviable, (2) pollen viability is maintained through

time at a level comparable to those in surrounding stamens, (3) pollen viability increases over time so that stamens evolve to increase reproductive output, or (4) pollen viability decreases over time as stamens become more staminode-like. To answer the above question and test the hypotheses, the student will be using a pollen-viability stain to count the proportion of inviable pollens in preserved flowers and then use a time-calibrated phylogeny that is produced as part of an NSF funded proposal to determine pollen viability and how it has changed through time. The goal is to have the student complete sampling and analyzing the data within the 12-week program, with the broader goal of publishing the results.

The 12-week project comes with a \$7,200 stipend to cover housing (the REU student will have to secure housing) and food. Eligible applicants must be enrolled, either part-time or full-time, in a degree program leading to a baccalaureate or associate degree. Furthermore, candidates must hold U.S. citizenship, U.S. national status, or be a U.S. permanent resident. Please note that individuals who have attained their bachelor's degrees and are no longer enrolled as undergraduates are typically ineligible to participate. Interested applicants should submit an online application that consists of a resume/CV, a cover letter that expresses their interest and addresses the minimum and preferred qualifications, and the names, email addresses, and phone numbers of two references to: <https://www.ohiouniversityjobs.com/postings/49413> Review of application materials will begin immediately, and the position will remain open until filled. For full consideration, please apply by April 15, 2024.

For more information, see: Schenk Lab website: <https://schenklab.weebly.com/> Environmental and Plant Biology at OU: <https://www.ohio.edu/cas/plant-biology> Our NSF funding: https://www.nsf.gov/awardsearch/showAward?AWD_ID=3D2117446 Application link: <https://www.ohiouniversityjobs.com/postings/49413> schenk@ohio.edu

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OmennPrize BestArticleEvolMedicine

Nominate your article or another that you admire for the \$5000 Gilbert S. Omenn Prize. The deadline is April 15,

2024. The form is simple, it takes only a minute.

The Prize is awarded annually 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 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/-shrRwFXDjU0RsXBD> –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/-shrRwFXDjU0RsXBD> 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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Passing of JohnDamuth

In Memoriam John Damuth, PhD. August 18, 1952 ??? April 2, 2024

Research Biologist Department of Ecology, Evolution & Marine Biology University of California, Santa Barbara

With great sorrow at the loss of a singularly sharp, clear-thinking, delightful, warm, witty, generous and wonderfully curious colleague and partner, we announce the passing of John Damuth, who died following 15 months of treatment to hold an insidious cancer at bay. John was an evolutionary biologist whose contributions included wide-ranging empirical, theoretical, and conceptual advances in the fields of comparative ecology, ecological allometry, levels of selection, macroevolution and paleontology.

John was a brilliant scientist whose wisdom extended not just to his academic endeavours, but also to his insights into people, culture and the world in general. John was born in Corpus Christi, Texas on August 18, 1952, and grew up in Prairie Village, Kansas, in Northport, Long Island and in Sewickley, Pennsylvania with his sister Laura and his parents John (John Douglas Damuth, Sr.) and Mary. John's curiosity about the world was directed towards science and history as a young boy, when he began to develop what became particularly deep interests in the ancient world, physical anthropology, linguistics, evolutionary theory, and paleontology. In 1970 he went to Yale University to study for a B.A. in anthropology, and then in 1974 to the University of Chicago, where he earned his Ph.D. in evolutionary biology. John always considered himself to have been extremely lucky to have been Leigh Van Valen's graduate student at Chicago, and he continued Leigh's tradition of eclectic scholarship by combining vertebrate paleontology with theoretical evolutionary biology. In John's own words, his approach was to seek out and investigate general processes and mechanisms that can be used to make reliable inferences about the remote past, but are based on demonstrable regularities in the present day. (see johndamuth.net)

While John was at the University of Chicago he first met Susan Mazer in 1977 through mutual friends at Yale; they soon became inseparable partners, living together in Davis from 1981 to 1985 while Susan completed her Ph.D. in plant evolutionary ecology at the University of California, Davis, and marrying in 1988. For 45 years,

they were a devoted couple who took great delight in each other's observations, critiques, and accomplishments.

Initially, John and Susan were both postdoctoral fellows at the Smithsonian Institution in Washington in the mid-1980s. They agreed that, no matter who first got a permanent faculty position at a research institution with a broad graduate program in evolutionary biology, the other would follow. Consequently, after Susan was offered a position at UC Santa Barbara in 1998, John accepted the position of Research Biologist in what was then the Department of Biological Sciences, and created a research career that worked for them both.

Although John began his career studying fossils, exploring the collections of Eocene and Oligocene mammals at the Field Museum, he soon found himself engrossed in the world of evolutionary biology, attracted to the challenge of finding and explaining regularities in community structure, specifically those relating to mammalian body size and population density (in both extant communities and fossil localities). John's first publication, completed while a graduate student (Nature, 1981), on Population density and body size in mammals became an instant and lasting classic that continues to be frequently cited (1446 citations to date).

John's most important and widely known ecological and evolutionary discovery, as first described in the 1981 paper, is widely referred to as Damuth's Law. John's characteristic humility prevented him from ever referring to this discovery as a "law", but many other investigators have accepted this distinction, and a brief description of it will justify this level of recognition. John's work on ecological allometries began with his discovery of the interspecific scaling of ecological population density with body mass among herbivorous mammals, which led him to realize that species' energy use among these species (at the population level) is independent of body size within communities.

The math and logic underlying this realization are relatively simple. Among ecologically similar species (e.g., herbivorous mammals), population density scales as the negative 0.75 power of body mass. The astonishing significance of this relationship becomes apparent when one applies another well-known scaling relationship (Kleiber's Law, discovered in the 1930s) to estimate, within communities, energy use by populations of species of different body sizes. Kleiber's Law states that the interspecific relationship between individual basal metabolic rates

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RoyalSocPubl more Releases

The following issue from Royal Society Publishing Philosophical Transactions B is now one of our most highly cited and widely read: Half a century of evolutionary games: a synthesis of theory, application and future directions compiled and edited by Xiang-Yi Li Richter and Jussi Lehtonen and the articles can be accessed at www.bit.ly/PTB1876 A print version is also available at the special price of £40.00 per issue from sales@royalsociety.org

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SouthAfrica VolunteerGiraffeConservation

Giraffe Guardians: Fieldwork Training Programme Dive into the heart of giraffe conservation with WildComm's Giraffe Guardians programme, where participants contribute to the understanding of giraffe populations and their conservation needs through data collection and research efforts.

WildComm (www.wildcomm.org) is a dynamic conservation organisation dedicated to fostering the next generation of conservationists. Through affordable fieldwork training opportunities, we empower individuals to actively engage in impactful research and conservation initiatives, bridging knowledge gaps and cultivating a shared appreciation for the natural world. We offer the opportunity to develop a range of skills, which is a perfect steppingstone for your future career in conservation, or simply to take time out whilst also giving back. We

are always looking for hands-on and passionate assistants to join our team and support our goals.

Key activities We currently have a limited number of positions for participants to train and assist on our research programme studying the conservation value of privately owned giraffe. Based within the Limpopo Province, South Africa, participants will develop essential fieldwork skills and gain practical experience in wildlife conservation. You will receive expert training and guidance from experienced staff, ensuring you are well-equipped to collect behavioural data and conduct regular population counts on giraffe, making meaningful contributions to giraffe research and conservation initiatives.

Whilst on this programme, you will also have the opportunity to get involved in a number of other activities, including rhino behavioural data collection, snare sweeps, invasive species removal, habitat surveys, litter picks and environmental education.

What we are looking for Everyone at WildComm is passionate about the work they do, so we are looking for someone who is excited to make an active contribution to the project. We are open to your background, what is important is that you are committed to the cause, willing to put in the hours, and dedicated to making a real difference. There are a few qualities that make you more relevant for the programme: prior experience with the project's field techniques or working in a southern African environment; being reliable, responsible and motivated to work hard; enjoy working as part of a team and be happy to operate under the authority of field research coordinators, whilst being competent working unsupervised; happy to work long and unsociable hours. Some activities involve long days of walking in hot and cold weather, so if you are applying for these activities, you must be prepared and able to cope with such conditions.

At WildComm, we pride ourselves on conducting serious and impactful research aimed at furthering conservation efforts. While we value camaraderie, social interaction, and an occasional beer under the stars, it's important to emphasize that our primary focus is on the research and conservation work at hand. If you're seeking a party atmosphere or are primarily interested in leisure activities, we encourage you to explore other opportunities that align more closely with those preferences. Our projects require dedication, focus, and a genuine passion for wildlife conservation, and we welcome participants who share these values and are committed to making a positive impact on the environment.

Participants are welcome to join us for any duration, but longer stays are encouraged for a more enriching

experience.

Costs Our fieldwork training programmes offer invaluable exposure to a variety of research techniques, making it an integral stepping stone for your next role. As we operate without external funding, participant fees not only cover their own expenses but also enable this vital research to proceed. Fees cover all training and research equipment, accommodation, and in-country transport. Fees do not cover food and participants are responsible for arranging their own airfare, as well as obtaining medical and travel insurance. Current fees are 1,000 per month. For stays of 3 months or longer, fees can be negotiated.

Accommodation is on a working farm, consisting of a communal area and kitchen stocked with crockery, cutlery, fridges, freezers, a stove and drinkable tap water. Rooms are shared (2-4 people) and include linens, hot showers and flushing toilets.

How to apply Immediate positions are available with ongoing opportunities. To apply or for further information, please contact applications@wildcomm.org. When applying, kindly include your CV along with a brief statement outlining your interest in joining our team, relevant experience or transferable skills, and how you envision contributing to our research programmes. PLEASE ALSO STATE WHERE YOU SAW THIS ADVERT.

Applications will be accepted until all positions are filled.

Embark on an unforgettable journey with WildComm's Giraffe Guardians

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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>

UMass Amherst PostdocProfessionalDevelopmentProgram

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

Best, Lisa

Lisa M. Komoroske, Ph.D. (pronouns she/her) Assistant

Professor, Dept. of Environmental Conservation University of Massachusetts Amherst phone: (413) 545-2491 | <http://lkomoroske.com/> Dear Colleagues,

We are excited to invite applicants for our second cohort of a professional development program at UMass Amherst: UNVEIL: Revealing the hidden curriculum of faculty job application, interviewing and negotiation to contribute to diversifying scientific leadership. This program is sponsored and hosted at UMass Amherst, but open to participants across North America.

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

More details on programmatic activities, eligibility, focal sub-fields, and the application can be accessed here: <https://forms.gle/SaGv3PyHhGpL8ep8>. The deadline for applications is May 3rd, 2024.

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

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

Respectfully,

Lisa Komoroske

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

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WildAnimalMicrobiomeEvolution ResearchExchangeFunding

Dear all,

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

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

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

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

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

KEY DATES: Deadline for applications 26th May 2024

Awards announced first week of June 2024

All costs must be claimed before June 2025

Best regards, WAME organising committee

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

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ArizonaStateU HumanAdaptation

Postdoctoral Research Scholar for the Stone Lab at ASU
 The Stone Lab (<https://stone.lab.asu.edu/>) is located on Arizona State University's Tempe campus and is directed by Dr. Anne Stone, Regent's Professor in the School of Human Evolution and Social Change. The central focus of the Stone laboratory is anthropological genetics. Currently, projects focus on human population history, understanding how humans have adapted to their environments, including their disease environments, improving methods for analyzing degraded DNA from forensic contexts, and examining the evolutionary dynamics of pathogens causing tuberculosis and leprosy. We are seeking applications for a full-time Postdoctoral Research Scholar to work under the supervision of Dr. Anne Stone. We are searching for a highly motivated researcher to join our group to work on projects related to forensic genetic analyses of samples from challenging contexts, conservation genomics and/or ancient DNA analyses of ancient pathogens.

The successful candidate will be working with ancient or degraded DNA, using molecular laboratory techniques (such as DNA extraction, library construction and capture) and conducting analyses of genomic data (with R, python, bash and bioinformatic software). The successful candidate will be engaged in mentoring graduate and undergraduate students, working with our collaborators, and will be provided opportunities to contribute to and/or develop external grant proposals.

This is an in-person, full-time, fiscal-year, term-limited 1-year position, which may be renewable for a second year, contingent on continued satisfactory performance, the availability of funding and the needs of the University. The anticipated start date is July 1, 2024. All Postdoctoral Research Scholar appointments are for one year, July 1st through June 30th.

The fiscal year (12-month) salary for this Postdoctoral Research Scholar position is \$55,000 along with competitive benefits through ASU, including health insurance, and paid vacation and holidays. This position is located at the Arizona State University at the Tempe campus.

Qualifications Minimum Qualifications

* A PhD in Anthropology, Evolutionary Genetics or

related fields.

* Applicants must be within five years of receipt of their PhD to be considered.

* Demonstrated commitment to working with faculty, staff, and student communities to advance the principles of the ASU Charter < <https://newamericanuniversity.asu.edu/about/asu-charter-mission-and-goals#:~:text=ASU%20is%20a%20comprehensive%20public,of%20the%20communities%20it%20serves>>

Desired Qualifications

- * Demonstrated experience with molecular laboratory analyses of ancient or degraded samples and bioinformatic analyses of genomic data.
- * Supervisory experience with student researchers.
- * Evidence of excellent organizational and project management skills.
- * Experience working independently and collaboratively in a team.
- * Experience working collaboratively with other departments and programs, across disciplines on grant-funded projects, publications or activities.
- * Evidence of commitment to creating and maintaining an inclusive environment.

Applications and Inquiries Initial review of applications will begin on May 17, 2024 if position is not filled, review of complete applications will occur every two weeks thereafter until the search is closed.

Only electronic submissions will be reviewed. Incomplete applications will not be considered. To apply, please submit application materials electronically to <http://apply.interfolio.com/144157> Required materials include:

1. a letter of interest describing how you meet the required and desired qualifications
2. a current curriculum vitae, and
3. up-to-date contact information (including email addresses) for three (3) professional references.

General questions about this position may be directed to Dr. Anne Stone: ACStone@asu.edu.

Background check is required for employment.

Arizona State University is a VEVRAA Federal Contractor and an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, protected veteran status, or any other

basis protected by law. (See <https://www.asu.edu/aad/manuals/acd/acd401.html> and

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Brno Czech FishEvolution

Brno_Fish_EcoEvo

POSTDOCTORAL RESEARCH POSITION - 18 MONTHS

TOPIC: Fish Evolutionary Ecology

REICHARD LAB (www.reichardlab.eu)

Institute of Vertebrate Biology, Czech Academy of Sciences, Brno

Full-time postdoctoral position for 1.5 years (funding until 31 Dec 2025) is available at the Institute of Vertebrate Biology of the Czech Academy of Sciences, located in Brno, Czech Republic. All applications submitted before 30 April 2024 will be fully considered. Selected candidates will be interviewed online.

This position is within a generous funding of Expro project of Czech Science Foundation to Martin Reichard on reproductive parasitism in fish (funded for 2021-2025). It uses two understudied fish brood parasitic systems: bitterling fishes (Acheilognathidae) and their mussel hosts, and cuckoo catfish (*Synodontis multipunctatus*) and their cichlid hosts from Lake Tanganyika.

The project aims at identifying the conditions for the origin and evolution of host specificity in brood parasites. Field and lab studies are combined with population genomics, phylogenetics and comparative methods.

Selected candidate will work in an international group consisting of two Ph.D students, three postdoctoral researchers, and several full-time researchers. There is flexibility in the specific focus within the broad terms of the project, although for this position, we would particularly welcome a candidate with expertise in:

1. population genomics or
2. genome biology or
3. diversification modelling and macroecology or
4. fish morphology, reproductive biology and behaviour

These topics are complementary to the expertise we already have in our research team.

We expect applications from candidates with a background in ecology and evolution. For experimental work, there is access to well-equipped fish breeding facility and outdoor battery of mesocosm tanks.

All research expenses, including fieldwork and conference travel, are covered from the project.

QUALIFICATIONS

PhD in Biology or related discipline

SALARY

50,000 CZK, c. 2,000 EUR per month (well above average for Czech living expenses), giving net earnings of approximately 42,000 CZK per month. Social and health insurance (additional 35%) are covered by the project funding.

APPLICATION PROCEDURE

Feel free to consult through informal enquires by email to reichard@ivb.cz (PI of the project).

For formal applications, please submit a CV with explanations of your previous work and motivation to apply for this position in your Cover Letter (1-2 pages).

Submit your application until 30 April 2024. Shortlisted candidates will be interviewed online in May.

Email your formal application to reichard@ivb.cz and polacikova@ivb.cz

Martin Reichard <reichard@ivb.cz>

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ClemsonU OralMicrobiome

ClemsonU.OralMicrobiome

Vincent Richards' lab in the Department of Biological Sciences at Clemson University is accepting applications for a postdoctoral position.

Position Description The overarching research theme focuses on the dental supragingival microbiome within the context of caries progression and HIV infection/exposure in children.

Postdoc candidates should have a strong publication record, a background in microbial community dynamics, experience analyzing next-generation sequence data (in

particular amplicon sequencing and metatranscriptomic data) and be well versed in Linux/bash. Moving forward, the postdoc will benefit from experience working with techniques developed to achieve strain level resolution for microbiome analyses. For example, PacBio long read data, DNA-DNA proximity capture (Hi-C), and targeted long read metatranscriptomics.

The position will be available July 15th, 2024. Currently, 12 months of support are available with the possibility to extend up to five additional years contingent upon available funding. Salary starts at \$54,000 and benefits are included.

About the University, Department, and Lab Located on Lake Hartwell in the foothills of the Blue Ridge Mountains, Clemson University is South Carolina's public land-grant University with access to multiple state and national parks and forests. As a Carnegie R1 Institution, Clemson has excellent research resources including the globally ranked Palmetto high-performance computing cluster, the Clemson University Genomics and Bioinformatics Facility, the Eukaryotic Pathogen Innovation Center, state-of-the-art light microscopy, electron microscopy, vivarium, animal, aquatic animal, and greenhouse facilities, and a multi-user analytical laboratory. There are many opportunities for collaboration across a wide group of partners on and off campus, including the Center for Human Genetics (<https://www.clemson.edu/science/research/chg.html>) and Prisma Health. Clemson is also launching a new College of Veterinary Medicine that will commence student enrollment in Fall 2026.

The Department of Biological Sciences at Clemson University harnesses faculty expertise across the areas of ecology, evolution, and organismal biology; microbiology; and molecular, cellular and developmental biology to advance the University's discovery mission and provide strong educational programs at both the undergraduate and graduate levels.

For more information about the Department and its programs, please visit the website <https://www.clemson.edu/science/academics/departments/-biosci/index.html> For more information about Clemson, please visit the website <http://www.clemson.edu/> For more information about the Richards' Lab, please visit the website <http://www.vprichards-lab.com> Application Instructions Review of applications will begin immediately; however, the position will remain open until filled. Applicants should submit the following items via Interfolio at (insert Interfolio link).

(1) Cover letter describing research interests, experience, and career goals. (2) CV (3) PDFs of representative publications (4) Contact information for three references

For more information, please contact Vincent Richards at vpricha@clemson.edu

Equal Employment Opportunity Statement Clemson University is an AA/EEO employer and does not discriminate against any person or group on the basis of age, color, disability, gender, pregnancy, national origin, race, religion, sexual orientation, veteran status or genetic information. Clemson University is building a culturally diverse faculty and staff committed to working in a multicultural environment and encourages applications from minorities and women.

vpricha@clemson.edu

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

Vincent Paul Richards <vpricha@clemson.edu>

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

HeinrichHeineU PlantAdaptation

Postdoc: HHU.PlantEcologicalGenetics_2024

The Institute for Plant Ecology and Evolution at the Faculty of Mathematics and Natural Sciences of Heinrich Heine University (HHU) Duesseldorf, Germany, invites applications for a

Postdoctoral Associate (w/m/d) (100 %, EG 13 TV-L, for 2 years - may be extended up to 3 years): Rapid Evolution to Changing Environments in Brassicaceae: Bridging Ecology and Genetics

To be filled as soon as possible

Our research focuses on the responses of plant populations to climate change and attempts at disentangling the relative contributions of adaptation, phenotypic plasticity, and range shifts. We also aim to identify the drivers of rapid contemporary evolution and uncover the genetic basis of climate change adaptation. To examine these themes, we combine traditional field- and greenhouse-based studies, as well as the resurrection approach, with quantitative genetics and ecological genomics. Our lab is integrated in the research initiative TRR 341 on Plant Ecological Genetics.

We are looking for a motivated postdoctoral associate to collaborate on ongoing research projects studying climate change adaptation in Brassicaceae. The postdoc is also encouraged to develop related projects within

the lab's research framework and to apply for independent third-party funding to develop their own research profile. The position has a teaching requirement of 4 SWS (contact hours per week). The courses cover basic ecology and evolutionary biology.

YOUR TASKS: - Use the resurrection approach to study rapid evolution in Californian Brassica rapa populations in response to drought - Conduct common garden experiments in the greenhouse and/or field to score phenotypic differences between Brassica rapa populations under different experimental conditions (i.e., water and nutrient limitations) - Conduct and support fieldwork for in situ sampling and scoring of local Brassicaceae species and populations to identify inter- and intraspecific trait and genetic variation underlying ecological diversification and local adaptation - Apply statistical and computational tools for the analysis of trait, environmental, and next-generation sequencing data - Present research results at conferences and publish in peer-reviewed scientific journals - Supervise and mentor students in the lab, coordinate and supervise student crews during experiments and fieldwork season

YOUR PROFILE: - PhD in the field of plant biology, ecology, botany, evolutionary or population genetics, quantitative biology or related - Experience designing and conducting large multi-factorial plant experiments (i.e., common gardens, reciprocal transplants, measure plant functional traits, etc.) - Experience in the use of statistical methods to analyze quantitative datasets and programming languages (e.g., R, Java, Python) - Experience with population genetics, NGS data, SNP calling, genome annotation, standard molecular techniques is desired - The languages spoken in the group are English and German - demonstrated ability to communicate effectively in both languages is important (written and spoken) since the position involves teaching at the undergrad level (mostly in German) - Good interpersonal skills (i.e., communication, cooperation, motivate others, open-minded, etc.) - Lawful ability to work in the EU (i.e., Schengen residence/work permit)

WE OFFER: - A unique, dynamic, and interdisciplinary research network in the field of Plant Ecological Genetics (TRR 341) that bundles the expertise of excellent scientists from seven different research institutions. - A comprehensive training program with targeted scientific education in the field of Plant Ecological Genetics as well as complementary training supporting your personal and career development (GEcoGen, iGRAD, JUNO, HeRA) - Family-friendly and multicultural working environment

TO APPLY: Qualified candidates should send their application (Cover Letter including statement of research interests - max. 2 pages, CV including publication list,

contact info of three references, BSc, MSc, and PhD certificates) by e-mail (one single pdf-file) until 30.04.2024 to elena.hamann@hhu.de.

If you have further questions on the project or position, please contact Prof. Elena Hamann and see lab website <https://www.biologie.hhu.de/institute-und-abteilungen/institute-hhu/pflanzenoekologie>. “Hamann, Elena” <Elena.Hamann@hhu.de>

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ISYEB Paris DistributionEffectSizesQTL

We offer a 2-years position, working as post-doctoral fellow to improve our ability to study the genetic architecture of complex traits, by developing a new method to study the distribution of the effect sizes of Quantitative Trait Loci (QTL).

The job will be mostly computational, based on statistical modelling and development, as well as assessing the performance of the method using simulated data. The candidate will work for the *École Pratique des Hautes Études* (PSL University), joining Pierre de Villemereuil’s team, at the Institute for Systematics, Evolution, Biodiversity (ISYEB), located within the *Muséum National d’Histoire Naturelle* (MNHN) in Paris. This position is funded as part of the *EvoGenArch* ERC Starting Grant. The position starts on 2024-09-16.

For more information and instructions to apply, see here: <https://euraxess.ec.europa.eu/jobs/225408> Pierre de Villemereuil <pierre.devillemereuil@ephe.psl.eu>

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JohnInnesCentre UK PlantBacteriaInteractions

Postdoctoral Researcher Salary: £35,300 - £43,750 per annum depending on qualifications and experience. Contract: 24 months, full time Location: John Innes Centre, Norwich, UK. Closing date: 16 May 2024 Ref-

erence: 1004657

Applications are invited for a Postdoctoral researcher to join the group of Prof Saskia Hogenhout (twitter: @SaskiaHogenhout) at the John Innes Centre (JIC) to study molecular processes in host-pathogen interactions.

This position provides an exciting opportunity to discover how an obligate bacterial plant pathogen modulates host development and immunity.

Our established system involves phytoplasmas that are insect-vectored plant pathogens. Phytoplasmas have the remarkable ability to dramatically alter plant development by modulating host cellular pathways, leading to, for example, leaf and stem proliferations, delayed aging and increased longevity. The resulting ‘Zombie plants’ (Nature Microbiology Reviews, New York Times) are under complete control of the phytoplasmas. We found that the phytoplasma virulence proteins are amazing tools to uncover cellular processes, including a novel way of targeted protein degradation, in diverse organisms, including humans. See the following recent publications for more information: Huang et al. 2021 (10.1016/j.cell.2021.08.029) Liu et al. 2023 (10.1073/pnas.2310664120) and Correa Marrero et al. 2024 (10.1111/tpj.16546).

The successful applicant will functionally analyse phytoplasma effectors and their targets in plant hosts and insect vectors. They will use biochemical and biophysical experiments in answering key questions such as: How do phytoplasma effectors bind and modulate specific host targets and how have these proteins evolved?

You must have or be close to finishing a PhD in molecular biology or a similar subject. Knowledge of cell- and microbiology, biochemistry and plant genetics are essential. Practical experience in recombinant DNA technology, protein engineering, plant stable/transient transformation techniques, and studying molecular processes in plant-biotic interactions, such as function-structure analyses of microbial effectors/virulence proteins and their targets, are required.

You will be part of a basic research environment that involves sharing outcomes via the writing of publications and reports. You will give research presentations at group, institute and (inter)national meetings.

You will have to work well within a collaborative team and have an interest in effectively communicating and sharing technologies and discoveries within this team and in campus/institute-wide expert and interest groups. You will be offered opportunities to teach, participate in student supervisory committees and outreach activities, and to engage with industry, entrepreneurs and investors.

About the John Innes Centre:

The John Innes Centre is an independent, international centre of excellence in plant and microbial sciences. We nurture a creative, curiosity-led approach to answering fundamental questions in bioscience, and translate that knowledge into societal benefits. Our strategic vision, Healthy Plants, Healthy People, Healthy Planet, sets out our ambitious long-term goals for the game changing impact of our science globally.

Our employees enjoy access to state-of-the-art technology and a diverse range of specialist training opportunities, including support for leadership and management. Click here to find out more about working at the John Innes Centre.

About the Hogenhout Group:

The Hogenhout group at the John Innes Centre focuses on understanding the mechanisms that drive interactions between plants and insects and the role of microbes in these interactions. We use a range of molecular, biochemical, cellular biology and bio-imaging techniques to study processes in live cells and whole organisms along with biophysical techniques to analyse and engineer protein-protein interactions.

Additional information:

Interviews will be held on 19 June 2024.

For further information and details of how to apply, please visit our website <http://jobs.jic.ac.uk> or contact the Human Resources team on 01603 450814 or nbi.recruitment@nbi.ac.uk quoting reference 1004657. This role meets the criteria for a visa application, and we encourage all qualified candidates to apply. Please contact the Human Resources Team if you have any questions regarding your application or visa options.

We are an equal opportunities employer, actively supporting inclusivity and diversity. As a Disability Confident organisation, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy. We are proud to hold a prestigious Gold Athena SWAN award in recognition of our inclusive culture, commitment and good practices towards advancing of gender equality. We offer an exciting,

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LaTrobeU InvertebrateEndemismEvolution

A postdoctoral research officer position is available at La Trobe University in Melbourne Australia.

This position contributes to the ARC linkage project “Identifying hotspots of endemism for invertebrate conservation in south-east Australia”, led by Prof. Heloise Gibb (La Trobe University) and including partners from Zoos Victoria, DEECA, Australian Museum, South Australian Museum, UNSW, Deakin and Monash University.

This project will inform conservation planning by identifying the distributions and drivers of forest invertebrate diversity and endemism in south-eastern Australia and providing solutions for biodiversity protection and restoration. Focussing on the poorly-known and dispersal-limited leaf litter invertebrates of south-eastern Australian wet forests, the project will: 1. Document and georeference biodiversity; 2. Identify hotspots of endemism for conservation prioritisation and model their relationship with contemporary and past environments; 3. a) Estimate the loss of phylogenetic diversity caused by past and future environmental threats; and b) Predict where undiscovered endemic species persist.

The position will contribute to field and lab collection and collation of data. They will model hotspots of endemism and how they relate to past environments and make predictions about how endemic species will be affected by global change. A key outcome will be publication of research in peer-reviewed journals that contributes to our understanding of current and future species distributions, including currently undescribed species. We are looking for applicants with a PhD in ecology, phylogenetics, biogeography or invertebrate biology, and specifically with skills in field collection, spatial analysis, DNA sequencing and phylogenetics and/or statistical modelling including analysis of phylogenetic endemism.

The link to this position is <https://careers.pageuppeople.com/533/caw/en/job/567129/-research-officer-postdoc> For further details contact Prof Heloise Gibb H.Gibb@latrobe.edu.au or Dr Nick Murphy n.murphy@latrobe.edu.au

La Trobe University | TEQSA PRV12132 - Australian University | CRICOS Provider 00115M

N.Murphy@latrobe.edu.au

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London UK EvolutionDNA methylation

An open post-doctoral position in the laboratory of Dr. Alex de Mendoza at Queen Mary University of London (United Kingdom). This is a European Research Council funded position under the project METHYLEVOL, aimed at understanding the evolution of DNA methylation in animals and other eukaryotes. This position is for 2 years.

For this position previous experience in molecular biology and/or bioinformatics is highly desirable. Alternatively, experience in functional genomic techniques is also welcome (e.g. ATAC-seq, bisulfite sequencing), virology or comparative genomics. Some bioinformatics experience would be a plus, but we can train the candidates and offer ample support on this aspect. Plenty of opportunities for gaining expertise in functional genomics.

The goal is to understand the role of DNA methylation in various organisms and its link to genome evolution, the project can be defined according to candidate's experience and interests. See some of our latest work here: <https://www.demendozlab.com/publications> The link to the position is:

<https://www.qmul.ac.uk/jobs/vacancies/items/-9528.html> Applications close on April 16th, but feel free to get in touch if you cannot make the deadline. Start could be from May-June 2024 onwards.

All you will need is your CV and a cover letter. No nationality restrictions.

Potential candidates are encouraged to get in touch with a.demendozasoler@qmul.ac.uk to discuss your interest in the post and the project.

Alexandre de Mendoza Soler
<a.demendozasoler@qmul.ac.uk>

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ing@mcmaster.ca)

NYU Abu Dhabi Two Comparative Genomics

The Evolutionary Genomics Laboratory in the Division of Science at New York University Abu Dhabi seeks to appoint TWO post-doctoral Associates starting September 1, 2024 (later starting dates are possible).

Position 1: Postdoctoral position in comparative genomics

The successful applicant will conduct comparative genomics analyses on a wide diversity of organisms studied in the lab, including vertebrates, insects and plants. The main foci of these analyses will be (1) the identification of genes and genomic features that have evolved adaptively and (2) the evolution of transposable elements in a phylogenetic context. The successful applicant will have the opportunity to develop an autonomous line of research related to the interests of the lab in evolutionary genomics. Motivated applicants with a strong background in evolutionary biology and who are interested in leading cross-disciplinary research are encouraged to apply.

Successful candidates must hold a Ph.D. degree in Biology. Significant experience in one or more of the following is strongly desired: comparative genomics, phylogenetics, transposable elements biology. Excellent communication skills in English, the ability to work in multi-disciplinary teams, and scientific creativity are essential.

Position 2: Postdoctoral position in population genomics

The successful applicant will conduct population genomics analyses on a wide diversity of organisms studied in the lab, including vertebrates, insects and plants. The main foci of these analyses will be (1) reconstructing population structure and demography and (2) identifying genes and genomic regions that have evolved adaptively. The successful applicant will have the opportunity to develop an autonomous line of research related to the interests of the lab in evolutionary genomics. Motivated applicants with a strong background in evolutionary biology and who are interested in leading cross-disciplinary research are encouraged to apply.

Successful candidates must hold a Ph.D. degree in Biology. Significant experience in one or more of the following is strongly desired: experience analyzing whole genome resequencing data, experience in demographic

inference from genomic data, experience in selection detection methods. Excellent communication skills in English, the ability to work in multi-disciplinary teams, and scientific creativity are essential.

How to apply:

For consideration, applicants need to submit a cover letter, curriculum vitae with full publication list, statement of research interests and three letters of reference, all in PDF format. If you have any questions, please email Prof. Stephane Boissinot at sb5272@nyu.edu.

The terms of employment are very competitive and include housing and educational subsidies for children. Applications will be accepted immediately and candidates will be considered until the position is filled. To be considered, all applicants must submit a cover letter, curriculum vitae, transcript of degree, a one-page summary of research accomplishments and interests, and at least 2 letters of recommendation, all in PDF format. Please visit our website at <https://nyuad.nyu.edu/en/about/-careers/postdoctoral-and-research.html> for instructions and information on how to apply. If you have any questions, please email: mrasras@nyu.edu.

About NYUAD:

NYU Abu Dhabi is a degree-granting research university with a fully integrated liberal arts and science undergraduate program in the Arts, Sciences, Social Sciences, Humanities, and Engineering. NYU Abu Dhabi, NYU New York, and NYU Shanghai, form the backbone of NYU's global network university, an interconnected network of portal campuses and academic centers across six continents that enable seamless international mobility of students and faculty in their pursuit of academic and scholarly activity. This global university represents a transformative shift in higher education, one in which the intellectual and creative endeavors of academia are shaped and examined through an international and multicultural perspective. As a major intellectual hub at the crossroads of the Arab world, NYUAD serves as a center for scholarly thought, advanced research, knowledge creation, and sharing, through its academic, research, and creative activities.

Stephane Boissinot, Ph.D.

Professor of Biology, NYU Abu Dhabi Global Network
Professor of Biology, Faculty of Arts and Science, NYU
Director, Center for Genomics and Systems Biology

Saadiyat Island campus

P.O. Box 129188 Abu Dhabi, United Arab Emirates

<http://www.boissinotlab.squarespace.com> <https://nyuad.nyu.edu/en/research/faculty-labs-and-projects/-nyuad-cgsb.html> Office (UAE): +971 2 628 4790

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OkinawaInstSciTech MachineLearningCoevolution

We are looking for a postdoctoral candidate to work on developing novel machine-learning approaches to model coevolution across biological scales. The successful candidate will join the Model-Based Evolutionary Genomics Unit (<http://bit.ly/mod2evol>) at OIST, a small, but prolific University with a unique interdisciplinary atmosphere (<http://bit.ly/oist1st>), and have the opportunity to develop their own project or join ongoing ones that:

- Continue and extend work on using Machine Learning to predict ancestral phenotypes based on ancestral gene content;
- Use protein language models, e.g. ESM models, to explore fitness landscapes with the goal of being able to reconstruct context-aware ancestral sequences;
- Design and train transformer models trained on extant gene content using a masked language modeling objective to produce robust and high-fidelity context-aware ancestral phenotype predictions and improve ancestral gene content reconstruction.

The 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 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, provided by the budget of the Model-based Evolutionary Genomics Unit.

The position is for two years with a possibility of extension.

To apply email gergely-szollosi@oist.jp with a CV including publications and three references, as well as a 1-2 page summary of your past research and your future plans by May 10, 2024. Position open until filled.

Context:

The Model-Based Evolutionary Genomics Unit's Research Objectives

Modelling the dependency between different levels of organisation is crucial for understanding the principles that govern living systems and central to understanding the evolution of Life on Earth, as the structure of biological systems today, from molecules to ecosystems, reflects Life's ascent on a "co-evolutionary ladder" of intertwined information-environment transitions that began 4 billion years ago (Lenton 2004). In recent decades the broad outlines of the major transitions on this co-evolutionary ladder have started to come into focus, from the early emergence of life to the rise of oxygen, eukaryotes and multiple transitions to multicellularity, but we lack an empirical framework within which to test hypotheses about how, when and why these major transitions in evolution have occurred based on the geochemical and fossil records and the wealth of genomic data available. The Model-Based Evolutionary Genomics develops data-driven models that take into account dependencies between different levels of organisation, which are currently neglected due to computational and modelling constraints. Going beyond model development we apply these methods to major outstanding questions across biological scales in collaboration with a multidisciplinary group of key interdisciplinary researchers.

The Okinawa Institute of Science and Technology

The Okinawa Institute of Science and Technology Graduate University (OIST; see 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://youtu.be/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.

OIST offers relocation support, on-campus child care, and a chance to be a part of a diverse international community (bit.ly/oistint) on a unique subtropical island (<https://okinawanaturephotography.com/>)!

For more information please email: gergely-szollosi@oist.jp

Gergely J. Szöllősi

Transitional Associate Professor Model-Based Evolutionary Genomics Unit <https://www.oist.jp/research/research-units/modevolgenom>

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OregonStateU GenomicsHostParasite

Genomics of host-parasite interactions in the snail-schistosome system

Postdoctoral Scholar position in Dept. Integrative Biology, Oregon State University, Corvallis, Oregon (must be within 5 years of PhD)

Michael Blouin's lab is seeking an individual with skills in genomics to help identify genes in the snail, *Biomphalaria glabrata*, at which allelic variation controls resistance to infection by the trematode parasite, *Schistosoma mansoni*. Candidate will bioinformatically characterize genomic regions that associate with resistance. Candidate will also help analyze genomic mapping and gene expression data to find additional genomic regions.

Additional, preferred qualifications include: Demonstrated ability to write manuscripts Background/interest in host-parasite relationships Some background in Statistical Genetics (e.g. gene mapping, gene co-expression network analysis).

Department: Integrative Biology Location: Corvallis, Oregon Appointment: 100% Basis: 12 months Start Date: June 1, 2024 Notes on Start Date: open until filled. Notes on End Date: one year from start date with possible renewal for 2nd year.

Salary will follow current NIH NRSA scale (<https://gradschool.oregonstate.edu/postdocs/stipends-and-benefits>). Candidate must be within 5 years of obtaining their PhD to be a postdoc scholar. Information about postdoctoral scholars at OSU can be found at <https://gradschool.oregonstate.edu/postdocs>. We foster work-life balance and opportunities for professional development. Corvallis is a safe, highly-educated and progressive community, with many restaurants, coffee

shops and parks. There is easy access to many outdoor activities from the coast to the Mountains.

For additional information, contact Mike Blouin at blouinm@oregonstate.edu. To apply, send to Mike a cover letter that describes your interests and background, a CV, and contact information for three references.

Michael Blouin <https://blogs.oregonstate.edu/blouinlab/>
 “Blouin, Michael”
 <blouinm@oregonstate.edu>

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OregonStateU PhylogenomicsOfHybridizingLemurs

This ad is available at the following link: <https://www.eversonlab.org/join-us> Postdoctoral Research Scholar - Phylogenomics of hybridizing lemurs

A postdoctoral scholar position is available in the research group of Dr. Katie Everson in the Department of Integrative Biology at Oregon State University. The position is funded by an NSF grant led by Dr. Everson and Dr. David Weisrock (University of Kentucky): DEB 2207198 “The role of hybridization in generating biodiversity: insights from genomics of Madagascar’s true lemurs (Eulemur)”

Researchers in the Everson Lab explore evolutionary patterns and processes in real-world systems. We use a variety of data types (e.g., genomics, morphometrics, and geographic information) with many groups of organisms (e.g., tenrecs, tiger salamanders, and lemurs).

The successful candidate will participate in a genomic study of true lemurs (genus *Eulemur*) from southeastern Madagascar. Hybridization is common among species in this radiation, and the candidate will explore how hybridization shapes the genome. The candidate will help with assembly and annotation of a high-quality genome as well as population-level analyses of low-coverage genomes. Field and lab work are largely complete, so the candidate would be expected to lead bioinformatics and manuscript writing efforts.

Please visit our websites for more details on our research: <https://www.eversonlab.org> and <https://weisrocklab.uky.edu>

Candidates must have a Ph.D. in biology or related fields, with a strong background in genomics and evolu-

tionary biology, as demonstrated by scholarly activities.

The start date of this position is somewhat flexible (between Summer 2024 and the end of the year). We will begin screening applications on May 3. This postdoctoral position will be available for an initial duration of one year with the possibility of extension for a subsequent year contingent upon satisfactory academic performance and fulfillment of job responsibilities.

To apply, please send the following to Katie Everson by email (eversonk@oregonstate.edu): - Cover letter detailing research interests, experience, and motivation relevant to the project - A current CV - Contact information for 3 professional references.

Informal inquiries before applying are welcome! Additional information: Dept. of Integrative Biology: <http://ib.oregonstate.edu/> Center for Quantitative Life Sciences: <https://cqsls.oregonstate.edu/> Oregon State University in Corvallis, OR is located within the traditional homelands of the Mary’s River or Ampinefu Band of Kalapuya. Following the Willamette Valley Treaty of 1855 (Kalapuya etc. Treaty), Kalapuya people were forcibly removed to reservations in Western Oregon. Today, living descendants of these people are a part of the Confederated Tribes of Grand Ronde Community of Oregon and the Confederated Tribes of the Siletz Indians.

Katie Everson <keverson.25@gmail.com>

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PasteurInstitute BacterialEvolutionaryGenomics

Postdoc: PasteurInsti-
tute.BacterialEvolutionaryGenomics.2024

The Microbial Evolutionary Genomics unit (head Eduardo Rocha) at the Institut Pasteur in Paris (CNRS UMR3525) is inviting applications for a postdoctoral position in comparative genomics, computational biology, and molecular evolution. The researcher will work within a multidisciplinary international team (both computational and experimental biologists), that focuses on understanding the future evolution of antibiotic resistance particularly through the action of mobile genetic elements. The project aims at characterizing gene flow among bacteria, its mechanisms, and how it can acceler-

ate or retard the evolution of novel antibiotic resistance. It will be done in interaction with a group of labs around the world with expertise in synthetic biology, antibiotic resistance, epidemiology, and genomics.

We are seeking a highly motivated candidate with a PhD in genomics, microbiology, bioinformatics, or a related field. The candidate should have expertise in evolutionary genomics or computational biology, and some experience on the analysis of bacterial genomes. Knowledge of horizontal gene transfer, mobile genetic elements, or antibiotic resistance are important. He/she should be proficient in programming languages commonly used in genomics research (e.g. Python or R) and have experience in working with bioinformatics software. Good knowledge of English is necessary. The successful candidate will be able to influence the direction of the project depending on his/her profile and strengths.

The position is funded by the JPIAMR. The monthly salary corresponds to the standard in the institute (3300 euro to 3900 euro before taxes, depending on experience post-PhD), including extended health coverage. The contract will be for 24 months, renewable at least for one further year. The position is available from June 2024, but the exact starting date is negotiable. Institut Pasteur has a dynamic and diverse scientific environment at the center of Paris. It has a service to support postdocs' career development.

To apply (or request information) please send to Eduardo Rocha an email with [Postdoc call] in the subject line and a single PDF document with: (1) a detailed CV including the full publication list, (2) a cover letter explaining motivation, research interests, skills and experience relevant to the position (1-2 pages), and (3) up to three names and contacts of researchers that can be references of your work. First round of applications' evaluation will take place the 22nd of April 2024.

Links and information: <https://research.pasteur.fr/en/-/job/postdoctoral-position-in-evolutionary-genomics-of-mobile-genetic-elements-and-antibiotic-resistance/erocha> <erocha@pasteur.fr>

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PennsylvaniaStateU ForestEvolGenetics

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

Applications are invited for a postdoctoral scholar to join the Leites lab and a highly dynamic team of scientists from Penn State University, Purdue University, University of Kentucky, and the US Forest Service, who are working on the multidisciplinary project "Future-proofing forests through a genetically informed reforestation/restoration decision network". The postdoctoral scholar will join the team to work on ecological genetics (a.k.a. genecology) of forest tree species, modeling population responses to climate in tree species native to the eastern US, and delineating climate-smart seed sourcing strategies for resilient forests. Duties include assembling and managing a large number of datasets from provenance and common garden trials for multiple species, statistical modeling and data science work, preparation and submission of manuscripts for peer reviewed journals, writing reports, oversight and coordination of activities with collaborators, serving as a role model and providing support to graduate students in the project, and performing other tasks as they arise. The postdoctoral scholar will have the opportunity to mentor undergraduate and graduate students, participate in extension and outreach activities, and participate in professional development activities as well as attend relevant and agreed-upon scientific conferences. This is a limited-term position funded for one year from date of hire with an excellent possibility of re-funding for a second year pending performance and funding availability. A minimum of one submission or publication in a peer-reviewed journal during the first year is required to be considered for contract renewal. This position will be located at Penn State in University Park, Pennsylvania (State College, PA).

Required Qualifications: * PhD in a relevant field such as forest ecology, forestry, or ecology, * Strong proficiency in statistical modeling and familiarity in data science, * Proficiency in R, * Record of publications in peer-reviewed journals, * Field experience in forest settings, * Excellent organizational skills, * Excellent teamwork, mentoring, and communication skills, * Committed to an ethical, inclusive, and nurturing work environment.

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

Start Date: Fall 2024 The Leites lab provides an intellectually rigorous and stimulating environment where we strive to be inclusive and welcoming so that all members can achieve their academic and professional goals. Visit our lab page for more information (<https://ecosystems.psu.edu/research/labs/leites-lab>).

Applicants are required to have a Ph.D. or equivalent doctorate in an appropriate field and be able to provide evidence that all requirements have been met for completion of the Ph.D. prior to the effective date of hire. To apply, visit Penn State University Careers (<https://hr.psu.edu/careers>) and search for position REQ.0000054453. For inquiries, please contact Dr. Laura Leites at lpl3@psu.edu.

“Leites, Laura P” <lpl3@psu.edu>

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RutgersU PredictingEvolution

Postdoctoral fellow in computational biology or statistical physics to study the predictability of evolution

Application review begins May 1, 2024

Download a PDF of the official job advertisement here: <https://qevomicrolab.org/wp-content/uploads/2024/04/Postdoc.advertisement.pdf> WHO ARE WE? We are the Quantitative Evolutionary Microbiology Laboratory (<https://qevomicrolab.org>), led by Dr. Michael Manhart. The QEM Lab aims to understand the fundamental principles of evolution in microbes. To this end we work at the interface of biophysics, evolutionary biology, and microbiology using theoretical, computational, and experimental approaches. We are based at Rutgers University in the Center for Advanced Biotechnology and Medicine, an interdisciplinary life science research institute. We are also affiliated with the Rutgers University Microbiome Program and the Center for Quantitative Biology.

This position is part of a collaboration with the labs of Dr. Meike Wortel (Swammerdam Institute of Life

Sciences, University of Amsterdam) and Dr. Daniel Charlebois (Department of Physics, University of Alberta).

WHO ARE WE LOOKING FOR? We are looking for a postdoctoral fellow to start in the summer or fall of 2024. By the start date, you must have a Ph.D. in a theoretical or computational field of science, including but not limited to physics, theoretical/computational biology, applied math, or computer science. Expertise in statistical physics, neural networks/machine learning theory, evolutionary theory, or bioinformatics is valuable. Previous experience in biology is not required, but you should have a strong interest in learning the biological foundations of this project. We encourage applications from a diverse range of candidates, even if you don't think you're a perfect fit.

For more information about what we look for in new lab members, please see our lab's website: <https://qevomicrolab.org/what-do-we-look-for-in-new-lab-members-our-labs-approach-to-evaluating-job-applications-and-interviews/> WHAT DO WE OFFER? We offer a postdoctoral fellow position on the predictability of evolution across biological scales of complex microbial ecosystems. You will develop a theory of evolutionary predictability, perform evolutionary simulations, and analyze high-throughput sequencing data from yeast evolution experiments to test the theory. You will present this work at local and international meetings, write papers, and apply for additional funding if necessary. You will also interact with other members of the QEM Lab at Rutgers, who are working on projects ranging from the evolution of microbial population dynamics to studying the effect of interactions on adaptation in microbial communities.

The salary will begin at \$61,805/year, with benefits including comprehensive health insurance and retirement contributions. The position is funded for 3 years.

WHERE ARE WE? Rutgers University is the eighth-oldest institution of higher education in the US and now one of the largest, with approximately 40,000 undergraduates, 20,000 graduate students, and over 8,000 faculty. Our center is based on the Piscataway/New Brunswick campus in New Jersey, part of the New York metro area and one of the most culturally and naturally rich areas of the country. We have convenient connections to the NJ Transit and Amtrak rail networks as well as to Newark Liberty International Airport.

HOW TO APPLY? Please fill out the application form at this link: <https://forms.gle/hMNgrh3Ja5dPUqfWA>

WHEN TO APPLY? Apply by May 1, 2024 to receive full consideration. If you have questions, please contact Dr. Michael Manhart at mmanhart@rutgers.edu.

Michael Manhart Assistant Professor Rutgers University
| Robert Wood Johnson Medical School Center for Advanced Biotechnology and Medicine Department of Biochemistry and Molecular Biology 679 Hoes Lane West Piscataway, NJ 08854, USA Office: CABM 306 Phone: (+1) 848-445-9835 Web: <https://qevomicrolab.org> mmanhart@rutgers.edu

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SGN Frankfurt AdaptationGenomics

Job Announcement Ref.#12-24004

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. The LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG), is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN) with five partner institutes from the Federal State of Hesse, aiming to intensify biodiversity genomics in basic and applied research. We establish a new and taxonomically broad genome collection to study genomic and functional diversity across the tree of life and make genomic resources accessible for societal demand driven applied research.

For the LOEWE funded Centre for Translational Biodiversity Genomics Centre (LOEWE-TBG), in the Genomic Biomonitoring project area, and starting as soon as possible, we are looking for a

Postdoctoral Researcher (m/f/d) in Adaptation Genomics

(full time / part-time options available)

We are looking for a talented and motivated applicant to work on a project on animal adaptation genomics using whole genome data with a focus on understanding species adaptation to extreme environmental conditions. Strong research interest in comparative or population genomics of animals will be favorable. The position is part of the Bista lab (Meta-OMICS group) and will be based in Frankfurt am Main. In the Meta-OMICS group, we work on environmental and comparative genomics focusing of animal taxa, including both vertebrates and invertebrates. We are part of TBG which maintains laboratory and bioinformatics infrastructures for reference genome sequencing at large scale, including genome lab,

robotic systems for high-throughput sample processing and HPC clusters for data analysis.

Your profile

PhD in Biology, Genomics, Bioinformatics or a related field Strong interest and skills on comparative, population or adaptation genomics Experience with analysis of large genomic and/or environmental datasets, Linux environment and shell scripting Experience with long read data analysis, transposon and gene family evolution is a plus Excellent written and oral communication skills in English

Place of employment: Frankfurt am Main Working hours: full time, part-time optional (at least 80%, 32 hours / week)

Type of contract: The position is available to start as soon as possible, and is limited to 1 year, with possibility of extension.

Salary: according to the collective agreement of the State of Hesse (pay grade E 13, TV-H)

What is awaiting you?

An interesting task in a dynamic team of researchers in an international research group and joining the LOEWE TBG excellence centre with its 20 new research groups Flexible working hours - opportunities for mobile working - leave of absence due to family reasons (certified by "auditberufundfamilie") - parent-child office - annual special payment - company pension scheme - Senckenberg badge for free entry in museums in Frankfurt. - leave of 30 days/year Senckenberg is committed to diversity. We benefit from the different expertise, perspectives and personalities of our staff and welcome every application from qualified candidates, irrespective of age, gender, ethnic or cultural origin, religion and ideology, sexual orientation and identity or disability. Women are particularly encouraged to apply, as they are underrepresented in the field of this position; in the case of equal qualifications and suitability they will be given preference. Applicants with disabilities ("Schwerbehinderung") will be given preferential consideration in case of equal suitability. Senckenberg actively supports the compatibility of work and family and places great emphasis on an equal and inclusive work culture. The employer for this position is the Senckenberg Gesellschaft für Naturforschung.

How to apply

Please send us your complete application documents as a single PDF file including: CV, list of publications, letter of motivation, academic transcripts, and contact details of two potential referees, by email at recruiting@senckenberg.de, quoting job reference number #12-

24004, or apply directly on our homepage using the online application form: <https://www.senckenberg.de/en/career/apply-online/> Applications to be submitted by 05.05.2024

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt a.M. E-Mail: recruiting@senckenberg.de

For more information about the position and requirements please contact Dr. Iliana Bista iliana.bista@senckenberg.de

For more information about the Senckenberg Gesellschaft für Naturforschung, please visit www.senckenberg.de For more information about the LOEWE-TBG, please visit <https://tbg.senckenberg.de>

Mit freundlichen Grüßen Sabine Heinrichsohn Referentin Recruiting/HR Department & Personalmarketing

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SouthAfrica Genetics MarineBiology

The Centre for Ecological Genomics and Wildlife Conservation at the University of Johannesburg invites expressions of interest for a joint postdoctoral fellowship to the value of R250 000 (~US\$ 13,400) per annum. The fellowship is awarded for up to 2 years, depending on performance.

Candidates should have 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 research field of their choice, which may include population genetics/genomics, phylogenetics/genomics and eDNA metabarcoding. Projects typically focus on marine/estuarine eukaryote species of conservation concern, commercially exploited species, or document biodiversity. Please see details about the center at <https://molzoolab.co.za/> and <https://www.uj.ac.za/members/peter-teske/> 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 can also gain experience in student supervision if they choose to become registered

co-supervisors of postgraduate students (MSc and PhD levels). The University of Johannesburg is Africa's top university in terms of the number of accredited research outputs published, and postdocs contribute significantly to this: <https://news.uj.ac.za/news/uj-achieves-historic-no-1-in-sas-accredited-research-outputs-2/> .

Interested candidates should please send the following documents to 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://beallist.net/standalone-journals/>) * Proof of having completed a PhD no earlier than 2019 (e.g. a scan of the PhD certificate or academic record); candidates who have not yet completed their PhD, but expect to do so soon, are encouraged to apply * A 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 May 1, and will then officially apply for this position at the departmental level (the closing date is May 15). The actual commencement of the postdoc position is flexible, but should be no later than 3 months after the outcome of the application has been announced.

Prof. Peter Teske Department of Zoology University of Johannesburg, Kingsway Campus Auckland Park 2006 South Africa Tel +27 (0)11 559 3373 <https://sites.google.com/view/petersteske/> For courier shipments: D3 LAB 339 (D LAB building on the far right (seen from D RING), two floors up, turn right through the glass door, last entrance on the left) Department of Zoology University of Johannesburg, Kingsway Campus (APK) Corner Kingsway and University Rd. Auckland Park 2092 Email: pteske101@gmail.com Tel.: 011 559 3373

Peter Teske <pteske101@gmail.com>

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Switzerland

TreeGeneEnvironmentInteractions

Switzerland.ForestTreesGeneEnvironmentInteractions

In the framework of the ERC Consolidator Grant “MyGardenOfTrees”, the Evolutionary Genetics Group offers a 2-year position starting 1 June 2024 or soon after a PostDoc position in evolutionary quantitative genetics of forest trees.

Evolutionary Genetics Group is interested in understanding the roles of demography and natural selection in shaping the life-histories and the genetic composition of forest tree populations across the landscape. The group uses field experiments, statistical models, and individual-based computer simulations to answer fundamental evolutionary questions and to aid adaptive forest management decisions.

How organisms adapt to their environments is the most fundamental question in evolutionary biology and is of utmost importance given current climate change threats. Identifying key traits involved in adaptations and understanding how they interact with each other, and with the environment, is a particularly urgent task for foundation and resource-production species, such as forest trees. Existing experiments, so-called provenance trials, assessing the local suitability of tree species and provenances lack scalability and predictability across the species range, and especially at the species range margins. MyGardenOfTrees proposes a novel participatory science approach. In 2023, an unprecedented “distributed” provenance trial was launched across Europe, where over 300 of voluntary foresters established a small common garden trial (a micro-garden) and evaluate the regeneration and early growth capacity of two forest tree species complexes (*Abies* spp and *Fagus* spp). Observations obtained from these trials will be combined with whole genome sequencing data from the seed source mother trees, and using tools borrowed from plant breeding, used to develop a prediction tool for foresters to help them build forests better adapted to climate change. See more information about the participatory aspects of the project at www.mygardenoftrees.eu This postdoc position will focus on addressing the role of gene-environment interactions in seedling performance using a combination of trait data, genomics, and environmental data. Three trait datasets will be available for analysis: one readily available from the pilot trials,

another also available from climate chamber trials, and lastly from the main trials, data from the first growing season by the end of 2023. Genomics data will be available for *Fagus* by March 2024 and for *Abies* by the end of 2024. Bioinformatics analysis will be performed in collaboration with two PhD students and with the Genetic Diversity Centre (GDC) of the ETH Zurich. The ultimate goal of the project is to estimate the reaction norms (phenotypic expression) of different populations and lineages across a large range of environments and incorporate this information into a genomic prediction model. The position involves only data analysis and statistical modeling. Some wet lab work is possible, depending on the candidate’s interests.

The ideal candidate holds a PhD degree in quantitative genetics/genomics, plant evolutionary biology, and/or forestry. Solid background (or strong motivation to develop skills) in plant/animal breeding methods (mixed-effects models), bioinformatics, and seedling development/physiology are necessary, as well as fluency in R/Python. Knowledge of ASReml-R is a plus. Experience in working with forest trees is not essential but is an advantage. We are looking for an enthusiastic and creative thinker who can make the most of this non-conventional and unprecedented trait and genomic data in hand. Capacity to produce scientific publications in top ranking journals is expected. The position will be based at WSL in Birmensdorf, close to Zurich, at the footsteps of the Swiss Alps. Zurich is home to a vibrant scientific community with its numerous universities (UZH, ETH) and research institutes (WSL, Eawag, Empa) and is famous for a high quality of living.

Applications, including a motivation letter, a summary of past relevant accomplishments, a CV, and the names and contact details of two referees should be uploaded here: <https://apply.refine.ch/273855/-1612/pub/4/index.html> Applications via email will not be considered. Dr Katalin Csilléry (project PI, katalin.csillery@wsl.ch, Tel. +41 44 739 23 43) will be happy to answer any questions or offer further information.

Katalin Csilléry, Group Leader, Evolutionary Genetics Group, Biodiversity and Conservation Biology Unit

Swiss Federal Research Institute WSL, Zürcherstrasse 111, 8903 Birmensdorf, Switzerland Office: Bi MG E floor, Tel: +41 44 739 2343, Email: katalin.csillery@wsl.ch

Web: evolgenetgroup and MyGardenOfTrees

Katalin Csilléry <kati.csillery@gmail.com>

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TrentU CaribouConservationGenomics

Post-Doctoral Fellows (PDFs)

The EcoGenomics (www.ecogenomicscanada.ca) research group under Principal Investigators Dr. Paul Wilson (Trent University) and Dr. Micheline Manseau (Environment & Climate Change Canada) is recruiting multiple PDFs in support of a nation-wide genomics research and monitoring project on caribou. The partners supporting this position include Canadian Wildlife Service (CWS); the Ontario Ministry of Environment, Conservation & Parks (MECP); Ontario Ministry of Natural Resources & Forestry (OMNRF), and other provincial and territorial jurisdictions; Indigenous organizations; industry; and funding agencies such as Genome Canada and NSERC.

The PDF positions will be based out of Peterborough, Ontario at Trent University or Ottawa, Ontario at the National Wildlife Research Centre (Science and Technology, ECCC).

Different areas of research for PDF recruitment include:

1. Wildlife conservation, population modelling for individuals with advanced experience in spatial/network analysis, population modelling, or deep learning. These methods will be used to model animal density using fecal DNA-based capture-recapture data along with a range of environmental variables. The research will contribute to 1) our understanding of the environment and its change on caribou population density and 2) the development of best practices for efficient sampling related to factors such as stratification and sample size needed for monitoring caribou density and various genetic indicators.
2. Conservation genomics for use in establishing metrics for large- scale and long-term Genomic Monitoring of caribou through the implementation of sequencing technologies, e.g. high/low coverage genomes, amplicon sequencing and the development of analytical pipelines supporting genomic indicator metrics. Strong genetic, genomic and bioinformatic skills are required. Areas of research focus will include indicators of diversity (e.g.

inbreeding, genomic erosion and load) and genetic connectivity.

3. Laboratory-based molecular genomics to implement protocols including processing high- and low-coverage genomes; characterizing a range of informative markers (e.g. SNPs, CNVs, Microhaplotypes); ageing from non-invasive sources; improving DNA extraction protocols through automated processing; protocol development on multiple platforms, e.g. Illumina and Oxford Nanopore MinIon; integration of workflows with an established database and automated scoring platform.

Education & Experience: The PDF positions requires a minimum of a PhD with work experience being considered an asset. Salary: \$55,000 - \$70,000 per year depending on qualifications. Positions to start as soon as possible.

To apply send a cover letter and CV to Dr. Paul Wilson (pawilson@trentu.ca) or Dr. Micheline Manseau (micheline.manseau@ec.gc.ca) by May 17th, 2024. Please note your full name and the job title in the subject line of your email (i.e. First and Last Name ??? Job Title).

Bridget Redquest <bridgetredquest@trentu.ca>

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UBologna MarineMetagenomics DeadlineApr30

Dear all, We would like to ask you to share among your students and colleagues the opportunity of the research fellowship position (up to two years) at CENTRO INTERDIPARTIMENTALE DI RICERCA INDUSTRIALE Fonti Rinnovabili, Ambiente, Mare ed Energia -FRAME, University of Bologna, UOS Ravenna.

The application is open (https://bandi.unibo.it/ricerca/assegni-ricerca?id_bando=67663) on “Innovative taxonomy and metagenomics approaches for the characterization of biodiversity in marine environments in Emilia Romagna” in the framework of the Emilia Romagna Region funded project StreamER -Sensori, Tecnologie Robotiche e mEtagenomica per l’ispezione di Ambienti Marini in Emilia Romagna.

The selection is open to candidates in possession of the following qualification: Master Degree or equivalent title in BIOLOGY; SCIENCE AND TECHNOLOGY FOR THE ENVIRONMENT AND TERRITORY;

NATURAL SCIENCES with appropriate scientific and professional curriculum.

The candidate should have proven experience in: - sampling in marine and/or coastal environments to study communities. - integrated taxonomy approaches of marine organisms; - molecular methods for the study of marine biodiversity (DNA extraction, amplification, Sanger sequencing and NGS) - statistical analysis of ecological data (multivariate) and molecular data (analysis bioinformatics) - writing scientific papers.

Applications can be submitted online by accessing the website: <https://concorsi.unibo.it>., after completing the registration process, following the web procedure instructions.

The last day available to submit the application is Tuesday, April 30, 2024 at 23:59

Brief project description Assessing the health of underwater habitats and the integrity of maritime infrastructures (i.e. ports, gas and oil pipelines, regasifiers and offshore platforms) is fundamental to determining the effects of climate change and human activities on natural resources and the security of energy supplies and transport of goods and people. The scenario is, however, complicated by the difficulties in using measurement instruments even continuously in a marine environment. Advances in sensor technologies have spurred the development of environmentally friendly inspection methods with the potential to complement or replace conventional and more invasive detection approaches. Sonar scanning or image collection provide information of great value for monitoring not only infrastructure but also for the study of biodiversity, offering not only presence/absence data, but also relative abundance. However, there are limitations in taxonomic resolution at the species level, due to sometimes insufficient image quality. Advances in robotic technologies offer the opportunity to reduce the use of underwater diving for prospecting and to deliver the most advanced sensory tools where necessary. The StreamER project will be based on a drone, Blucy, characterized by a modular and reconfigurable architecture in its hardware and software. This vehicle will act as a testing platform for new and advanced sensors such as flow cytometers and samplers for metagenomic analysis, will be able to coordinate simpler units and finally will be equipped with a new architecture for real-time processing of the collected data. The project represents a contribution in the Blue Growth field because it directly addresses the need to develop innovative technologies to monitor and sustainably manage marine ecosystems. The Blucy drone developed in StreamER could represent, as a whole or through its subsystems, the progenitor of a series of innovative solutions for the monitoring

and detection of marine biodiversity with the aim of improving the coexistence of human activities with the environment marine/aquatic in open environments (e.g. offshore platforms, underwater infrastructures) or confined environments (ports, basins, water systems, water and mariculture). This will result in better knowledge of the effects of human activities and climate change on aquatic ecosystems. At the same time, this will contribute to better management of resources, promoting the sustainable development of the blue economy and the achievement of the sustainable development goals of the United Nations 2030 Agenda.

For more information please contact us: alessia.cariani@unibo.it; federica.costantini@unibo.it; massimo.ponti@unibo.it

Hoping to reach your interest, we thank you for your kind attention

Alessia Federica and Massimo Alessia Cariani Laboratory of Genetics & Genomics of Marine Resources and Environment (GenoDREAM) Dept. Biological, Geological & Environmental Sciences (BiGeA) Alma Mater Studiorum - Università di Bologna Via Sant'Alberto 163, 48123 Ravenna, Italy Ph. +39 0544937321 - Mobile +39 320 6951145 - Fax +39 0512086327 skype contact: [alessiacariani](https://www.skype.com/contact)



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UCalifornia Berkeley PlantEcologicalGenomics

The Plant & Microbial Biology Department at the University of California, Berkeley seeks applications for a Postdoctoral Scholar in the Blackman Lab, in the area of plant ecological genomics, at 100% time, with an anticipated start in summer or fall 2024.

Applying tools from evolutionary genomics, molecular genetics, and field ecology in sunflowers and monkeyflowers, our research addresses the following questions: How do plants cope with daily and seasonal environmental fluctuations? How and why do these responses evolve along environmental gradients? How are multi-trait adaptations assembled over evolutionary time?

The Position: The postdoc will contribute to current NSF-funded work in the lab that seeks to understand the diversity of mechanisms by which natural populations of monkeyflowers have adapted to historic and contemporary drought stress using a combination of population genomics, transcriptomics, resurrection experiments, and genome editing. The aims of the position will be tailored to the expertise of the successful applicant and complement the Blackman Lab's broad interests in the genetic basis of adaptation and domestication, the ecology and evolution of plant development, and mechanisms of organism-environment interaction.

Responsibilities: The postdoc will work closely with the PI, collaborators, and lab personnel to design and lead research in the lab and field on the genetics and ecology of natural variation in drought resistance strategies in the common monkeyflower, *Mimulus guttatus*. The position also involves preparing grant proposals and manuscripts, data management and dissemination, organization and content development for workshops with land managers, and mentoring graduate and undergraduate students. The ideal candidate will demonstrate the ability to integrate across biological disciplines, identify and troubleshoot promising new methodologies independently, and use the appointment to develop and pursue novel, exciting questions.

Basic Qualifications (By application date): PhD (or equivalent international degree) or enrolled in a PhD (or equivalent international degree) program.

Additional Qualifications (By start date): PhD (or equivalent international degree) required by the appointment start date. No more than 2 years of post-degree research experience by start date.

Preferred qualifications -Demonstrated expertise in evolutionary and ecological genomics. -Expertise in analysis of genomic or transcriptomic datasets. -Programming for bioinformatics, biostatistics, image analysis, machine learning. -Plant physiological ecology, GWAS, genome editing, or gene expression studies. -Excellent writing and communication skills.

Appointment: The initial appointment will be at 100% time for two years with the possibility of extension based on satisfactory performance and availability of funding.

Salary and Benefits: Salary will be commensurate with qualifications and experience and based on UC Berkeley Postdoctoral salary scale. Generous benefits are included <https://vspa.berkeley.edu/postdocs> Job Location: Berkeley, CA

To Apply: Visit: <https://aprecruit.berkeley.edu/-JPF04404> Specific questions regarding the recruitment can be directed to bblackman@berkeley.edu

UC Berkeley is committed to diversity, equity, inclusion, and belonging. The excellence of the institution requires an environment in which the diverse community of faculty, students, and staff are welcome and included. Successful candidates will demonstrate knowledge and skill related to ensuring equity and inclusion in the activities of their academic position (e.g., teaching, research, and service, as applicable).

The University of California, Berkeley is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age, or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: <http://policy.ucop.edu/doc/4000376/-NondiscrimAffirmAct> In searches when letters of reference are required all letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided via a third party (i.e., dossier service or career center), to the UC Berkeley statement of confidentiality < <http://apo.berkeley.edu/-ucb-confidentiality-policy> > prior to submitting their letter.

As a University employee, you will be required to comply with all applicable University policies and/or collective bargaining agreements,

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UCaliforniaDavis MosquitoEvol

Postdoctoral Research Fellow Position Mosquito Ecology
University of California, Davis

The Vector Genetics Laboratory (VGL) at the University of California, Davis is seeking applications for a post-doctoral research scholar position in the area of MOSQUITO ECOLOGY. The VGL is dedicated to research and training in the areas of population & molecular genetics, genomics and bioinformatics of insect vectors of human and animal disease. The VGL research agenda is aimed at expanding knowledge that may be applied to improving control of disease vectors

and at the same time addresses problems of interest in the field of evolutionary genetics. The VGL has links to multiple Graduate Groups and Centers on the UC Davis campus, including the Center for Population Biology, Department of Evolution and Ecology and the One Health Institute. Find out more about the VGL at: <https://vectorgeneticslab.ucdavis.edu/> Background: The VGL is a member of the University of California Malaria Initiative (UCMI) which is a collaborative group comprised of members from four UC campuses (UC Berkeley, UC Davis, UC Irvine, and UC San Diego) plus Johns Hopkins University. UCMI researchers have proposed and developed a cost-effective, sustainable, and environmentally responsible strategy for the eradication of human malaria from Africa. This strategy is based on genetically modifying populations of the mosquito that transmits malaria by introducing two genes that encode products that destroy the malaria parasite as it develops in the mosquito vector. These anti-parasite genes are coupled with a Cas9-based gene drive which facilitates their introduction and spread through natural populations. The objective is elimination of malaria transmission by elimination of the parasite within the mosquito but not the mosquito itself. Details about UCMI may be found on our website, <https://stopmalaria.org/> The VGL's role in UCMI is to conduct field trials of the modified mosquitoes. The island nation of São Tomé and Príncipe (STP) was ultimately identified as an ideal field site. These two oceanic islands are located in the Gulf of Guinea, roughly 300 kilometers off the coast of west Africa. The VGL project has a team of mosquito biologists and state-of-the-art laboratory and insectary facilities on-site in STP where field and laboratory research has been ongoing since 2019. In addition, we have a very large local team of community and stakeholder engagement workers.

Project Description: The Mosquito Ecology post-doc will be part of a project that is focused on the ecology and genetics of populations of the primary malaria vector, *Anopheles coluzzii* and species with which this mosquito interacts on São Tomé and Príncipe islands. The goal of the ecology project is to assess the impact of introducing genetically engineered *An. coluzzii* both on natural populations of this species as well as potential impacts on non-target species with which *An. coluzzii* may interact. The Mosquito Ecologist will interact with our mathematical modeling and population genomics groups, and it is hoped that these interactions will synergize the individual work of each group.

Job Description: We are seeking a person with a strong background in quantitative ecology, an interest in island ecology and experience in conducting field work. The Mosquito Ecologist will be responsible for providing lead-

ership in the conduct of all field work. He/she should be capable of dealing with the logistical challenges often faced while conducting field work in the tropics and be capable of managing field collection teams. The effort at each field site will include intensive collection of adult and larval *An. coluzzii*, sampling and identification of non-target macro- and microorganisms sharing the aquatic environment with *An. coluzzii*, identifying collection sites and scheduling field collection work. On return to the lab at Davis the mosquito ecologist will be responsible for DNA extraction and utilization of established molecular methods to: (i) identify *Plasmodium* infected individuals, (ii) identify insecticide resistance genotypes, and (iii) identify blood meal sources. We have developed multiplex molecular assays for this work.

The Mosquito Ecologist will be working as part of an interdisciplinary team that includes expertise in population genetics, molecular genetics, genomics, bioinformatics, mathematical modeling and the acquisition and analysis of remotely sensed data. The team is located across the University of California system including UC Irvine, UC Berkeley, UC San Diego and of course UC Davis. The person filling this position will be based at the Vector Genetics Laboratory at UC Davis. The candidate should be available to spend periods of up to 3 months at a time in the field.

Candidate qualifications include the following: (i) quantitative methods

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UCalifornia LosAngeles PopulationGeneticsMicrobiome

Postdoc: UCLA.PopulationGenetics/Microbiome

A postdoctoral research position is available in the lab of Dr. Nandita Garud in the Department of Ecology and Evolutionary Biology at the University of California, Los Angeles. We are broadly interested in understanding the evolutionary dynamics of natural populations. A considerable focus is on microbiomes, however, we also work with other systems, including *Drosophila* and ancient human DNA. The lab develops statistical and

computational methods to gain insight into evolutionary processes from population genomic data.

The successful candidate will have substantial input in the specific nature of their research project. However, the project should broadly fit within the lab's goals of learning about evolution in natural populations. Applicants with an interest in machine learning are also encouraged to apply.

Additional information can be found at: <http://garud.eeb.ucla.edu> The Ecology and Evolutionary Biology department at UCLA offers a cutting-edge research environment with many opportunities for collaboration. The lab will have affiliations with the Microbiome Center at UCLA and the Institute for Quantitative and Computational Biology at UCLA.

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

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

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

- A letter describing your background and motivations pursuing a postdoc in the Garud Lab
- CV that includes a brief 1-2 sentence description of your contribution to past research projects.
- Contact information for two referees who can provide references upon request
- A description of your programming background.
- A description of your evolutionary coursework
- brief descriptions (e.g. 2 sentences each) of possible project ideas you would be interested in pursuing.

Nandita Garud <nandita.garud@gmail.com>

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UChile Evolutionary Genetics

Call for Postdoc in Evolutionary Genetics Research Ring in Insect Pests and Climate Change (PIC2) Anillo ATE230025

PIC2 aims to investigate the genetic, phenotypic, and ecological bases that explain the redistribution and adaptations in response to temperature and management practices in insect pests relevant to food security and public health. PIC2 is interested in the adaptation of insect pests such as the spotted wing fly (*Drosophila suzukii*), the grain aphid (*Sitobion avenae*), the domestic kissing bug (*Traitoma infestans*), and the horn fly (*Haematobia irritans*). The PIC2 team is made up by Luis Castañeda and Carezza Botto (Universidad de Chile), Christian Figueroa and Eduardo Fuentes (Universidad de Talca), Hugo Benítez and Margarita Correa (Universidad Católica del Maule), and Paula Irlés (Universidad de O'Higgins).

We are looking for a postdoc to investigate how changes at the genomic and microbiota composition facilitate the adaptation of pest insects to the application of insecticides in a context of climate change.

Candidates for the position must:

- Be Chilean or foreigner with permanent or temporary residence in Chile and domiciled in the country from the moment the contract begins.
- Possess a doctorate degree in areas related to Genetics, Ecology and/or Evolution, with particular emphasis on the study of insects or similar animal models. The selected person must have a doctorate degree at the time of hiring.
- Demonstrate proficiency in the English language (written, reading and oral).
- Demonstrate autonomy, organization, leadership, and responsibility.
- Demonstrate experience in writing scientific articles independently (for example, having articles as first and/or corresponding author).
- Have a solid background in evolutionary biology and/or population genetics.
- Demonstrate experience in bioinformatics analysis in any of the following topics: genome-wide association analysis (GWAS) using SNPs, metabarcoding and genotype-environment association studies.

The application deadline is 6 May 2024 and the selected person is expected to begin the postdoc in July or August, although this date is negotiable.

Please send CV, letter of intent, doctoral certificate, and name and contact information of two references to Luis

Castañeda (luis.castaneda@uchile.cl).

The contest rules (in Spanish) can be reviewed at <https://cutt.ly/qw728b7v> For more information about the position and requirements please contact Dr. Luis Castañeda (luis.castaneda@uchile.cl) Faculty of Medicine University of Chile

Luis E. Castañeda, PhD. Programa de Genética Humana -Instituto de Ciencias Biomédicas Facultad de Medicina - Universidad de Chile

Research Ring in Pest Insects and Climate Change (PICÁ²)

Teléfono: +56 2 297 89630 GoogleScholarSociedad Chilena de EvoluciónDrosEU

“Luis E. Castañeda” <luis.castaneda@uchile.cl>

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UC London GeneticsEvolutionEcol

The Research Department of Genetics, Evolution and Environment, (GEE) at University College London (UCL) is organised into six Centres, with cross-cutting research interests, and close links with other organisations, including the Francis Crick Institute, the Natural History Museum, and The Zoological Society of London. The department has a long and rich history across many biological topics, a summary of which can be found here.

GEE is grouped into six centres that are especially interested in the following research areas:

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

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

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

evolution.

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

About the role

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

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

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

The deadline for this round is 29 April 2024.

Applications need to be submitted via this link <https://www.ucl.ac.uk/work-at-ucl/search-ucl-jobs/-details?nPostingId'12&nPostingTargetId!267&id=-Q1KFK026203F3VBQBLO8M8M07&LG=-UK&languageSelect=UK&mask=ext> *Important* Salary is provided by the external award that is secured in future applications to the relevant fellowship schemes. UCL will not provide salary whilst the supported fellows apply for the fellowship schemes.

About you

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

If selected as a suitable candidate following pre-assessment, you will be invited to deliver a research

talk to present your recent work and fellowship plans. This is planned to occur in early June 2024. You will get the chance to meet our staff and students and view our facilities. In addition, you will get the opportunity to meet current GEE fellows, including those who have progressed to permanent positions within the department, and learn about the supportive and stimulating environment we offer. Where a visit is not possible, the discussion will be conducted online. Following a positive outcome of the visit, we will identify a sponsor(s) to support your fellowship application.

Eligibility:

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

To apply, please ensure to attach the following:

- Your CV - A brief (2 page maximum) document outlining your research proposal that will form your first fellowship application.
- A list of fellowship schemes you are planning to apply for

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UCologne PlantComputationalBiology

Postdoc:

Computational Biology - Developing a multi-scale modelling framework to study the adaptive potential of the ecological performance in *A. thaliana*

The project “Adaptive potential of the ecological performance in *Arabidopsis thaliana* investigated by multi-scale modeling ” will be conducted in association with the CRC 341: Plant ecological genetics (<https://trr341.uni-koeln.de/>).

The project aims to increase our understanding of *Arabidopsis thaliana*'s/ adaptive potential in ecological performance through in silico analyses using a multi-scale life cycle model. You will quantify the effect of selected traits and genes on plant adaptation to resource availability such as light and nitrogen and predict and

analyze life history strategies, growth strategies, and fitness levels in various environments under current and future conditions. This shall provide a mechanistic understanding of ecological relationships by providing a framework for disentangling complex interactions.

The University of Cologne one of the largest and oldest universities in Europe and one of the most important employers in our region. Our broad range of subjects, the dynamic development of our main research areas and our central location in Cologne make us attractive for students and researchers from around the world. We offer a wide range of career opportunities in science, technology, and administration. The “Metabolic Reconstruction and Flux Modeling” group at the Institute for Plant Sciences and the Cluster of Excellence on Plant Sciences (CEPLAS) uses computational tools to study plant metabolic networks and their interactions and works closely with experimental labs.

YOUR TASKS - You will be responsible for developing a multi-scale modelling framework to study the adaptive potential of the ecological performance in *A. thaliana*. - You will communicate closely with colleagues and collaboration partners. - You will present your results at conferences and in scientific articles. - You will be engaged in writing independent research proposals. - You will be involved in the supervision training and teaching of students.

YOUR PROFILE - PhD in Physics, Mathematics, Computational Biology or a related discipline - experience in modelling metabolic networks or other physiological and physical processes - excellent programming skills - knowledge in plant physiology - high degree of self-initiative and individual responsibility - excellent oral and written communication skills in English

WE OFFER - participation in a stimulating, dynamic, international, enthusiastic and collegial team - a diverse working environment with equal - opportunities - support in balancing work and family life - extensive advanced training opportunities - occupational health management offers - flexible working time models - opportunity to work remotely

The University of Cologne is committed to equal opportunities and diversity. Women are especially encouraged to apply and will be considered preferentially in accordance with the Equal Opportunities Act of North Rhine-Westphalia (Landesgleichstellungsgesetz LGG NRW). We also expressly welcome applications from people with disabilities / special needs or of equal status. The position is available immediately on a full-time basis (39,83 hours per week). The contract is to be filled for a fixed term until 31.12.2025 with option to extend. If the applicant meets the relevant wage require-

ments and personal qualifications, the salary is based on remuneration group 13 TV-L of the pay scale for the German public sector. Please apply online with proof of the required qualifications without a photo under: <https://jobportal.uni-koeln.de>. The reference number is Wiss2402-25.

The application deadline is 02.05.2024.

For further inquiries, please contact Professor Dr Nadine Töpfer (ntoepfer@uni-koeln.de). Postdoctoral Researcher - Computational Biology (f/m/x) Faculty of Mathematics and Natural Sciences Institute for Plant Sciences/CEPLAS

Nadine Töpfer <ntoepfer@uni-koeln.de>

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ULaRochelle ComparativeOncology

*POSTDOCTORAL POSITION IN COMPARATIVE ONCOLOGY: *

EVOLUTION OF CANCER RESISTANCE AND SOMATIC MUTATION RATE IN MAMMALS

The research teams led by Mathieu Giraudeau (LIENSs, University of La Rochelle, France) working on the evolution of cancer resistance in wild organisms and by Alex Cagan (University of Cambridge, UK) working on the accumulation of somatic mutations are recruiting a new postdoctoral researcher. The position is fully funded for 2 years by a Chaire d'Excellence Nouvelle Aquitaine to Mathieu Giraudeau. The postdoc hired will spend time in France and the UK (the time spent at each university can be discussed). We are looking for candidates with a background in evolutionary biology who could ideally start between September and December 2024, though this is open to discussion.

Project information

The etiology of cancer in humans and laboratory model organisms (e.g. rats) has received ample attention, but many aspects of cancer remain poorly understood or seriously understudied. For instance, it is now widely recognized that cancer not only affects humans but also occurs in nearly every vertebrate species of the animal kingdom, from rodents to whales, in various stages from precancerous lesions to final stages, called metastatic cancers. However, despite increasing interest, our knowledge of cancer in wildlife is extremely lim-

ited, even regarding its prevalence in major vertebrate clades, its causes, consequences, life history, genetic or physiological

predictors or how environmental change contributes to emerging cancer cases. Accurate estimates on cancer in wildlife promise extremely valuable information on oncogenic processes, as the limited research conducted on non-standard model organisms already provided tremendous insights into the natural mechanisms of cancer resistance. For example, very low cancer rates are ensured by duplications of the TP53 tumour suppressor gene in elephants, overproduction of high molecular mass hyaluronan in the naked mole rats⁹, interferon-mediated concerted cell death in the blind mole rat and reduced growth hormone insulin-like growth factor-1 signaling and microRNA changes in bats. Despite its value, robust cancer prevalence data on animals was surprisingly limited until the publication of our recent paper with information for nearly 200 species of captive mammals (<https://www.nature.com/articles/s41586-021-04224-5>). Our study demonstrates the universality and high frequency of oncogenic phenomena in mammals and reveals substantial differences in cancer mortality across major mammalian orders, strongly suggesting that some species are more resistant to cancer than others. Our results also highlight that cancer mortality risk is largely independent of both body mass and adult life expectancy across mammalian species. This might appear surprising since larger bodied and long-lived animals have larger cell numbers and undergo more cell divisions during their lifetime, resulting in an increased probability of accumulating somatic mutations, potentially leading to cancer. Our study thus suggests that natural

selection on large size or extended longevity might have been associated with the evolution of more efficient anticancer defences. The most likely mechanism being a slower rate of mutational accumulation in large, long-lived taxa.

All organisms accumulate mutations in the cells in their DNA as they age. While most of these mutations are thought to have no impact on organismal function, mutations in certain genomic regions can transform healthy cells into cancer cells. It has only recently become possible to directly study this transformation from healthy cells into malignant ones through advances in the accuracy of genome sequencing technologies. This work is revealing how different cell types accumulate mutations at different rates (<https://www.nature.com/articles/s41586-021-03822-7>) and how cells carrying cancer causing mutations can spread to colonize apparently healthy tissues as we age (<https://pubmed.ncbi.nlm.nih.gov/30337457/>). While we are learning much about how

these processes operate in humans we know virtually nothing about other species. We recently found that somatic mutation rates vary greatly across mammalian species (<https://www.nature.com/articles/s41586-022-04618-z>), which may partially explain differences in cancer risk that have been observed between species (<https://www.nature.com/articles/s41586-021-04224-5>). While this work has advanced our understanding of how mutation rates vary across species it was limited to one cell type in 16 mammalian species. A more

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UMinnesota Duluth EvolutionPlantApomixis

POSTDOC: UMinnesota.Duluth.EvolutionPlantApomixis*

The Grusz Lab at the University of Minnesota Duluth, on the shores of Lake Superior, welcomes applications for a postdoctoral researcher to join a collaborative systematic study focused on examining whether abiotic environment shapes repeated origins of obligate apomixis in plants.

JOB DESCRIPTION:

The Department of Biology at the University of Minnesota Duluth (UMN-D) has an opening for a postdoctoral research associate. This is a P&A position, job code 9546. This is a full-time, 12-month position with an anticipated funding period of one year, supported through the National Science Foundation (NSF-DEB 2232106). The selected applicant would be an employee of UMD, advised by Dr. Amanda Grusz. We seek a strong candidate to collaborate on a drought-driven study focused on the evolution of reproductive mode (obligate apomixis) in plants, using ferns as a model system. The position will encompass the analysis of existing data and the generation of new information from laboratory and field studies. The goals of this research are:

- (1) to generate a robust phylogeny for the focal clade using target enrichment and phylogenomic approaches;
- (2) to assess climatic and reproductive traits across the focal clade using field observations and herbarium

voucher specimens; and

- (3) to train next-generation undergraduate and graduate student researchers in classical and cutting-edge systematic techniques.

The successful candidate will also have the opportunity to join the PI and graduate students in developing a course based undergraduate research experience focused on plant cytogenetics. An ideal candidate will have experience conducting cytogenetic surveys, fieldwork, and herbarium studies. The primary research sites for this work will be at UMN-D (Duluth, MN) and in the southwestern United States.

Major Job Duties:

Fieldwork: Collecting voucher specimens and conducting microhabitat monitoring (15%); Data collection and analyses: Herbarium surveys, molecular and phylogenomic analyses (35%); Graduate and undergraduate supervision and mentorship (25%); Writing articles for peer-reviewed scientific journals (20%); Presenting research findings at meetings/conferences (5%). The Employer retains the right to change or assign other duties to this position.

REQUIRED QUALIFICATIONS:

PhD in biology, botany, bioinformatics, or a related field from an accredited college or university at the time of hire; * Demonstrated experience using classical and cutting-edge systematic approaches (e.g., chromosome counts, flow cytometry, fuelgen microdensitometry, target enrichment, phylogenomics, bioinformatics); * Excellent communication skills and ability to work well within a collaborative team; * Evidence of leadership in teaching, research, and/or mentoring.

Preferred (not required) qualifications:

* Background mentoring undergraduate students * Skills in molecular systematics and/or pteridology * Experience conducting population genetic and/or phylogenetic comparative analyses integrating spatial, environmental, and morphological data * Proficiency in Spanish (writing, reading, and/or speaking)

For details regarding this 1-year NSF-funded postdoctoral position, or to apply, go to <https://-humanresources.umn.edu/jobs> and search for job ID 358216. Please provide a cover letter, your C.V., a brief research statement, and the names and contact information for three professional references. For more information regarding this position, please contact Dr. Amanda Grusz (algrusz@d.umn.edu).

Review of completed applications will start April 26, 2024, and continue until the position is filled. The anticipated start date for this appointment is July 1, 2024

(some flexibility is possible).

HOW TO APPLY:

Applications must be submitted online. To apply, go to <https://humanresources.umn.edu/jobs> and search for job ID 358216. First, submit the application with a cover letter and CV/resume in pdf format. Then, return to the “My Job Applications” page to attach any additional documents, also in pdf format. Complete applications include the online application, cover letter, and resume/CV. Even if you provide this information within the application, you must also attach the requested additional document(s). Please do not miss this important step in the application process. Applications missing any of these documents may not be reviewed.

ABOUT U OF M:

University of Minnesota, Duluth (UMD)

Overlooking Lake Superior, UMD is a regional comprehensive land- and sea-grant state university, one of five coordinate campuses within the State of Minnesota system and with a total enrollment of approximately 9,000 students. There are significant opportunities for fostering existing and creating new ties with local, regional, and national industry

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UMontpellier GeneFlowConservationQuantitativeGenetics

Postdoctoral position at ISEM Montpellier France

Can assisted gene flow rescue an endangered plant from extinction in a changing climate?

*Starting date: *September 2024-(no later than December 2024)

*Duration:*24 months

*Location: *Institut des Sciences de l'Evolution, Montpellier, France

*Net income—:*from 2300 to 3300 euros per month depending on experience. Benefits include pension and health insurance

*Overview:*The postdoctoral researcher will analyze several data sets on phenotypic and genomic variation in the endemic endangered plant *Centaurea corymbosa*/, with the general aim of assessing if assisted gene flow has the potential to halt the decline of the species. Estimates from the statistical analysis will be used to parametrize models of evolutionary rescue for that species. This post-doctoral project of 24 months is part of the project FloRes - Gene Flow to the Rescue: Assessing the need, effectiveness, risks and ethical implications of manipulating gene flow to improve adaptation to climate change for long-lived plants (ANR 2022-2026). The selected candidate will be based at the Institut des Sciences de l'Evolution (ISEM), Montpellier, France. They will be supervised by Ophélie Ronce, Eric Imbert, François Rousset and Agnès Mignot with interactions with other collaborators from the FloRes project.

Keywords: quantitative genetics, conservation genomics, evolutionary rescue, statistical analysis, adaptive potential, heterosis, outbreeding depression, gene flow, life history traits, population dynamics, fitness, structured populations, population reinforcements, translocations.

*Context:*Climate change may become a major driver of species extinction in the near future. Recurrent episodes of drought and high temperatures in particular accelerate the decline of the highly endemic plant *Centaurea corymbosa*/, an endangered perennial plant whose entire fragmented range is limited to 3km² on a small massif near Narbonne. The population dynamics of the species has been surveyed by our team for more than 30 years, which allows parametrizing demographic models that predict a high probability of extinction for most of the 6 extant populations in the next two decades. Demographic and genetic surveys have shown that gene flow is very rare between these 6 populations. Given the critical situation of the species, managers have undertaken a reinforcement of all 6 extant populations in 2018, 2019 and 2021, planting about 40 000 seeds, obtained from free crosses between all populations in a common garden. /Our aim is to test whether such admixture between multiple genetic sources could improve the populations survival and capacity to adapt to climate change/.

To answer this question, we have: (i) developed and parameterized eco-evolutionary models for the species predicting how much genetic variation for critical adaptive traits must be increased within each population for adaptive evolution to rescue the populations from rapid extinction, (ii) set up a quantitative genetic experiment with seeds from the same progenies as used for the reinforcements to estimate the amount of genetic variation for life history and functional traits in the reinforcements in a common garden, (iii) performed

controlled crosses between the different populations and measured the fitness of F1 and F2 progeny in controlled conditions, (iv) measured the complete life history in the field of individuals that have been introduced in the natural populations. Genotyping, using NGS, of leaf samples from individuals in the common garden and in the wild is under way.

***Objectives:** We expect data sets, including genotyping, to be nearly completed at the beginning of the contract and the contribution of the postdoctoral researcher to data acquisition to be marginal, their contribution being focused on data analysis (including bioinformatics analyses) and statistical modelling and inferences. The postdoctoral researcher will use the genotyping and phenotypic data sets to 1) estimate genetic relatedness between individuals and identify the population of origin of each parental line in the reinforcements, 2) test if offspring from crosses between different populations have a higher fitness under stressful conditions, 3) test if mixing sources in the reinforcement increases heritable variation for adaptive traits. These estimates of hybrid vigor and genetic variation for different life history traits will be used to predict the demographic consequences of assisted gene flow with the eco-evolutionary models developed by other collaborators in the project. To put these results in context, genomic data could also be used to infer the recent demographic history of the 6 extant populations of *C. corymbosa*.

***Working environment*:** The postdoctoral research will join the Evolution&Demography team at ISEM, led by Ophélie Ronce



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UOttawa PDF PhD NetworkResilienceDiversity

Postdoctoral and PhD opportunities - Resilience and diversity of complex biological networks - University of Ottawa, Ottawa, Canada

Application Deadline: May 1st 2024

The Lefebvre < <https://www.uottawa.ca/faculty-science/professors/jeremie-lefebvre> > and Kharouba <

<https://kharoubalab.weebly.com> > labs are seeking candidates to fill ONE Postdoctoral and ONE PhD (Biology) fully funded positions to explore how resilience and heterogeneity influences the dynamics of complex biological networks. These interdisciplinary projects will combine computational (e.g., data analysis, modelling, data-informed simulations) and potential field experiment approaches used in ecology and other fields to study how diversity contributes to the stability and resilience of biological function(s). The overall objective of the projects is to better understand the role played by diversity in the genesis of critical events (e.g., ecological collapse) and identify potential intervention strategies.

The successful candidate will join the Lefebvre and Kharouba labs in the Departments of Biology and Physics at the University of Ottawa, as well as an extensive network of existing experimental and clinical collaborations with both internal and external groups. The research will be conducted in the uOttawa Bioscience Complex, a teaching and research hub hosting dozens of state-of-the-art experimental and computational interdisciplinary research facilities in downtown Ottawa, Canada. Successful candidates will be immersed in a highly interdisciplinary environment, with access to many additional training and networking activities, and be associated with Centre for Neural Dynamics, the Ottawa-Carleton Institute of Biology, the uOttawa Brain and Mind Institute as well as the Krembil Brain Institute.

Details

Postdoctoral position: as early as July 1st 2024

PhD position: September 1st 2024.

Position Description:

Trainees will be expected to work in-person for most of the position. Trainees will be expected to participate in the lab's scholarly activities (i.e., workshops, meetings), and to support other lab member's work whenever applicable. We expect applicants to demonstrate the ability to work respectfully with others in teams to carry out project goals and contribute to an inclusive lab environment. Additional details of the projects will be provided during the interview process. Please don't hesitate to reach out at [Jeremie.Lefebvre \[at\] uottawa.ca](mailto:Jeremie.Lefebvre[at]uottawa.ca) for any questions.

Requirements

The ideal candidates are expected to possess strong mathematical OR computing, writing and presentation skills, and express a vivid interest in eco-evo modelling, applied mathematics, and/or computational biology.

Applicants must meet the required qualifications for

admission to graduate/postgraduate studies at the University of Ottawa, and comply with international regulations regarding traveling, studying and working in Canada whenever applicable. Successful candidates must be eligible to work in Ontario as of July 1st 2024 (or at a mutually agreed date).

Funding

Postdoctoral position: This position is fully funded for 2 years (July. 2024 - June. 2026, or mutually agreed date) with a stipend of \$48,000 CAD per year plus benefits.

PhD position: This position is fully funded for 4 years (Sept. 2024 - Aug. 2028) with a stipend of \$30,000 CAD per year, including teaching assistantship duties. The successful candidate will be eligible to apply for Teaching Assistant (TA) positions and/or other scholarships, such as entrance scholarships.

Accommodations and Accessibility

Should you require a copy of this posting in an alternate format, please contact us as soon as possible and we would be happy to get one to you in a timely manner. We believe in the importance of supporting on-the-job success for the incumbent and are pleased to discuss and/or provide specific tools, resources, or other requirements for day-to-day work requirements, as needed.

How to Apply

Interested candidates are invited to submit their application by May 1st 2024 to [Jeremie.Lefebvre\[at\]uottawa.ca](mailto:Jeremie.Lefebvre@uottawa.ca), using the subject "Resilience position".

In your dossier, please include:

1. A cover letter stating your interest and explaining why you are a good candidate for this position, and specify clearly which position (Postdoc, PhD) you are applying for
2. Up to date CV including a list of publication, if applicable
3. Contact information for 2 references

Applications will be reviewed until the position is filled. Only candidates selected for an interview will be contacted.

Heather Kharouba <kharouba@gmail.com>

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UppsalaU PolyploidGenomics

Postdoctoral position in polyploid genomics

A 2-year position as a postdoctoral fellow in polyploid genomics, financed by a grant from the Swedish Research Council, is available at the Department of Ecology and Genetics, Plant Ecology and Evolution, Uppsala University, Uppsala, Sweden.

The Department of Ecology and Genetics is an international environment with staff and students from all over the world. Our research spans from evolutionary ecology and genetics to studies of ecosystems. For more information, at www.ieg.uu.se . Project description

Polyploidization, the increase in genome size caused by the inheritance of an additional set (or sets) of chromosomes is a major force in evolution. Allopolyploidy corresponds to two processes altering fundamentally the hereditary material: whole genome duplication (WGD) and hybridization. Transition to allopolyploidy is also often accompanied by a mating system shift, from outcrossing to selfing. Three major transitions at once seem a tall order. Yet, our recent genomic studies in natural shepherd's purse (*Capsella bursa-pastoris*) as well as with resynthesized allopolyploids, together with studies in other allopolyploid species, have demonstrated the absence of genomic shocks. Instead, there is a strong parental legacy and a gradual evolution of both allopolyploidy and the selfing syndrome. Hence, understanding the evolution of these two transitions implies understanding more subtle processes, in particular, how the genetic architecture of quantitative traits is altered by the joint effect of WGD, hybridization and mating system shift. We propose here (i) to leverage recent progress in the analysis of the architecture of complex traits and carry out genomewide association studies (GWAS) in *C. bursa-pastoris* and its parental diploid species (ii) to take advantage of our series of resynthesized *Capsella* polyploids to cross these resynthesized polyploids with established *C. bursa-pastoris* to identify genes associated with the progressive evolution of the selfing syndrome.

Duties

Fieldwork, lab work (plant growing and measurements), bioinformatics, population and quantitative genetics analyses. The applicant will be responsible for fieldwork, lab work, generating new genomic data, and for their bioinformatics and population genetics analysis,

and for writing and publishing articles.

Requirements

PhD degree or a foreign degree equivalent to a PhD degree in population genomics or evolutionary biology. The degree needs to be obtained by the time of the decision of employment. Those who have obtained a PhD degree three years prior to the application deadline are primarily considered for the employment. The starting point of the three-year frame period is the application deadline. Due to special circumstances, the degree may have been obtained earlier. The three-year period can be extended due to circumstances such as sick leave, parental leave, duties in labour unions, etc. Candidates must be able to express themselves fluently in spoken as well as written English. We attach great importance to personal qualities such as ability to work in a group.

Additional qualifications

Good fieldwork and lab skills as well as proficiency in programming (bash, Python, R) and/or statistical and modelling skills will be highly valued.

About the employment

The employment is a temporary position for 24 months, with a possibility to an extension up to a maximum of 36 months, if funds are available, according to central collective agreement. Scope of employment 100%. Starting date 2024-07-01, or as agreed. Location: Uppsala

For further information about the position, please contact: Professor Martin Lascoux, martin.lascoux@ebc.uu.se.

Please submit your application by 15 May 2024, UFV-PA 2024/1151.

Submit your application through Uppsala University's recruitment system:

<https://uu.varbi.com/en/what:job/jobID:716603/> Last application date 2024-05-15

Martin Lascoux Department of Ecology and Genetics EBC, Uppsala University Norbyvägen 18D 75236 Uppsala Sweden Tel +46 (0) 18 471 64 16 Fax +46 (0) 18 471 64 57 <https://lascouxlab.wordpress.com> När du har kontakt med oss på Uppsala universitet med e-post innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: <http://www.uu.se/om-uu/-dataskydd-personuppgifter/> E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: <http://www.uu.se/en/about-uu/data-protection-policy> Martin Lascoux <martin.lascoux@ebc.uu.se>

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URennes CNRS France SVdiversityGenomics

Dear Colleagues, We are opening a post-doctoral position for 2 years within an ERC-funded project investigating the role of structural variants in evolution.

We are looking for a candidate with a strong interest in evolutionary biology and genomics, with skills in bioinformatics. There is flexibility in the starting date and the specific focus of the post-doc project. Please feel free to contact me for more information at claire.merot@univ-rennes.fr.

The full offer is posted on the CNRS portal <https://emploi.cnrs.fr/Offres/CDD/UMR6553-BERDIC-014/-Default.aspx?lang=EN> (where applications are received until April 23rd).

The position will be based at the University of Rennes (France) within the institute Ecobio (<https://ecobio.univ-rennes.fr/en>). More information about the whole project and environment can be found on my website https://www.normalesup.org/~cmerot/-recherche_en.html Best regards, Claire M₂rot

Claire M₂rot <claire.merot@gmail.com>

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UStAndrews ComputationalModelling

Dear All,

We have a research opportunity open at the University of St Andrews' Centre for Biological Diversity Biodiversity (CBD), School of Biology working in the research team of Carolin Kosiol.

Applications are sought for a committed Post-doctoral Research Fellow conducting research for a BBSRC International Partnership on AI funded project entitled “Deep learning: Linkage effects and balancing selection”.

Our research team focuses on the development of computational methods to investigate adaptations occurring at both inter- and intraspecies timescales, in particular we have developed an approach called Polymorphism-aware phylogenetic models (PoMos). Presently, we incorporate Deep Learning (DL) methodologies to examine the phenomenon of balancing selection across diverse species.

The detection of balancing selection is an exciting problem challenging evolutionary geneticists for decades. It is often intertwined with linkage disequilibrium (LD), which connects genetic sites. This project focuses on using Ancestral Recombination Graphs (ARGs) to generate testing and training data for DL with balancing selection while accounting for LD. We will develop a DL method, which draws upon Voznica et al. (2022) and will be trained on the data generated, to detect balancing selection in the populations of great apes and fruit flies.

This post will suit a candidate who can think flexibly and implement new software. Ideally, the candidate should have solid grasp of programming languages (eg. C, C++, Java, Python, R), but a desire to extend their capabilities into new areas and methods is highly desirable and there will be many opportunities to develop specific skills. An interest in phylogenetics and population genomics is a plus.

You will have the opportunity to publish first author papers, contribute as a co-author, and present your work at international meetings. In particular, visits to the collaboration partners Olivier Gascuel (Paris Artificial Intelligence Research Institute, France) and Adam Siepel (Cold Spring Harbor Laboratories, US) are planned. You must be able to independently manage your work, meet deadlines, and prepare internal reports and draft publications. You will have good communication skills. This is an outstanding opportunity to develop your research skills, ask exciting scientific questions and drive forward novel research at the cutting edge.

Applications should include:

- (i) A cover letter expressing your interest in the position
- (ii) a current CV
- (iii) the names and contact details of two referees.

See

<https://www.vacancies.st-andrews.ac.uk/-Vacancies/W/6599/0/425572/889/research-fellow->

[in-bioinformatics-ar2977nb](#) Deadline 26th April 2024. The position is available for 15 months but might be extended.

Informal enquiries can be directed to Dr Carolin Kosiol, ck202@st-andrews.ac.uk

Dr Carolin Kosiol Reader in Bioinformatics Centre for Biological Diversity School of Biology University of St Andrews St Andrews, Fife KY16 9TF, Scotland/UK Email: ck202@st-andrews.ac.uk Web: <https://biology.st-andrews.ac.uk/kosiol-lab/> Carolin Kosiol <ck202@st-andrews.ac.uk>

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UToronto Scarborough FishGenomics

Postdoctoral Position

Genomics of Fishes and Fisheries in the Great Lakes Basin

Department of Biological Sciences, University of Toronto Scarborough

The Lovejoy and Mandrak labs (mandraklab.ca) seek a postdoctoral scholar to lead genomic studies on fishes and fisheries of Lake Huron, Ontario. The main project will use DNA metabarcoding to investigate the diets of Whitefish and Lake Trout, addressing fisheries and conservation questions. The project offers outstanding partnership opportunities with Indigenous, provincial, industrial, and federal collaborators and is funded by GEN-FISH (gen-fish.ca). The scholar will join a dynamic, collegial research environment with strong mentorship training possibilities. The position is for one year and available immediately, and has the potential to be extended

Candidates are expected to have demonstrated bioinformatics expertise, project organization skills, and some genetic laboratory experience, excellent written and oral communication skills, quantitative skills, and other relevant skills.

The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ2S+ persons, and others who may contribute to the further diversification

of ideas.

The University strives to be an equitable and inclusive community, and proactively seeks to increase diversity among its community members. Our values regarding equity and diversity are linked with our unwavering commitment to excellence in the pursuit of our academic mission.

Interested candidates should send a letter of intent and cv to Nathan Lovejoy (nathan.lovejoy@utoronto.ca).

Nathan Lovejoy <nathan.lovejoy@utoronto.ca>

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UYork UK Plant Genomics Introgression

Adaptive introgression in the Anthropocene

We are looking for a 3 year postdoctoral research associate (PDRA) to work on a NERC-funded project “Adaptive introgression in the Anthropocene” led by Kanchon Dasmahapatra at the University of York. The main aim of the project is to understand the prevalence and impact of gene flow between native and non-native flowering plant species in the British Isles making use of newly generated genome assemblies and large whole genome resequence datasets.

Human translocation of species and anthropogenic climate change are resulting in some of the fastest rates of species distribution changes ever seen, causing many native and non-native species to be brought together. While the ecological consequences are often well-documented, the evolutionary impacts of hybridization and gene flow between native and non-native species are usually less visible. In this ambitious project we will leverage reference genomes produced by the Darwin Tree of Life project and combine high-throughput sequencing with the latest bioinformatic methods to address a major question of growing importance: What is the extent of gene flow between native and non-native flowering plant species, and is this gene flow of adaptive value to native or non-native species? These data will be used to parameterise models predicting the rate of gene flow between native and non-native species, and test model estimates of cryptic gene flow among species pairs that have not been observed to hybridize. The British flora is intensively studied, and its well charac-

terised distributions, hybrids and ecology make it an ideal model system to build predictive models exploring ecological and genetics factors affecting the rates and effects of gene flow between native and non-native species.

The PDRA will be based in York at the Leverhulme Centre for Anthropocene Biodiversity (<https://www.york.ac.uk/anthropocene-biodiversity/>), and be supervised by Kanchon Dasmahapatra (<http://www.york.ac.uk/res/dasmahapatra/>).

Project co-investigators and partners: Alex Twyford and Simon Martin (University of Edinburgh), Pete Hollingsworth and Markus Ruhsam (Royal Botanic Garden, Edinburgh), Chris Thomas (University of York), Mark Blaxter (Wellcome Sanger Institute), Kevin Walker (Botanical Society of Britain and Ireland).

Closing date: 15th May 2024. Start Date: 1st August 2024 (negotiable).

For informal enquiries email kanchon.dasmahapatra@york.ac.uk.

To apply click the “Apply now” button at the bottom of the University of York job advertisement: <https://jobs.york.ac.uk/vacancy/research-associate-in-evolutionary-biology-556527.html> Prof Kanchon Dasmahapatra (kanchon.dasmahapatra@york.ac.uk) Professor of Evolutionary Biology Director of Postgraduate Research (Biology) Department of Biology University of York York YO10 5DD Tel: +44 (0)1904 328635

New publications : Rosser N, Seixas F, Queste LM, Cama B Dasmahapatra KK (2024) Hybrid speciation driven by multilocus introgression of ecological traits. *Nature *<https://doi.org/10.1038/s41586-024-07263-w> Page E, Queste LM, Rosser N, Salazar PA, Nadeau NJ, Mallet J, Srygley R, McMillan WO Dasmahapatra KK (2024) Pervasive mimicry in flight behavior among aposematic butterflies. *PNAS *121 (11) e2300886121 <https://doi.org/10.1073/pnas.2300886121> I choose to work flexibly and send emails outside normal office hours, but I do not expect you to respond outside your working hours. Prof Kanchon Dasmahapatra Professor of Evolutionary Biology Director of Postgraduate Research (Biology) Department of Biology University of York York YO10 5DD Tel: +44 (0)1904 328635 <http://www.york.ac.uk/res/dasmahapatra/> Kanchon Dasmahapatra <kanchon.dasmahapatra@york.ac.uk>

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UZurich EvolutionaryGenomics

Graduate position: 2 year postdoctoral researcher (0.8 FTE) in Evolutionary Genomics

University of Zurich, Department of Evolutionary Anthropology - Evolutionary Genetics Group

The Evolutionary Genetics Group (www.michaelkruetzenlab.org) at the Department of Evolutionary Anthropology (www.iea.uzh.ch) at the University of Zurich, is seeking a highly motivated Postdoctoral Researcher to join our dynamic and collaborative group consisting of postdocs, PhD and MSc students. Our group focuses on advancing our understanding of evolutionary processes through genomic analyses, with a particular emphasis on the genetic diversity and adaptation of dolphins and orangutans. Position Overview: The successful candidate will play a key role in conducting evolutionary genomic analyses, utilizing existing genomic data from orangutans and dolphins (www.sharkbaydolphins.org). The position requires expertise in handling and analyzing large scale genomic data and proficiency in coding languages (Python, Bash, R). The researcher will actively contribute to ongoing projects, collaborate with team members, and to some extent also will be able to independently pursue research in the field of evolutionary genetics using existing dolphin and orang-utan data. Qualifications:

* PhD in Evolutionary Genomics or a related field. * Expertise in handling and analyzing large scale genomic data. * Proficiency in coding languages: Python, Bash, and R. * Strong analytical and problem-solving skills. * Excellent written and verbal communication skills. * Ability to work independently and collaboratively. Remuneration: The remuneration for this position is in accordance with the University of Zurich's salary scales (18/03, 0.8 FTE, CHF 80'192 pa). Starting date of the position is 1 August 2024. The position is initially for two years but could potentially be extended depending on the acquisition of additional funding.

About the Evolutionary Genetics Group: Our group combines important questions in classical behavioural ecology (cooperation, culture, drivers of social structure) with genomic approaches (eDNA, aDNA, full genome sequencing), dedicated to unraveling the genetic mechanisms driving adaptation and diversity in non-human populations. We combine long-term fieldwork data with

computational approaches to address fundamental questions in evolutionary biology.

About the University of Zurich: The University of Zurich is one of Switzerland's leading research universities. Renowned for its academic excellence and commitment to innovation, the university provides a vibrant, diverse, and inclusive academic environment. The Department of Evolutionary Anthropology fosters interdisciplinary research and collaboration, offering state-of-the-art facilities and a supportive community for scientific exploration.

Living in Switzerland: Switzerland is known of its beautiful landscapes, high quality of life, and multicultural atmosphere. Zurich, the largest city in Switzerland, offers a unique blend of urban sophistication and natural beauty. With excellent public transportation, cultural attractions, and a reputation for safety, Zurich provides an ideal setting for both professional and personal growth.

Application Deadline: Applications should be submitted by 30 May 2023. To apply, please send a motivation letter, CV, a copy of the PhD certificate and contact information for at least two references to michael.kruetzen@uzh.ch in one single document.

The University of Zurich is an equal opportunity employer and welcomes applications from candidates of all backgrounds. We encourage diversity and inclusion in our workplace.

Michael Krützen <michael.kruetzen@aim.uzh.ch>

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

UZurich PopulationGenomics HumansAndPlants

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

Please apply from this link, which has more information and web links <https://jobs.uzh.ch/-offene-stellen/postdoc-in-population-genomics-and->

[bioinformatics-on-language-evolution/08d2f305-50fc-4bf0-8c4f-a93840c64feb](https://doi.org/10.1093/molbev/msad001) The NCCR is a Swiss National Center of Competence in Research with the goal of creating a new discipline, Evolutionary Language Science, that targets the past and future of language. The center consists of leading scientists from traditionally separated academic domains, which allows us to harvest the diverse expertise from the humanities, social sciences, computational sciences, natural sciences and medicine towards a broadscale interdisciplinary collaboration. Your responsibilities

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

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

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

What we offer The University of Zurich offers a highly international, mostly English speaking and an inter-

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

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

Place of Work Pending budgetary approval, the positions are primarily located at the Department of Evolutionary Biology and Environmental Studies at the University of Zurich (UZH) but the NCCR supports exchange with other departments in its network.

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

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

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

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

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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>

Workshops Courses

Berlin FlowerMorphologySystematics Jun3-14	86	Online IntroAncientMetagenomics Aug5-9	92
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Berlin FlowerMorphologySystematics Jun3-14

Dear colleagues,

There are still a few places available on this workshop.

Please distribute widely.

Best wishes,

Louis Ronse De Craene and Julien Bachelier

Berlin Summer Course in Flower Morphology and Systematics 3-14 June 2024

This is the second version of a highly successful two-week workshop held in 2023. The course is based at the Biological Institute of the Freie Universität Berlin and the Berlin Botanical Garden, which offer extensive facilities, including functional microscopy laboratories and a huge plant collection of more than 20,000 species. The course is set up as lecture-based, laboratory taught, and interactive visits of the living collections.

FORMAT: 2-week workshop, lectures and hands-on practical sessions.

INTENDED AUDIENCE: Final year undergraduate students, PhD students, post-doctoral and advanced researchers, professionals (but no formal restriction). A basic knowledge of botany is preferred but not essential.

The course will run with a minimum of 8 and a maximum of 20 participants.

REGISTRATION FEE: euro 800 (euro 600 for Undergraduate and Master students)

(Registration includes coffee breaks, daily lunches with snacks, and visits, but does not include travel and accommodation).

HOW TO APPLY AND SECURE A PLACE: Please contact Dr. Louis Ronse De Craene (l.ronsedecraene@gmail.com) to request an application form.

Payment to be made by May 1st 2024.

COURSE INSTRUCTORS AND CONTACT:

Dr. Louis Ronse De Craene, Research Associate Royal Botanic Garden Edinburgh (l.ronsedecraene@gmail.com)

Prof. Julien Bachelier, Freie Universität Berlin (julien.bachelier@fu-berlin.de)

PROGRAMME:

Course Description and outline:

This short course will introduce students to the structure and development of flowers, with a focus on floral diversity and evolution and the significance of flowers for systematics. Major plant families will be identified within the framework of the main lineages of seed plants to understand their evolution and diversification. Additionally, students will learn to analyse, describe, and study the structure of inflorescences, flowers, and fruits, and based on their observations, to identify the main

evolutionary patterns underlying their tremendous morphological diversity, as well as their potential pollination and dispersal mechanisms.

Course objectives and learning outcomes:

Through this course students will acquire the following skills:

- a guide to identifying plants using morphological characters in the context of the molecular classification system.
- a better understanding of the origin and evolution of floral structures, including their importance for classification, and of the main developmental patterns and evolutionary trends which underlie the tremendous diversity of reproductive structures.
- an ability to observe and recognise key characters through the study of live floral material and the building up of floral diagrams.

Course outline:

Daily activities will be in the following format:

9-12 Lecture, seminar and discussion of paper.

12-13 Lunch break

13-18 Plant collecting and observation.

Monday 3 June: Student presentations - introduction to morphology of vegetative structures and flowers, inflorescence and flower structure (floral diagrams and formulas).

Tuesday 4 June: Overview of major groups of flowering plants; major characteristics of Flowers and special attributes (phyllotaxis, aestivation, merism, symmetry, floral tubes and hypanthia).

Wednesday 5 June: Floral evolution from the ANITA grade to Mesangiosperms I

Thursday 6 June: Floral evolution from the ANITA grade to Mesangiosperms II

Friday 7 June: Monocot evolution: variations on a theme

Saturday 8 June: Basal eudicots and rise of the core eudicots

Sunday 9 June: Visit of the paleontological collections of the Museum of Natural Sciences

Monday 10 June: Rosid diversification I

Tuesday 11 June: Rosid diversification II

Wednesday 12 June Rosid-Asterid transition

Thursday 13 June: Asterid diversification I

Friday 14 June: Asterid diversification II - Conclusions

and wrap-up

Recommended Textbooks and Reading:

Please note that this list is not exhaustive, and that these books will be available in class:

Endress, P.K. 1996. Diversity and evolutionary biology of tropical flowers. Cambridge University Press, Cambridge.

Leins, P. & Erbar, C. 2010. Flower and fruit: morphology, ontogeny, phylogeny, function and ecology. Schweizerbart Science Publishers, Stuttgart.

Ronse DeCraene LP. 2022. Floral Diagrams: An Aid to Understanding Flower Morphology and Evolution. 2nd Edition. Cambridge University Press.

Simpson MG. 2019. Plant systematics. 3th Edition. Elsevier.

Soltis DE, PS Soltis, PK Endress, MW Chase, S Manchester, W Judd, L Majure, E Mavrodiev. 2018. Phylogeny and evolution of angiosperms. Revised and updated edition. Chicago: The University of Chicago Press.

Disability Accommodation and dietary restrictions:

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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>

Lausanne LandscapeGenomics Jun17-21

Dear all,

Our Landscape Genomics course is scheduled to take place in the beautiful Lausanne (Switzerland), at the EPL, from June 17th to 21st!

Course website: (<https://www.physalia-courses.org/-courses-workshops/course17/>)

During this course, participants will delve into various aspects of landscape genomics analysis. Initially, you'll learn to acquire environmental data from public databases and process it using Geographic Information Systems (GIS). Subsequently, you'll explore different methodologies for obtaining genetic data and discover how to analyze genetic variation and population structure using R. Additionally, you'll receive training in

two statistical approaches for studying local adaptation: Sambada and LFMM. The course will also address the crucial task of interpreting and validating results, along with essential considerations and best practices for planning a landscape genomics experiment, such as sampling design.

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/-course17/>)

If you have any questions, please feel free to reach out to us.

Best regards, Carlo

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MNHN Paris BigDataIntegrativeTaxonomy Jun10-14

The course “Integrative taxonomy in the ”big data“ era” will be from the 10th to the 14th of June, 2024, at the MNHN of Paris, France.

The course is in English. To register, please fill the form on the website of the course <https://sites.google.com/-site/coursbarcode/home>

If you have any question, please contact: Nicolas Puillandre (puillandre@mnhn.fr) Sarah Samadi (sarah@mnhn.fr)

Nicolas PULLANDRE <nicolas.puillandre@mnhn.fr>

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Online BiodiversityWithR Sep5-11

Dear all,

registrations are now open for the Physalia course “Analysing Biodiversity Through Time and Space using R”: (<https://www.physalia-courses.org/courses-workshops/biogeography-in-r/>)

This online course (Sept 5-6, 9-10-11) equips researchers and enthusiasts with the skills to analyze biodiversity patterns across time and space using R.

In this course, you will learn how to: Build automated workflows for data acquisition, cleaning & analysis (R) Interrogate data for errors & sampling biases Estimate diversity & diversification rates Visualize data for clear communication Understand processes shaping biodiversity (past & present) For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/biogeography-in-r/>)

Best regards, Carlo

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Online ConservationGenomics Jul22-25

Dear all,

We are excited to announce our upcoming online course on Conservation Genomics, scheduled for July 22nd-25th, 2024.

Course website: (<https://www.physalia-courses.org/courses-workshops/course62/>)

This course will provide a comprehensive introduction to utilizing population genomics tools in conservation efforts. Our instructors will cover study design, genomic data collection, SNP filtering, and various analyses including population structure, local adaptation, effective

population size, inbreeding, and relatedness. Through hands-on exercises, participants will gain essential bioinformatics skills and learn to interpret genomic data in a conservation context.

The course is tailored for graduate students and researchers interested in applying genomic tools to conservation biology. Previous experience in UNIX-based command line and R is required. Hands-on exercises will be run in a Linux environment on remote servers and data analysis and visualization will be run in R using RStudio.

Learning Outcomes: 1. Study design and genomic data collection methods 2. Handling raw genomic data to produce SNP datasets 3. Assessing population structure and adaptation signals 4. Estimating effective population size, inbreeding, and relatedness

For the full list of our courses and workshops, please visit: <https://www.physalia-courses.org/courses-workshops/course62/> Best regards, Carlo

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Online Eukaryotic Metabarcoding Jul1-5

Dear all,

We are excited to announce our upcoming online workshop on Eukaryotic Metabarcoding, scheduled for July 1-5, 2024.

Course website: (<https://www.physalia-courses.org/courses-workshops/course4/>)

This workshop provides a comprehensive overview of metabarcoding procedures, focusing on practical problem-solving and hands-on analysis using real datasets. By the end of the workshop, participants will gain the skills to understand the potential of metabarcoding, run complete analyses, and design their own projects.

Participants should have some experience with Unix commands and basic knowledge of R (preferably RStudio) for plotting and statistical procedures.

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/course4/>)

Best regards, Carlo

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Online Food Traceability Using Genomics Jul2-5

Dear all,

We are thrilled to announce our upcoming online course on “Food Traceability Using Genomic Tools”, scheduled from 2nd to 5th July 2024.

Course website: (<https://www.physalia-courses.org/courses-workshops/food-traceability/>)

The global seafood and wildlife trade, valued at over US\$676.20 billion annually, faces challenges in regulation and sustainability. Our course offers an overview of the seafood industry’s evolution and introduces genomic tools for traceability. From Sanger sequencing to advanced Illumina and Nanopore technologies, participants will gain practical skills to ensure food integrity and safety.

Designed for researchers, food safety officers, quality control technicians, and supply chain managers, this course requires basic molecular biology understanding. While familiarity with genomics and data analysis is beneficial, it’s not mandatory.

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

Best regards, Carlo

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Online GeneralizedLinearModelsInR May6-10

Dear all,

It is still possible to join us for our online course on Generalized Linear Models in R in May (6-10).

Course website: (<https://www.physalia-courses.org/-courses-workshops/glm-in-r-1>)

The course is aimed at graduate students and researchers with basic statistical knowledge that want to learn how to analyze experimental and observation data with generalized linear regression models in R. Basic knowledge means that we assume knowledge about foundational statistical concepts (e.g. standard error, p-value, hypothesis testing) that are usually covered in a first introductory statistics class. Participants should also be familiar with Rstudio and have some experience in programming R code, including being able to import, manipulate (e.g. modify variables) and visualize data.

At the end of this course, attendees will be able to:

1. Specify and fit generalized linear regression models in R, choosing the appropriate distribution and link function according for your data.
2. Interpret the parameter estimates of the fitted models, including the correct interpretation of categorical predictors (e.g. contrasts, ANOVA, post-hoc testing), and calculate predictions from your model.
3. Understand the principles of model selection to choose the correct model / regression formula for your question.
4. Visualize the fitted models to check assumptions, communicate results, and increase understanding.
5. Acquire the foundations and some first ideas to move on to more complex regression models (e.g. Generalized Linear Mixed Models, Generalized Additive Models, Bayesian modeling) in the future.

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/-glm-in-r-1>)

Best regards, Carlo

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Online GenomeAnnotation May13-16

Dear all,

There are still 4 seats available for the onlinec course on Genome Annotation, which will run from the 13th to the 16th of May.

Course website: (<https://www.physalia-courses.org/-courses-workshops/genome-annotation/>)

Recent technological advancements in long-read DNA sequencing, coupled with a significant reduction in costs, have rendered the generation of genome assemblies financially viable and computationally feasible. As a result, genome assembly no longer poses the primary obstacle to evolutionary analysis for many non-model organisms. The greater challenge lies in accurately annotating a draft genome assembly after its construction.

In this course, we will delve into the essential processes and strategies required to start the annotation of your target genome addressing challenges posed by genome characteristics and specificities.

By the end of this course, attendees will :

- 1) have the basic knowledge and practical skills necessary to start the annotation process of your genome of interest;
- 2) be able to tackle genome specific challenges;
- 3) understand the vital role that high-quality genome annotations play in advancing our understanding of biological processes, paving the way for groundbreaking discoveries and research.

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

Best regards, Carlo

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Online Geometric Morphometrics In R May 2-10

Dear colleagues,

There are 3 slots available for Transmitting Science's online course "Geometric Morphometrics in R". This course can be of interest to any evolutionary biologist interested in quantifying/comparing shapes across populations, species, etc.

Dates and schedule: Online live sessions 2nd, 3rd, 6th, 7th, 8th, 9th, and 10th of May from 12:00 to 17:00 (Madrid time zone).

Instructor: Dr. Julien Claude, author of the book "Morphometrics with R [1]" (Institut des Sciences de l'Évolution de Montpellier, France).

Course Overview

Concepts in geometric morphometrics will be taught using a series of original data sets and working in R for solving a series of tasks. The course will start with an introduction to R and rapidly go into shape analysis with measurements, landmark data, and outlines. The participants are welcome to bring their own data and problems so that we may find R solutions.

Full program here: <https://www.transmittingscience.com/courses/geometric-morphometrics/geometric-morphometrics-r/#toggle-id-1> More information and registration: <https://www.transmittingscience.com/courses/geometric-morphometrics/geometric-morphometrics-r/> or writing to courses@transmittingscience.com

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Transmitting Science Full list of courses: www.transmittingscience.com/-courses 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

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Online Interactive Maps With R 17-18 June

Dear all,

Registrations are now open for the next edition of our online course on Interactive Maps with R, taking place on June 17-18, 2024.

Course website: (<https://www.physalia-courses.org/-courses-workshops/interactive-maps-with-r/>)

In this course, you'll learn how to craft dynamic and engaging interactive maps using R. Here's what you can expect:

- Understand the fundamentals of interactive maps and their applications - Hands-on experience in creating customized maps with provided and your own spatial data - Dive into practical sessions with live lectures and exercises - Ongoing support through Slack to address queries and enhance your learning experience

Basic R and spatial data knowledge are recommended, but worry not $\frac{1}{2}$ “ we'll provide fully annotated R scripts and installation guidance beforehand.

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/-interactive-maps-with-r/>)

Best regards, Carlo

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Online IntroAncientMetagenomics Aug5-9

Dear all,

The SPAAM Community in collaboration with Friedrich Schiller Universität $\frac{1}{2}$ t Jena (Germany) and Harvard University (USA) is happy to again offering a new 5 day virtual summer school course sponsored by the Werner Siemens Foundation: Introduction to Ancient Metagenomics.

DATE AND SCHEDULE Online from Monday 5th to Friday 9th of August 2024 from 09:00 to 17:00 (CEST, Leipzig time zone).

ORGANISERS Prof. Dr. Christina Warinner (Harvard University, Max Planck Institute for Evolutionary Anthropology) and Dr. James Fellows Yates (Max Planck Institute for Evolutionary Anthropology, Leibniz Institute for Natural Product Research and Infection Biology Hans Knöll $\frac{1}{2}$ ll Institute).

INSTRUCTORS Hi $\frac{1}{2}$ bner, Dr. Arthur Kocher, Dr. Betsy Nelson, Clemens Schmid, Dr. Giulia Zampirolo, Gunnar Neumann, Jasmin Frangenberg, Keri Burge, Dr. Kevin Nota, Dr. Maxime Borry, Dr. Meriam Guellil, Dr. Nikolay Oskolkov, Dr. Remi Denise, Dr. Theseas C. Lamnidis, Tessa Zeibig, and Dr. Vilma Pi $\frac{1}{2}$ rez.

OVERVIEW: Ancient metagenomics applies cutting-edge metagenomic methods to the degraded DNA content of archaeological and paleontological specimens. The rapidly growing field is currently uncovering a wealth of novel information for both human and natural history, from identifying the causes of devastating pandemics such as the Black Death, to revealing how past ecosystems changed in response to long-term climatic and anthropogenic change, to reconstructing the microbiomes of extinct human relatives. However, as the field grows, the techniques, methods, and workflows used to analyse such data are rapidly changing and improving.

In this hands-on summer school (block praktikum) we will go through the main steps of ancient metagenomic bioinformatic workflows, familiarising students with the command line, demonstrating how to process next-generation-sequencing (NGS) data, and showing how to perform de novo metagenomic assembly. Focusing on host-associated ancient metagenomics, the course consists of a combination of lectures and hands-on exercises, allowing participants to become familiar with the types of questions and data researchers work with. Round table discussions with experts at each stage of the workflow will be held to allow participants to get advice on their own projects and research.

By the end of the course, participants will have an understanding of how to effectively carry out the major bioinformatic components of an ancient metagenomic project in an open and transparent manner. Attendees will be eligible for ECTS points (awarded by the JSMC Graduate School, Friedrich-Schiller University, Germany) or a certificate of completion (Max Planck - Harvard Research Center, MHAAM).

ELIGIBILITY The course is aimed at masters students and early-stage PhD students, to a maximum of 40 participants. Course instruction will take place online. There are no fees.

APPLICATIONS Applications are now open until May 31 2024. To apply, please visit our website: <https://-spaam-community.org/wss-summer-school/> For questions or more information, contact James Fellows Yates (james_fellows_yates@eva.mpg.de) or Christina Warinner (christina_warinner@eva.mpg.de)

Kind regards

James and Christina

Dr. James A. Fellows Yates

Microbiome Sciences Group, Dept. of Archaeogenetics
Max Planck Institute for Evolutionary Anthropology

Dept. of Paleobiotechnology Leibniz Institute for Natural Product Research and Infection Biology Hans Knöll $\frac{1}{2}$ ll

Institute

James Fellows Yates <james_fellows_yates@eva.mpg.de>

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Online ManipulationOfNGSData Jun5-14

Dear colleagues,

Registration is open for the course “Manipulation of NGS Data for Genomic and Population Genetics Analyses” - 5th edition

Schedule: Online live sessions 5th, 7th, 12th, 13th, and 14th of June, 2024; 13:00 to 17:00 (Madrid time zone).

Instructors: Dr. François Sab [1]ot [1] (Institute of Research for Development, France) and Julie [2] Orjuela (Institute of Research for Development, France)

More information and registration: <https://www.transmittingscience.com/courses/genetics-and-genomics/manipulation-ngs-data-genomic-population-genetics-analyses/> Course programme:

* Introduction to NGS sequencing platforms. * Introduction to basic command lines. * Basic raw data manipulations (counting sequences, listing files). * Raw data QC & Cleaning. * Introduction to TOGGLE, a NGS pipeline framework. * Mapping: principle, tools, execution. * Mapping: cleaning, data control, realigning, duplicates marking. * SNP calling: raw calling, cleaning calling, filtering. * VCF manipulations: filtering on MAF, heterozygosity . * Impact of SNPs on genes. * Population genomics using sNMF. * Context-based analyses. * Piping large scale analyses for multiple samples using TOGGLE. * Testing new tools and different conditions to answer different biological questions. * Questions.

With best wishes

Sole

– Soledad De Esteban-Trivigno, PhD Transmitting Science www.transmittingscience.com [3]

Check all Transmitting Science’s courses here: <https://www.transmittingscience.com/courses/> 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

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Links: — [1] <https://www.transmittingscience.com/instructors/francois-sabot/> [2] <https://www.transmittingscience.com/instructors/christine-tranchant-dubreuil/> [3] <http://www.transmittingscience.com>

Online MethylationInEvolution Sep16-20

Dear all,

We are pleased to announce the upcoming online course on “DNA Methylation in Ecology and Evolution,” taking place from September 16th to 20th.

Course website: (<https://www.physalia-courses.org/courses-workshops/dnamethylation/>)

This course will delve into various methodologies for obtaining and analyzing DNA methylation data, including bisulfite sequencing using Illumina, as well as long-read technologies such as PacBio and Oxford Nanopore. From data acquisition to statistical analyses for identifying differentially methylated sites and regions, participants will gain comprehensive insights into interpreting methylation data in the context of ecology and evolution.

The course spans five days, blending theoretical lectures with practical hands-on sessions. Each day will commence with an introductory lecture followed by interactive class discussions. The practical sessions will involve both guided demonstrations by instructors and individual exercises to reinforce learning. While primarily focusing on non-model organisms with draft reference genomes, the examples and applications explored in the course will be broad-ranging and applicable across diverse contexts.

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

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>

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

Poland AgentBasedModels Jul29-Aug2

Dear all,

We're excited to announce our upcoming five-day course on Agent-Based Modelling Using NetLogo, happening from July 29th to August 2nd, 2024, at the Faculty of Biology and Environmental Protection, University of Lodz, Poland.

Course website: (<https://www.physalia-courses.org/courses-workshops/course52/>)

Agent-based modeling (ABM) is a powerful technique for unraveling the dynamics of complex systems, spanning natural and social sciences. Led by renowned experts, Professors Volker Grimm and Steve Railsback, this course will equip you with the knowledge and skills to design, implement, and evaluate ABMs tailored to your research and teaching needs.

Here's what you can expect: In-depth instruction in ABM principles and practice Hands-on tutorials and exercises using NetLogo, a leading ABM software platform Open discussions and independent project work

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

course52/)

Best regards,

Carlo

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TheNetherlands PhenotypicPlasticity Apr29-May3

Are you also fascinated by phenotypic plasticity?

PE&RC is organizing a course “The ecology and evolution of phenotypic plasticity” from April 29th to May 3rd in Ede, The Netherlands. The course is aimed for PhD candidates and postdocs, and there are still some spots left!

For more info see: <https://www.pe-rc.nl/Ecology-Evolution-of-Phenotypic-Plasticity> . Best regards, Judith Smit (j.a.h.smit@vu.nl)

“Smit, J.A.H. (Judith)” <j.a.h.smit@vu.nl>

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UFlorida PolarGenomics Jul22-23

NSF-sponsored Workshop: Detecting adaptive evolutionary events in genomes of polar species at the Whitney Laboratory for Marine Bioscience, St. Augustine, Florida A series of workshops were funded by the National Science Foundation through awards#1935635and#1935672. Below is the information for the upcoming 2024 workshop: A two-day workshop will be held at the Whitney Laboratory for Marine Bioscience (University of Florida) in 2024 (July 22 & 23). Participants should plan to arrive on the afternoon of July 21st and depart in the morning or afternoon on July 24th. The workshop organizers, Dr. Scott Santagata and Dr. Joseph Ryan, will lead participants

through a series of computational exercises using our SELECTINGS pipeline (<https://github.com/josephryan/-SELECTINGS>) having the following goals: (1) Construct orthologous gene assignments (OrthoFinder), prune paralogous genes (PhyloPYPruner), align orthologous gene (MAFFT), and multi-gene phylogenetic relationships (IQ-TREE); (2) Establish collaborative research groups to test for genes under positive selection from diverse organisms and habitats (e.g., polar, terrestrial, marine, tropical) using genomic and transcriptomic datasets; (3) Evaluate current analytical methods for determining positive selection (e.g., PAML, HyPHY) and their statistical significance;

Participants are encouraged to work with their own NGS-based datasets, but sample datasets will also be provided and analyzed using a bioinformatics platform. Applicants with transcriptomic datasets that span ecological boundaries (e.g. high vs. low latitudinal habitats, marine vs. freshwater habitats, deep vs. shallow water habitats, etc.) will be given priority. However, anyone who is interested in learning these techniques is encouraged to apply. Lodging will be provided at the Guy Harvey Resort in St. Augustine Beach, FL and participants will be reimbursed for lodging and travel after the workshop. We will provide transportation between the hotel and the Whitney Laboratory where the workshop will take place. Funds will also be provided to offset the costs of round trip travel based on the number of participants and demonstrated need. Workshop facilities and housing are in accordance with ADA guidelines and we will work with any participants needing accommodations. Details for reimbursable costs will be provided upon acceptance. Researchers from underrepresented groups and/or with disabilities are particularly encouraged to apply. Workshop will include a code of conduct to help ensure a safe and inclusive space. The workshop will incorporate structured participation to ensure balance in participation and encourage inclusion. It will include activities that facilitate interaction within small groups. Mentorship opportunities will be facilitated through encouraging post-workshop interaction and mentoring. To apply please visit http://ryanlab.whitney.ufl.edu/-polar_workshop/. The application (due date: May 17, 2024) requires: A) Current CV, B) 400-word description detailing your research experiences and how this workshop fits into your overall career goals, and C) Estimated funds needed for round trip travel.

Scott Santagata, Associate Professor Department of Biology Life Sciences Building, Room 261 Long Island University-Post 720 Northern Blvd. Greenvale, NY 11548-1300 Phone:516-299-3029 Website: <https://sites.google.com/site/-scottasantagata/Labpage> Researchgate: [\[www.researchgate.net/profile/Scott_Santagata\]\(http://www.researchgate.net/profile/Scott_Santagata\) Scott Santagata <Scott.Santagata@liu.edu>](https://-</p>
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UOslo GenealogiesARG Aug17-20

Hi everyone,

What We're holding a course on *Genealogies and Ancestral Recombination Graphics*

When August 17-20 this year *Fees* Totally free, thx to EBP-Nor and Norbis. We sponsor housing and food. *Deadline* for signing up May 31st *More Info* Here < <https://github.com/ebp-nor/GARG/blob/main/README.md> > *Why* Haplotypes are revolutionizing our field, as they allow to bypass the issues of focusing only on SNPs.

My very best, Josi $\frac{1}{2}$

jcerca.github.io

Google Scholar < <https://scholar.google.pt/citations?user=3DZIIvWPEAAAJ&hl=en> >

Evolutionary Biologist

University of Oslo

Out on Rxiv (Jan 2024) ::: Consistent accumulation of transposable elements in species of the Hawaiian Tetragatha spiny-leg adaptive radiation across the archipelago chronosequence < <https://www.biorxiv.org/content/10.1101/2024.01.03.574070v1> >

Recently published (Oct 2023) ::: Understanding natural selection and similarity: Convergent, parallel and repeated evolution < <https://onlinelibrary.wiley.com/doi/10.1111/mec.17132> >

jose.cerca@gmail.com

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UReading Systematics Assoc Jun19-21

Workshops for attendees at the Systematics Association Biennial. University of Reading, 19th-21st June 2024. Closing date for registration 1st May. <https://systass.org/events/biennial/> Choose one of the 3hr workshops: BayesTraits Distribution and maps in R

<https://systass.org/events/biennial/programme/> Julie Hawkins <j.a.hawkins@reading.ac.uk>

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Vairao Portugal Plant Evolutionary Genomics May13-17

Dear all

We have still some places available and have thus prolonged the application deadline for our TRAINING AND RESEARCH WORKSHOP IN “EVOLUTIONARY GENOMICS FOR PLANT MODELS AND CROPS”.

New registration deadline :Friday 19th April

May 13-17, 2024 | CIBIO-InBIO, Vairão, 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 Vairão, 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 19, 2024

All applicants will be notified about whether they are accepted until 23, 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

Best regards,

Raquel Tavares

Raquel Tavares <raquel.tavares@cibio.up.pt>

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Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral

positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly 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. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email `evolDir@evol.biology.McMaster.CA`. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most 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^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.