
E v o l D i r

June 1, 2023

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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Ingelheim Evolution Unisexual Reproduction Jul1-13

Registration and abstract submission for the Gutenberg Workshop on the Evolution of Unisexual Reproduction, July 11-13, 2023, Ingelheim is now open

REGISTER AND SUBMIT AN ABSTRACT NOW!

Registration closes May 18, 11:00pm (CEST).

Evolution of Unisexual Reproduction

While the topic of unisexual reproduction has fascinated many of us for a long time, recent advances from diverse systems make this a great time to bring a group of scientists together who have moved the field forward and will enjoy scientific exchange and discussions. In addition to an emphasis on having diverse systems represented at the workshop, we are also looking forward to the exchange between those focused on experimental and modelling approaches.

Confirmed Speakers

Tuliana Brunes, U of Texas at Arlington, USA

George Constable U of York, UK

Susanne Foitzik, JGU Mainz, GER

Matthew Hartfield, U of Edinburgh, UK

Michael Kearney, U of Melbourne, ASTL

Craig Moritz, ANU, ASTL

Manfred Schartl, U of W??rzburg, GER

Ingo Schlupp, U of Oklahoma, USA

Isabelle Sch??n, Royal Belgian Institute of Natural Sciences, BE

Tanja Schwander, Universit?? de Lausanne, CH

Sen Xu, U of Texas at Arlington, USA

Scientific Organizers

Anthony Barley, ASU, USA Peter Baumann, JGU Mainz, GER
Hanna Kokko, JGU Mainz, GER

Anthony Barley <Anthony.Barley@asu.edu>

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London Infection Circadian Rhythms Sep25-26

On 25 ??? 26 September 2023, Professor Sarah Reece, Dr Rachel Edgar and Professor Annie Curtis will lead a scientific meeting on the topic of circadian rhythms in infection and immunity.

The timing of infections can have a serious impact on the outcome for hosts, but little is known about how timing impacts host-pathogen interactions. This meeting will include presentations by leaders in the fields of circadian biology, immunology, microbiology, parasitology, virology and evolutionary ecology to explore how and why rhythms in pathogen activities and host immune responses drive disease processes.

Registration is free and this event is intended for researchers in relevant fields. Advance registration is essential. There is also a poster session which may be

of interest to early career researchers and students.

More information about the speakers, programme and how to register for this meeting can be found on the Royal Society website.

Kindly note, the Royal Society will process your data in line with our privacy policy. If you do not wish to be contacted about providing promotional support for our events, please let us know. For any queries, please contact the Scientific Programmes team by emailing scientific.meetings@royalsociety.org.

Kind regards,

Annabel

Annabel Sturgess Senior Scientific Programmes Officer

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Scientific Meetings <scientific.meetings@royalsociety.org>

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MonteVerita Switzerland EvolutionInAction Jun11-15

Dear all,

We would like to draw your attention to the INTERNATIONAL CONFERENCE 'EVOLUTION IN ACTION' taking place on Monte Verità, Switzerland, from June 11-15, 2023.

ABSTRACT SUBMISSION IS POSSIBLE UNTIL MAY 12.

The conference (<https://www.evolution.uzh.ch/en/-conference.html>) aims to bring together a diverse, international group of researchers to foster interdisciplinary discussions about aspects of evolutionary biology based on genomic and computational approaches. The program comprises oral and poster sessions on the following topics:

ADAPTATION TO CHANGING ENVIRONMENTS
EMERGING TRENDS IN EVOLUTION DOMESTI-

CATION POLYPLOIDY & EPIGENETIC EVOLUTION
PATHOGEN EVOLUTION

The conference also hosts keynote speeches on ANTHROPOLOGICAL GENETICS and EVOLUTION OF PLANT REPRODUCTIVE TRAITS as well as a workshop on machine learning in evolution.

On behalf of the Conference Committee The Coordination Office of the URPP Evolution in Action (coordination@evolution.uzh.ch)

EVOLUTION coordination
<coordination@evolution.uzh.ch>

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MountainLakeBioStation SEPEEG Sep22-24

Registration is now open for the 2023 SouthEastern Population Ecology and Evolutionary Genetics Conference (SEPEEG). SEPEEG will be from September 22-24th at Mountain Lake Biological Station (MLBS) in Pembroke, VA. Capacity is limited, so register early.

More information and registration at <https://mlbs.virginia.edu/SEPEEG-2023>. SEPEEG 2023 Organizing Committee: Helen Murphy Josh Puzey Karen Barnard-Kubow Priscilla Erickson Mandy Gibson

Karen Barnard-Kubow, PhD James Madison University
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"Barnard-Kubow, Karen Beth - barnarkb@jmu.edu"

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Portugal LittorinidEvolution Jul23-27

We are pleased to announce the 13th edition of ISOLBE, the International Symposium on Littorinid Biology and Evolution, hosted by Rui Faria at CIBIO ? Research

Centre in Biodiversity and Genetic Resources ??” InBIO Associate Laboratory, University of Porto, Portugal.

During four days of conference, we will discuss recent scientific findings of evolutionary significance within a highly polymorphic group of organisms with remarkable variation in life history traits.

The informal and inspiring scientific atmosphere of ISOLBE enables researchers and students of different disciplines but with a common interest in Littorinids to present their work in a series of talks and posters, as well as opportunities for group discussions/brainstorms on participants-selected topics of interest.

The conference will be in a hybrid format with possibility of attending both in situ or remotely. However, to fully benefit from interactions among researchers we recommend a visit to Portugal.

Future promising avenues of research using Littorinids as models to understand evolutionary process driving our understanding of biodiversity, together with state-of-the-art tools to address them will be discussed. Altogether, XIII ISOLBE will contribute to reinforce the recognition of Littorinid species as key models to understand the forces influencing evolution .

For more information visit the conference website: [<https://isolbexiii.com/>]

Important information:

Dates: 24-27 th of July 2023

Location: Vila do Conde-Porto, Portugal

Deadline for abstract submission: 14 th of May

Deadline for registration: 31 st of May

In case of doubts please e-mail us: [isolbexiii@cibio.up.pt]

On behalf of the organizing committee, Rui Faria, CIBIO/InBIO, Research Center on Biodiversity and Genetic Resources University of Porto, Portugal

ruifaria@cibio.up.pt

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TexasAMU SMBE
DeNovoGeneBirth Nov6-9

Dear all,

We are pleased to announce that registration and abstract submission for the first Society of Molecular Biology and Evolution Satellite Meeting on De Novo Gene Birth.

The meeting will be held at Texas A&M University, College Station, TX, on November 6-9, 2023.

The abstract deadline is June 30th.

For further details, including the lineup of speakers, visit: <https://agriferegister.tamu.edu/website/56645/> De novo genes represent a major source of genetic variation with a profound impact on adaptation, phenotypic variation, and evolutionary innovation.

This meeting will fulfill the need to (i) provide a synthesis of the current knowledge of de novo gene evolution and function; (ii) develop shared guidelines concerning the annotation of de novo genes, particularly those encoding small proteins; (iii) identify critical areas and compelling questions at the intersection of evolutionary biology, functional genomics and other disciplines where future interdisciplinary research efforts should concentrate; (iv) promote novel opportunities for collaborations among investigators from different fields; (v) provide recommendations for improved annotation tools to identify functional de novo genes.

This meeting is supported by the SMBE, the National Science Foundation, the Department of Ecology and Conservation Biology at Texas A&M University, the Graduate Program in Genetics and Genomics at Texas A&M University, the Texas A&M University School of Veterinary Medicine and Biomedical Sciences, and Visit College Station.

The organizing committee: Claudio Casola, Texas A&M University Li Zhao, Rockefeller University Victor Luria, Yale University Nikolaos Vakirlis, BSRC Alexander Fleming

For questions email Claudio Casola at ccasola@tamu.edu

Claudio Casola, Ph.D. (he/him/his) Associate Professor Department of Ecology and Conservation Biology Texas A&M University email: claudio.casola@agnet.tamu.edu <http://agriflife.org/casolalab/> Claudio Casola <Claudio.Casola@ag.tamu.edu>

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UAuckland FishGeneticsEpigenetics Nov20-24

Kia ora colleagues,

We would like to invite you to submit your abstracts to our special session:

“Facing environmental changes: what are the genetic and epigenetic mechanisms providing resilience in fishes?”

at the Indo Pacific Fish Conference and the Annual Conference of the Australian Society for Fish Biology, to be held 20-24 November at the University of Auckland, New Zealand (<https://www.ipfc11-asfb.ac.nz/>).

The ability to cope with environmental changes is essential for fish resilience, and one of the key mechanisms allowing fishes to face such variations is acclimation through phenotypic plasticity. Whether acute, developmental or transgenerational, plasticity is usually associated with dynamic changes in transcription regulation and/or epigenetic modifications. This session will showcase the latest findings on the genetic and epigenetic mechanisms involved in fish responses to changing environments, and highlight the links between molecular and physiological approaches. Among others, we will discuss topics such as: the role of gene expression and transcriptional regulation in environmental acclimation, the impact of the environment on the epigenome, and the potential of genetic adaptations and/or epigenetic modifications to enhance fish resilience in a changing planet.

With this session we hope to attract experts in the fields of fish biology, ecology, genetics, epigenetics and conservation. Our aim is to provide a space for scientists that work on a variety of fish species, habitats and environmental stressors, both in the wild and in controlled laboratory experiments, to present their latest findings on the genetic and epigenetic mechanisms involved in the responses to changing environments.

Abstract deadline: 11th June 2023 -> <https://www.ipfc11-asfb.ac.nz/submissions/> We look forward to see you in New Zealand!

Cheers, Special session organizers Lucrezia Bonzi, Alyssa Budd and Moisés Bernal

Lucrezia Bonzi <lucrezia.bonzi@gmail.com>

ULinz Austria MathStatBiology Aug31-Sep1

We are pleased to announce that registration and abstract submission for the Annual Workshop on Mathematical and Statistical Aspects of Molecular Biology \ddot{u} ₂ (MASAMB 2023) \ddot{u} ₂ is now open.

Please see <https://conferences.jku.at/masamb23/> for further details.

We would be happy to welcome you after a long Covid break in Linz!

Please submit your abstracts by the end of May.

On behalf of the committees

\ddot{u} ₂ Andreas Futschik

Andreas Futschik <andreas.futschik@univie.ac.at>

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UNAM Mexico PopGenetics Oct12-13

Dear fellow evolutionary biologists

We are pleased to announce the sixth edition of the Mexican Population Genetics Meeting #MexPopGen6, which will be held as a hybrid event on October 12-13 at the Center of Genomic Sciences, UNAM located in Cuernavaca, Mexico. This year, thanks to the financial support of SMBE, MexPopGen6 has funding to provide travel awards that will cover travel and lodging expenses for a set of selected participants in the early stages of their scientific career. These travel awards will be available to promote and guarantee the participation of students and researchers from other states of the Mexican Republic, as well as from Central and South America.

Participation is free of charge after successful registration. Registration will be open starting Friday, May 26th

until June 26th 2023. For more details, to submit your abstract and/or apply for travel awards, visit the MexPopGen6 website: <https://www.mexpopgen.com.mx> We look forward to meeting you all in person in Cuernavaca, Mexico, or online through our streaming platforms.

Please save the date and spread the word!

Organizing committee MexPopGen6

Idalia Rojas rojas@evolbio.mpg.de

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UOxford InvertebrateBiogeography Sep26-27

Registration and abstract submission for the Invertebrate Biogeography Conference on September 26-27, 2023 at University of Oxford, UK is now available at <https://www.eventbrite.co.uk/e/invertebrate-biogeography-conference-tickets-617008327517> 26 Sep: Talks including the keynote speakers Mark Lomolino (SUNY College of Environmental Science and Forestry) and Rosemary Gillespie (University of California, Berkeley). 27 Sep: Workshops discussing the future roles of collections (hosted by Scott Miller, Smithsonian Institution), molecular applications and invertebrate conservation.

Registration deadline: August 1

Accommodation is available at Jesus College, Oxford for a discounted price. Any questions should be directed to: Tim.Coulson@biology.ox.ac.uk, Bryony.Blades@biology.ox.ac.uk or Tabitha.Taberer@biology.ox.ac.uk.

This conference is hosted by the African Natural History Research Trust (ANHRT) and University of Oxford. ANHRT conference page weblink: <https://anhrt.org.uk/african-natural-history-research-trust-news/conference> Tabitha Taberer <tabitha.taberer@jesus.ox.ac.uk>

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UWolverhampton EuropeanCongressHerpetology Sep4-8

Dear all, We are pleased to announce that registration and abstract submissions for the 22nd European Congress of Herpetology are now open <https://www.sehcongress23.com/> VENUE: University of Wolverhampton, UK CONFERENCE DATE: 4 - 8 September 2023 ABSTRACT DEADLINE: 16 June 2023 EARLY BIRD DEADLINE: 30 June 2023 REGISTRATION CLOSE: 4 August 2023

We welcome abstracts for talks and posters from any aspect of herpetology. Additionally we have three dedicated symposia which build on the presentations from our plenary speakers (Richard Griffiths, Katharina Wolvenberg Valero, Patrick Campbell, Jeffrey Streicher): (1) Rewilding and reintroductions, (2) The role of museums in the age of extinction, (3) Adapting to a changing climate.

For regular updates please visit our website <https://www.sehcongress23.com/> or follow our Social Media accounts (Twitter https://twitter.com/SEH_2023, Facebook <https://www.facebook.com/Seh2022>).

Simon Maddock On behalf of the Local Organising Committee sehcongress23@gmail.com

“Maddock, Simon” <S.Maddock@wlv.ac.uk>

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WhistlerBC TransposableElements Sep3-7

To Evolutionary Biologists Interested in Mobile DNA:

Registration and abstract submission for the Keystone Symposia Meeting “Transposable Elements at the Crossroads of Evolution, Health and Disease”, September 3-6, 2023, Fairmont Chateau Whistler, British Columbia, Canada is now available at <https://keysym.us/KSTransposons24> Deadlines: June 1, short

talk abstract submission and scholarship application; July 6, early registration at discounted rates. Lodging for attendees is reserved until July 18.

We look forward to an exciting meeting! Please help us spread the word: #KSTransposons24

Kathy Burns, Harmit Malik, Irina Arkhipova, organizers
Irina Arkhipova <iarkhipova@mbl.edu>

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LMU Munich ShrimpEvolutionaryHistory	13	UReading PlantDiseaseEpidemiologyEvolution	24
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ArcticU Norway EcosystemGenomics

UiT the Arctic University of Norway has started a trans-disciplinary research school “Changing Arctic” in August 2022, with PhD candidates and supervisors from all seven university faculties. The research school has a focus on renewable energy, food security, health, and welfare.

‘Changing Arctic’ will collaborate with actors in the private and public sector. The research outcomes will contribute to resilience and transformation in the Arctic and will thus operationalize Sustainable Development Goals.

The training will provide PhD candidates with knowledge, professional and transferable skills, and general

competences that enables them to contribute to innovative and sustainable solutions for the Arctic. The research school will arrange courses, seminars, workshops, and excursions, and will organise secondments in private enterprises, NGOs, and public institutions. This is to ensure the relevance of project outcomes and enhance the employability of the PhD graduates.

The position is a fixed term position for a duration of four years. One year is distributed as 25 % each year and will consist of teaching (10 %) and other duties such as secondments and interactions with the industry or the public sector. The objective of the position is to complete research training to the level of a doctoral degree. Admission to the PhD programme is a prerequisite for employment, and the programme period starts on commencement of the position.

The workplace is at UiT Campus Tromsø. You must be able to start in the position within a reasonable time after receiving the offer. The Research School has its kick-off the week of 28.08 - 01.09.2023. The successful

applicant's participation is mandatory.

The position's affiliation and field of research While being a member of the research school, you will be employed at the Arctic University Museum of Norway, UiT.

You will conduct research as a part of the newly established Norwegian Centre for Arctic Ecosystem Genomics (ArcEcoGen) and will be part of the terrestrial working group.

Research at the ArcEcoGen focuses on the combined effect of humans, climate, and biota on northern ecosystem dynamics in the past, present, and future using environmental DNA (eDNA) techniques. A key goal of ArcEcoGen is to build up a diverse, rigorous, and internationally leading research group in ecosystem genomics. Norway has among the world best cover of local flora and fauna in DNA reference libraries, with near 20 000 species barcoded. In addition, the large natural history collections at The Museum will be available for creating complementary reference libraries. Our collections also include sediment samples from arctic and alpine lakes as well as important archeological finds linked to pre-historic times of Northern Norway. We also have fully equipped laboratories and infrastructure for recovery and analyses of modern, ancient, and eDNA, as well as field equipment for sediment coring. We are currently recruiting PhDs, Post Docs, and associate professors as a part of a recent Aurora Centre funding award.

The shift from hunting to the domestication of reindeer in Arctic Europe is a multifaceted human and socio-ecological story that has yet to be fully unravelled. However, there are opportunities to tackle both cultural and environmental aspects from well-preserved archaeological materials in Northern Norway using new techniques. This project will be connected to an existing PhD studying the genomic basis of eco-evolutionary responses to changing environments in arctic plant-herbivore systems but expand more into human interactions using sedaDNA and archaeological data.

It will address the relative importance of reindeer, sheep, and other domesticates (including food crops and wild plants) as well as fishing and hunting in the Arctic diets of the past in different cultural contexts.

The approach will be multi-tiered using several genomic techniques including metabarcoding, shotgun sequencing and possibly target-capture. This may be supplemented by using genome-wide SNP genotyping of suitable reindeer samples. Both the full domesticated and wild assemblages as well as reindeer provenance/lineage relate strongly to the cultural history of reindeer exploitation and lifeways. An overarching question of

great ecological and cultural importance is the representation of reindeer as a keystone species over time during which it was semi-domesticated.

Qualifications This position requires:

1. A master's degree in biological sciences or subject relevant to the research description (see specifications below)
2. Excellent English language skills (written and spoken)
3. Qualification with a master's degree is required before commencement in the position.

If you are near completion of your master's degree, you may still apply and submit a draft version of the thesis and a statement from your supervisor or institution indicating when the degree will be obtained.

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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>

GriffithU Australia FeralCatAncientDNA

We have a fully funded 3-year PhD Fellowship in ancient DNA of feral cats available at Griffith University, Brisbane, Australia.

Title: Feral cats in the Australian Anthropocene

Supervisors: A/Prof Julien Louys, Dr Mark de Bruyn, Dr Tim Maloney, Prof Nicole Boivin

We are currently looking for a PhD candidate to join our research team in the examination of feral cat distribution in Australia using ancient DNA (aDNA) techniques. The primary focus of this role is to investigate the impact of feral cats on the Australian ecosystem during the Anthropocene, the current geological age characterised by significant human impact on the planet. This project includes analysing aDNA from cat remains obtained from various archaeological and palaeontological sites across Australia to reconstruct the historical distribution and genetic diversity of feral cats.

Requirements:

The selection of applicants for the award of higher degree research scholarships at Griffith University involves consideration of your academic merit and research background. To be successful research project on aDNA and the impact of feral cats in Australia, you will be

able to demonstrate a strong foundation in genetics and molecular biology, as well as familiarity with conservation biology, archaeology/palaeontology, and wildlife management. You will have evidence of a passion for biodiversity conservation and a desire to address the negative impact of feral cats on Australian wildlife. You will ideally have experience in fieldwork, data collection, and analysis, as well as the ability to work independently and collaboratively with stakeholders from diverse backgrounds. with a strong desire to undertake research in making a positive impact on the environment.

Expressions of interest are welcome from domestic and international applicants. - Applicants must have completed, or expect to complete, a bachelors degree with honours equivalent to first class honours or a - Masters degree (AQF Level 9) incorporating a significant research component of a standard comparable to a bachelor honours degree or be regarded by Griffith University as having an equivalent level of attainment in accordance with Schedule One of the HDR - Scholarship Policy. For further information on the eligibility requirements for the program refer here.

International applicants should ensure that English Language Proficiency requirements for the program are met before formally applying. Applicants to research programs will need to show they meet:

1. A minimum overall band score of 6.5 on the IELTS (Academic) with no band score less than 6.0 OR
2. A minimum score of 575 on the paper-based TOEFL including a score of no less than 5.0 on the TWE OR
3. A score of 79 on the internet-based (iBT) TOEFL with no sub-score less than 19

The scholarship: The 2023 Griffith University Postgraduate Research Scholarship has an annual stipend of AU\$32,192 (indexed) for a period of up to three years of full-time study. Please see the GUPRS Conditions of Award for more information.

A successful International applicant will also be awarded a Griffith University International Postgraduate Research Scholarship to cover tuition fees for up to three years. Please see the GUIPRS Conditions of Award for more information.

How to apply:

All expressions of interest must be submitted to A/Prof Julien Louys and Dr Mark de Bruyn containing:

Statement addressing your suitability for the project/scholarship Research proposal Evidence that you have completed a program with the required grades as detailed in the about you section A curriculum vitae (CV) using the Griffith CV template. Names of

two referees

The closing date for expressions of interest is: 11.59pm Friday 30 June 2023.

The preferred applicant will then be invited to apply for the program and scholarship on-line

Julien Louys j.louys@griffith.edu.au

Mark de Bruyn m.debruyn@griffith.edu.au

Mark de Bruyn <m.debruyn@griffith.edu.au>

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HongKong MicrobialPopGenomics

Fully-funded PhD position at the Chinese University of Hong Kong, in collaboration with the University of Hong Kong and University of South Australia

Topic:

Developing next-generation probiotic marine bacteria for sustainable marine bivalve mollusc aquaculture under climate change

We are seeking an enthusiastic and highly motivated PhD student with interests in both the fundamental and applied aspects of marine microbiology, population biology, symbiosis, and organism responses to global change to join our group. Funding has been secured to support a PhD student for three years for candidates with a Master degree or four years for candidates with a Bachelor degree, with annual studentship of HK\$216,300 (approx. US\$27,730). The project will be jointly supervised by Haiwei Luo (haiweiluo@cuhk.edu.hk) and Laura Falkenberg (laurafalkenberg@cuhk.edu.hk) at The Chinese University of Hong Kong (CUHK), and in collaboration with Bayden Russell (brussell@hku.hk) at The University of Hong Kong (HKU). The PhD student will be primarily based at CUHK, will work at the Simon F.S. Li Marine Science Laboratory of CUHK (www.msl.sls.cuhk.edu.hk) and the Swire Institute of Marine Science of HKU (www.swims.hku.hk), and will have the opportunity to perform collaborative work at University of South Australia where a new lab will be established by Laura Falkenberg. CUHK is a long-standing English-speaking institution and ranks as one of the top Universities in Asia.

Competences: The successful candidate will have a Bachelor degree with at least one year of laboratory research

experience or a Masters degree in biological sciences. We are seeking a highly motivated candidate with background in microbiology, marine biology, and/or bioinformatics. He/she should have a good work ethic and organisational skills to transition between different work settings (laboratory, mesocosm, field, bioinformatics).

About the project:

Probiotics have been extensively used as an alternative to antibiotics in aquaculture to improve growth performance, immune response, disease resistance, and feed efficiency. However, concern exists around safety issues because commercially available probiotics for aquaculture commonly carry virulence genes that may have adverse effects on human health. Despite this concern, few efforts have been made to find alternative probiotics that are free of these risks. Moreover, the efficacy of probiotics - either traditional or emerging - may be modified in the future as a consequence of climate change.

In this project, we aim to identify next-generation probiotic marine bacteria and evaluate their effects on mussels, a representative bivalve mollusc used in aquaculture. Here, next-generation probiotics are defined as autochthonous host-associated bacteria that are increasingly dependent on, and restricted to, the hosts. Although many kinds of bacteria are found associated with mussels, bacterial associates having the hallmarks of early-stage symbiosis have only recently been recognized.

The marine bacterial genus *Ruegeria* is prevalently associated with marine invertebrate hosts. We recently discovered that some *Ruegeria* populations carry the genomic signatures of early symbiosis. During host adaptation, *Ruegeria* members use their own tools (i.e., insertion sequences) to disable and eliminate virulence genes in their genomes, thereby having the potential to become sustainable next-generation probiotics.

Key words:

mussel, *Ruegeria*, marine bacteria, population genomics, symbiosis, probiotics, seafood, aquaculture, global change

Expectation:

The PhD student will be responsible for the implementation of the practical work of the project, with support from the PIs and their lab members. Specific activities will be to: (1) strategically collect mussels from the field along Hong Kong's coastline and perhaps part of the South Australian coastline from which, (2) the PhD student will extract and build a comprehensive mussel-associated *Ruegeria* culture collection. In the next component, (3) population genomic methods will

be used to identify *Ruegeria* populations under early symbiosis with mussels. Following their identification, (4) the mesocosm systems at the Marine Science Laboratory of CUHK and the Swire Institute of Marine Science of HKU will be used to expose mussels to different conditions anticipated under global change scenarios (i.e., warming and acidification), with some of the exposed organisms inoculated with the next-generation probiotics to identify if - and how - they modify the mussel response. The PhD student will also take the lead in drafting manuscripts for publication and present the results at academic conferences.

Start date: 1st January 2024

How to apply: Please send your application to haiweiluo@cuhk.edu.hk or laurafalkenberg@cuhk.edu.hk with "Application PhD mussel-*Ruegeria*" in the

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JagiellonianU Poland InsectMicrobiome

Ph.D. Student Position: The ecological dynamics and roles of microbiota in Arctic insect communities

The Symbiosis Evolution Research Group (<https://-symbio.eko.uj.edu.pl>) at the Institute of Environmental Sciences of Jagiellonian University (www.eko.uj.edu.pl) in Kraków, Poland, led by Dr. Piotr Lukasik, is seeking a motivated Ph.D. Student in Evolutionary Biology. The Student will join the project "Micro-allies during mega-crisis? The role of the microbiome in insect community responses to climate change", funded by the Polish National Science Centre (NCN) Opus 22 project no. 2021/43/B/NZ8/03376.

We know that microorganisms can play essential roles in insect biology, affecting insects' ability to respond and adapt to various environmental challenges. However, our understanding of the microbiome diversity, distribution, transmission, and functions across wild insect communities remains limited. This project aims to describe the roles of microbial symbionts in responses of multi-species insect communities to the changing climate. It focuses on East Greenland - an area that is warming

rapidly, and where we can plausibly capture and characterize most insect species. Specifically, we ask about the microbiome composition across the taxonomic diversity of insects, the transmission of microbial strains across species, and the effects of seasonal changes, geographic variation, and environmental factors on the microbiota of selected broadly distributed insect species.

We will address these questions using large numbers of historical and newly sampled insects from several areas of Greenland, that will be characterized using innovative high-throughput sequencing-based approaches, custom bioinformatics solutions, and advanced statistical models. The Ph.D. Student will work initially on the analysis of existing, extensive marker gene amplicon datasets for diverse Greenland insects, developing and consolidating their bioinformatics skills. Later, depending on interests, they may participate in field collections, laboratory work, analysis of expanding marker gene datasets, phylogenomics and comparative genomics characterization of broadly distributed microbial clades, or the development and implementation of statistical models. The Student will be encouraged to work closely with other team members and Polish and international project collaborators, including Tomas Roslin (Swedish Agricultural University) and Brandon Cooper (University of Montana). The available samples, expertise, research funding, and collaborations offer great potential for motivated students to explore their own ideas and evolutionary questions related to insect diversity and symbiosis and acquire cutting-edge research skills.

The Student will be enrolled in the Ph.D. Program in Biology at Jagiellonian University (https://science.phd.uj.edu.pl/en_GB/recruitment/phd-biology). They will also join a dynamic, multi-lingual, collaborative research team based at one of the top research institutes in the fields of Ecology and Evolution in Central Europe, in a medieval city known as the cultural capital of Poland, with good access to outdoor recreation opportunities and well-connected to the rest of Europe. The Ph.D. Student will be supported by a four-year stipend from the Ph.D. Program, they may also receive an additional stipend from the research project. The official start date is 1st October 2023.

The successful candidate will have an M.Sc. degree in a relevant field by July 2023; a demonstrated interest in Evolution, Entomology, Microbiology, and/or Genomics; experience with or a keen interest in learning, Bioinformatics, and Computational Biology; and strong English language, communication, and organizational skills. Previous experience with insect ecology, evolution and especially symbioses, molecular biology, microbiome surveys, phylogenomics and/or comparative genomics, and statistical modeling is advantageous, as

is the willingness to travel.

The candidates are requested to send a letter explaining their experience and interest in the project, a CV, and the details of two references, to Dr. Piotr ukasik (p.lukasik@uj.edu.pl), before 12th June 2023. The applicants recommended for the Ph.D. The Program will then need to formally apply through the University system by 21st June 2023.

Make sure also to check other proposed projects within the Ph.D. Program in Biology at Jagiellonian University (https://science.phd.uj.edu.pl/en_GB/recruitment/phd-biology), and contact their PIs if interested!

dr hab. Piotr ukasik Symbiosis Evolution Research Group Institute of Environmental Sciences Jagiellonian University ul. Gronostajowa 7 30-387 Kraków Poland

Phone: +48 12 664 5195, +48 798 104 743

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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>

KU Leuven EvolutionDevelopmentalPlasticity

Molecular mechanisms and evolution of developmental plasticity <https://www.kuleuven.be/personeel/jobsite-jobs/60216055> PhD position

Project We are pleased to announce the availability of a PhD position that focuses on studying the molecular mechanisms and evolutionary aspects of developmental plasticity, with a particular emphasis on the water flea *Daphnia magna* and its response to varying environments.

The successful candidate will be responsible for conducting controlled experiments that expose *Daphnia* clones to different environments to examine their plastic developmental response. This will involve morphometrics, behavioural assays, and functional genomics to test and analyse the response patterns. Furthermore, the project will also involve a comparative analysis of patterns of plasticity evolution on a larger geographic scale.

To achieve this, the PhD candidate will employ advanced techniques such as RNA-seq, ATAC-seq, and Hi-C to construct Gene Regulatory Networks that play a role in developmental plasticity.

If you are a highly motivated individual with a passion for developmental biology, genomics, and evolution, we encourage you to apply for this PhD opportunity.

Profile We are seeking a highly motivated student with an outstanding academic track record, a keen interest in evolutionary ecology and genomics, and excellent laboratory and bioinformatics skills. Proficiency in both written and spoken English is essential.

This is a full-time position with an initial duration of one year, which may be extended up to a total of four years upon good evaluations. Funding is available through the FWO Odysseus program, and we also provide assistance to applicants seeking personal scholarships.

Applicants must hold a Flemish master's degree with distinction or equivalent credentials.

The group You will be embedded in the research group of Prof. Steven Van Belleghem (<https://bio.kuleuven.be/eeb/sv>) and an international, enthusiastic and dynamic team and community with ample expertise in using aquatic invertebrates as model systems to address key questions at the intersection of ecology and evolution (<https://bio.kuleuven.be/research> - Division Ecology, Evolution & Biodiversity Conservation). Our team has excellent research facilities including temperature-controlled rooms and well-equipped molecular laboratories. You will be co-supervised by Prof. Robby Stoks (<https://bio.kuleuven.be/eeb/rs>), Prof. Ellen Decaestecker (https://kulak.kuleuven.be/nl/onderzoek/Onderzoeksdomeinen/aquatische-biologie/personal_pages/Prof_Ellen_Decaestecker), and Prof. Luc De Meester (<https://bio.kuleuven.be/eeb/ldm>) who have strong expertise in studying *Daphnia*.

Leuven Leuven is a beautiful historical university city with a very high and pleasant standard of living (<https://www.kuleuven.be/english/living>). Leuven is a 15-minute train ride away from Brussels International Airport and a 20-minutes train ride from Brussels itself. Brussels is one of the best-connected cities in Western Europe; Amsterdam, Paris and London are all reachable within 2 hours by train. The university, founded in 1425, has a top research and teaching standard (<http://www.kuleuven.be/english>). The KU Leuven features consistently in Europe's top-15 universities and has been elected by Reuters as most innovative university in Europe.

Interested?

Please send your CV, a 1-page letter of motivation including relevant experience, a transcript of your bachelor and master study results, and the contact information of two referents as a single PDF to Prof. Steven Van Belleghem (Steven.VanBelleghem@kuleuven.be) with

the subject 'PhD_Application_NAME'. Shortlisted applicants will be interviewed. The application deadline is 31 July 2023. The starting date is 1st of November 2023 (but can be negotiated).

KU Leuven wants to provide an inclusive environment in which all talents can develop to the fullest, regardless of gender, age, cultural origin, nationality or disability. If you have questions about accessibility or support options, you can contact us at diversiteit.HR@kuleuven.be.

Steven Van Belleghem
<steven.vanbelleghem@kuleuven.be>

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LIB Hamburg GastropodEvolution

PhD in Evolution and Systematics of Land Snails at the Leibniz Institute for the Analysis of Biodiversity Change (LIB), Hamburg (deadline 11.06.2023)

The Leibniz Institute for the Analysis of Biodiversity Change (LIB) formed by the merger of the Zoological Research Museum Alexander Koenig (ZFMK), Bonn and the Centre for Natural History (CeNak) of the University of Hamburg, is an internationally operating research institute. As a research museum of the Leibniz Association, the LIB contributes to taxonomic and molecular biodiversity research and to the conservation of global biodiversity, documents and analyses evolutionary and ecological biodiversity change and participates in public communication about biodiversity change and its possible causes.

The LIB has a vacancy for a doctoral student (f/m/d) at the Hamburg location, limited to three years TzBfG, 65% hours, remunerated according to E13 (TV-L).

PhD Student (f/m/d) in the DFG-funded project "Exploration of genomic methods for species delimitation in terrestrial snail radiations". In the project, the systematics, evolution and biogeography of land snail radiations in Indonesia will be investigated with the help of various genomic methods. The project is supervised by Prof. Bernhard Hausdorf (B.Hausdorf@leibniz-lib.de), who is also happy to answer project-related questions.

Your work tasks are in particular: * Generate genomic datasets using methods such as ddRAD and target capture. * Species delimitation and reconstruction of evolution and biogeography of land snail radiations using

generated genomic data * Evaluation of advantages and disadvantages of different methods for species delimitation and optimisation of methods

Our requirement profile: * Qualifying university degree (master's degree/diploma) in biology, genetics, bioinformatics or a related field * Experience with molecular biology methods, especially genomic methods such as ddRAD or target capture * Experience with the analysis of population genetic and genomic data * Programming skills are an advantage

Applications should be submitted in English. The documents should include a covering letter (including the date when the position can be started and the motivation for this position), a CV in table form, final certificates and a reference contact.

In addition to an exciting task in an excellent research institution, we offer you the company supplementary pension scheme VBL and further training opportunities. Our institution is certified according to the "Work and Family" audit. Remuneration is based on the applicant's qualifications up to pay group E 13 of the TV-L. Applications from women are expressly welcome. Severely disabled persons will be given preference in case of equal suitability. Please send your application only digitally via our applicant portal to Ms Katharina Ostermann: <https://leibniz-lib.de/karriere/>. For organisational reasons, only online applications will be accepted. The closing date for applications for this position is 11.06.2023. You can find more information about our institution on the internet at <https://leibniz-lib.de/>. Stiftung Leibniz-Institut zur Analyse des Biodiversitätswandels Postanschrift: Adenauerallee 127, 53113 Bonn, Germany

Stiftung des öffentlichen Rechts; Generaldirektion: Prof. Dr. Bernhard Misof (Generaldirektor), Adrian Gräter (Kaufm. Geschäftsführer) Sitz der Stiftung: Adenauerallee 160 in Bonn Vorsitzender des Stiftungsrates: Dr. Michael Wappelhorst

Bernhard Hausdorf <B.Hausdorf@leibniz-lib.de>

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LMU Munich Shrimp Evolutionary History

PhD position, 75% TV-L E13 LMU Munich, Faculty of Biology, Zoology Starting date: 1 September 2023 End of application: 10 June 2023

Doctoral position (f/m/x) - Reconstruction of the evolutionary history of tadpole shrimps (Notostraca) and their relatives, important components of ephemeral freshwater habitats

We are seeking a highly motivated PhD student to take part in the investigation of tadpole shrimps, including extant and fossil representatives. The project is funded by the German Research Foundation (DFG).

The project aims at using high-resolution imaging for a wide array of fossil and extant tadpole shrimps and their closer relatives. Based on these data, the project will establish a morphometric framework for reconstructing the evolutionary history of the group Notostraca. These findings will provide deeper insights into the presumed long-term stability of the specific habitat of ephemeral ponds, which seems to have played an important role for the last 365 million years.

Specimens will be provided via scientific collections as well as by breeding in the lab, fieldwork is not considered. Techniques to be applied are various imaging methods (digital microscopy, super-macro-photography, μ CT-scanning and other up-to-date methods).

The prospective PhD student does not necessarily need to have experience with the imaging methods or specific systematic groups, but is expected to gain expertise early in the course of the project. The project includes a distinct amount of traveling to collections in Germany and abroad. The results of the project are expected to be presented regularly at national and international conferences by the prospective PhD student as well as published in peer-reviewed journals.

We are especially seeking for a good team worker being able to cooperate closely with people in the workgroup and national and international colleagues of a wide network.

The successful candidate will be based in the workgroup of Systematic Zoology at the campus Martinsried (part of municipality Planegg) south-west of Munich, in close proximity to Munich. Child care facilities as well as

schools are nearby.

We offer: DFG-funded PhD position (75%) for 36 months; interdisciplinary research project and working environment; modern imaging equipment (macro and microscopic)

We expect: MSc (or equivalent) in Biology or Palaeobiology; good English communication skills (oral and written); ability to work in teams; high motivation; keen interest in zoological evolutionary questions

The position is limited to 36 months with a presumed starting date of September 01, 2023.

Applications of women are strongly encouraged. We actively promote gender equality. Severely challenged persons will be given preference in case of otherwise equal qualifications.

Please send your application to chaug@bio.lmu.de until June 10, 2023. The application should include CV, transcript of records, letter of motivation and the names and contact details of two potential referees.

For further information contact: Prof. Dr. Carolin Haug, LMU Munich, Faculty of Biology, Großhaderner Str. 2, 82152 Planegg-Martinsried, Germany, Phone : +49-89-2180-74132; Email: chaug@bio.lmu.de <https://www.en.syszoo.bio.lmu.de/index.html> <https://www.palaeo-evo-devo.info/> Prof. Dr. Carolin Haug LMU Munich Biocenter - Faculty of Biology Großhaderner Str. 2 82152 Planegg-Martinsried Germany

GeoBio-Center at LMU Richard-Wagner-Str. 10 80333 München Germany

Phone 1: +49-89-2180-74227 Phone 2: +49-89-2180-74171 Email: chaug@bio.lmu.de carolin.haug@palaeo-evo-devo.info

Website of Carolin and Joachim T. Haug: <http://www.palaeo-evo-devo.info> Carolin Haug <chaug@biologie.uni-muenchen.de>

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OaklandU Michigan MicrobialPangenomics

The Battistuzzi Lab is looking for a PhD or MS student to join her research group in Fall 2023. The position is fully funded (stipend + tuition waiver).

We focus on the evolution of microbial organisms, primarily Bacteria and Archaea. Using comparative genomics, we seek to reconstruct the early timeline of life's evolution, understand speciation mechanisms, and identify genomic evolutionary patterns over long evolutionary timescales.

The graduate student who will be joining the lab will work on a project focusing on the pangenomics of microbes. This is a large-scale project whose primary focus is to explore the use of pangenomics to reconstruct the timeline of early life. We are a fully computational research group thus prior experience in bioinformatics research or coursework is preferred. Knowledge of evolutionary processes is required.

The Lab is in the Department of Biological Sciences at Oakland University (OU), Michigan (USA). Oakland is a high research intensive institution (R2) with a strong extramurally funded research program in the sciences. OU is located in Rochester (MI), a welcoming suburban area approximately 45 minutes north of Detroit. OU is a lively community with opportunities to live on and off-campus, strong local community connections, and many opportunities for collaborations within the Biology department and with other units on campus (e.g., Chemistry, Bioengineering, Center for Data Science and Big Data Analytics).

To apply, please send your CV or resume, unofficial transcripts, and a brief (~1 page) statement of interest to battistu@oakland.edu by June 11, 2023.

For additional information please contact Dr. Fabia Battistuzzi at battistu@oakland.edu.

Fabia U. Battistuzzi, Ph.D. CAS Interim Associate Dean Associate Professor, Department of Biological Sciences Affiliated Faculty, Department of Bioengineering Oakland University battistu@oakland.edu 248-370-2148

battistu@oakland.edu

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OxfordBrookes UK DrosophilaEyeDevelopment

Want to do a PhD in a friendly and supportive environment, using state-of-the-art techniques in the best model system? We are looking for a graduate student to work with us at the interface of evolutionary biology,

developmental biology, bioimaging, and genomics. A central question in evolutionary biology is how changes in cis-regulatory sequences facilitate phenotypic evolution. A crucial piece of the puzzle is understanding transcription factor (TF) binding and function. This project will study paralogs of Pax6, a gene that plays a central role in animal eye development and regulation of eye size, to gain further insight into the evolution and functional divergence of TFs. The *Drosophila* Pax6 genes, *eyeless* (*ey*) and *twin of eyeless* (*toy*), are crucial for the initiation of eye development and are individually sufficient to induce ectopic eye formation. However, these paralogs have at least partially distinct functions in eye and head development.

A comprehensive comparison of expression patterns, binding motifs and direct target genes for *Ey* and *Toy* is required to gain further insights into how evolutionary diversification of TF paralogs can lead to sub- and neo-functionalisation of TFs. This will be addressed using state-of-the-art methodologies including CRISPR-mediated protein tagging, CUT&RUN sequencing and bioinformatic analyses, as well as confocal and electron microscopy.

The supervisory team has extensive experience in *Drosophila* genetics, imaging, and developmental biology as well as bioinformatic analyses. The student will be embedded in a larger group of *Drosophila* labs at Oxford Brookes and benefit from shared facilities and close collaborations with the Centre for Functional Genomics and the Centre for Bioimaging.

Please visit <https://www.brookes.ac.uk/courses/-research/dissecting-the-genetic-regulation-of-eye-dev> for further details and contact Maike Kittelmann (maike.kittelmann@brookes.ac.uk) or Sebastian Kittelmann (skittelmann@brookes.ac.uk) for informal inquiries. The application deadline is 31st May.

skittelmann@yahoo.de

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Poznan Poland Butterfly Evolution

Name of unit: Faculty of Biology, Adam Mickiewicz University in Poznan

Position name: PhD student

We are looking for a PhD student on the

OPUS 22 National Science Centre research project (2021/43/B/NZ8/00966) "Success of a widespread butterfly: Local adaptation or phenotypic plasticity?" funded by the National Science Centre. The aim of the project is to determine how the widespread butterfly *Melanitis leda* (L.) (Nymphalidae: Satyrinae) has colonized its range and adapted to varying climates and habitats <https://melanitisleda.amu.edu.pl/>. Requirements:

- MSc in Biology or a related field
- a demonstrated interest in evolutionary ecology and field biology
- strong interpersonal skills and a good level of English are important, given the international team
- a driving license and interest in left-side and off-road driving will also be a plus

Task description:

The Ph.D. student will perform fieldwork and lab experiments in Africa and India, coordinate a network of volunteers and collaborators, and perform data management, and data analysis. The Ph.D. student will also be involved in the preparation of manuscripts.

Conditions of employment:

The workplace is in the Faculty of Biology of Adam Mickiewicz University in Poznan which is among the best institutes in evolutionary biology and ecology in Poland. The Ph.D. student will be part of an international team of experts with complementary skills.

The doctoral school includes coursework and requires some hours of teaching practice. The scholarship of 5000 PLN per month (gross) for four years is comfortable in Poland, and Poznan is a pleasant city.

- Planned date of starting work: October 1st, 2023

To be hired in the project, the candidate must pass entry exams to the Doctoral School of Natural Sciences at the Adam Mickiewicz University.

Required documents:

- CV with a cover letter
- scan of the Master's diploma
- a (draft) publication or report
- the names and e-mail addresses of two references
- a signed consent to the processing of personal data: "In accordance with Article 6(1)(a) of the General Data Protection Regulation of 27 April 2016 (Journal of Laws of the EU L 119/1 of 4 May 2016) I agree to the processing of personal data other than those indicated in Article 221 of the Labour Code (name(s) and surname;

parents' names; date of birth; place of residence; address for correspondence; education; previous employment), included in my job offer for the purpose of current recruitment."

Application:

- The required documents should be sent to the following email address: fremol@amu.edu.pl (prof. Freerk Molleman), by May 8th, 2023.
- Applications will be evaluated by a scholarship committee appointed by the Principal Investigator.
- The results of the competition will be announced no later than August 2nd, 2023.
- The scholarship will be awarded in accordance with the rules contained in the Regulations for the awarding of scholarships in research projects financed from the funds of the National Science Centre introduced by the resolution of the NSC Council No. 25/2019 of 14 March 2019.

The selection procedure will have four stages, the first three involving the scholarship committee, and the fourth stage will be with a recruitment committee of the Doctoral School of Natural Sciences at the Adam Mickiewicz University (July 2023). First, the scholarship committee will preselect candidates based on the application materials. Second, these candidates will be invited for a virtual interview and to have recommendation letters submitted. Third, the most promising candidates will prepare a presentation and brief research plan, and will then be given a chance to improve these, guided by the PI. The scholarship committee will then choose the best 1-2 candidates to pass the recruitment to the Doctoral School of Natural Sciences at the Adam Mickiewicz University which includes the aforementioned presentation and research plan.

RODO information clause:

According to Art. 13 of the general regulation on the protection of personal data of April 27, 2016 (Journal of Laws EU L 119 of 04.05.2016), we inform that:

1. The administrator of your personal data is the University of Adam Mickiewicz in Poznań with its registered office at ul. Henryka Wieniawskiego 1, 61-712 Poznań.
2. The personal data administrator has appointed a Data Protection Officer supervising the correctness of personal data processing, who can be contacted via the e-mail address: iod@amu.edu.pl.
3. The purpose of processing your personal data is to carry out the recruitment process for the indicated position.
4. The legal basis for the processing of your personal

data is Art. 6 para. 1 lit. a of the general regulation on the protection of personal data of April 27, 2016 and the Labor Code of June 26, 1974 (Journal of Laws of 1998, N21, item 94, as amended).

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SEVAB Toulouse MouseLemurEvolution

We are seeking motivated candidates interested in applying to the PhD project subject to competitive recruitment of the SEVAB Doctoral School (Toulouse, France)

Title:

Unravelling the mechanisms of cryptic diversification in mouse lemur (genus *Microcebus*, Cheirogaleidae, Primates)

Full description:

[<https://shorturl.at/CFGNZ>]

Abstract:

Madagascar is a renowned model for biodiversity diversification. Various hypotheses, such as climatic oscillations, watersheds, elevation, and rivers, have been proposed to explain the remarkable biodiversity and spatial distribution of Madagascar's flora and fauna. Recently, an integrative framework shed light on the cryptic diversification of the highly speciose mouse lemur primate genus (*Microcebus*), revealing that climatic fluctuations and a humid rainforest species-pump effect during the late Pleistocene may have facilitated mouse lemur diversification, despite morphological stasis. However, interspecific gene flow has been inferred along the mouse lemur radiation, but not among sympatric species, raising questions about the timing and nature of reproductive isolation. This PhD project seeks to comprehensively understand the evolutionary mechanisms driving the rapid cryptic radiation of mouse lemurs, using genomic data at the genus scale. The study will explore the geographic and molecular mechanisms driving mouse lemur diversification and evaluate the contributions of shifts in reproductive and sensorial recognition mechanisms to this exceptional radiation.

How to apply:

[https://ed-sevab.univ-toulouse.fr/as/ed/page.pl?site=edsevab&page=info_concours]

Contact:

jordi.salmona@ird.fr & [jerome.murienne@univ-tlse3.fr]

Dead line: May 31 2023

Jordi SALMONA - IRD - EDB

Laboratoire i₂volution & Diversit*é* Biologique - UMR5174 IUCN SSC Primate Specialist Group - Madagascar jordi.salmona@ird.fr / jordi.salmona@univ-tlse3.fr +33 (0)561556758

Jordi Salmona - IRD - EDB <jordi.salmona@ird.fr>

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Experience in the study of microscopic animals, marine biological fieldwork, analysis of nucleotide sequence data, molecular lab techniques and a strong interest in biodiversity are important qualifications.

The position is for four years. A new position as a PhD student is first for one year and then normally renewed for up to two years at a time. Closing date for the application is 15 June

For more information, please contact Ulf Jondelius (ulf.jondelius@nrm.se) We accept digital applications only. More information, instructions on how to apply, and a submission form are at <https://recruit.visma.com/spa/public/-apply?guidAssignment=b59cf808-cb54-4ab6-935e-d4a76cc29dbd> Ulf Jondelius <Ulf.Jondelius@nrm.se>

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StockholmU MeiofaunaSpeciesDiversity

PhD student in Zoological Systematics

We invite applications for a four-year PhD position based at the Swedish Museum of Natural History in Stockholm. PhD students at the museum are admitted to the PhD programme at the Department of Zoology, Stockholm University.

The project is aimed at analysing species diversity of the marine meiofauna group Acoelomorpha in Sweden, estimate the phylogeny of select groups and describe new species. The project includes fieldwork at marine labs where specimens will be collected, identified, documented, and prepared for downstream analyses. The successful candidate will be supervised by Prof. Ulf Jondelius.

Qualifications In order to meet the general entry requirements, the applicant must have completed a second-cycle degree, completed courses equivalent to at least 240 higher education credits, of which 60 credits must be in the second cycle, or have otherwise acquired equivalent knowledge in Sweden or elsewhere. In order to meet the specific entry requirements, the applicants must have completed at least 120 higher education credits in biology, and at least 30 credits from a degree project within zoological systematics, marine biology, evolutionary biology, bioinformatics, or a similar subject.

UBremen Germany ButterflyUrbanEvolution

PhD in urban evolution of Lepidoptera at the University of Bremen (Deadline: 9 June 2023)

I (Matthew Nielsen) am starting a new research group at the University of Bremen in Germany which will use insects to study evolutionary and plastic responses to global change. As part of this group, I am hiring a PhD student for a project on urban evolution in butterflies.

The PhD project will study the adaptation of butterfly seasonal plasticity to cities across Europe using a combination of field research and laboratory common garden experiments. As part of the project, the student will get to participate in field work in cities across Europe with an international network of collaborators.

Please read the full posting here for more information about the project and qualifications: https://matthewnielsen.net.files.wordpress.com/-2023/05/nielsen_bremen_phd-hiring-description.pdf
Application:

To apply, please send the following to nielsen.matthew@gmail.com: 1) Cover letter (at most 2 pages) describing your interest in the position and relevant experience and qualifications, 2) CV, 3) unofficial transcripts (or other listing of courses taken), 4) a sample of your scientific writing, and 5) contact information for two references (who may be contacted

during the review of applications). All materials should be in English. The scientific writing sample could be your Master's thesis or something else you have already written. It does not need to be the length of a full thesis, and if your thesis is not written in English, it could be a short (~1 page) English-language summary of your thesis work or something else that demonstrates your writing.

Materials should be submitted by Friday, 9 June 2023 for full consideration. The position is available immediately, but the starting date is flexible (ideally by September 2023).

If you have any questions about the position, the application, or anything else, please contact me at the above email address.

Matthew Nielsen soon-to-be Junior Professor Faculty of Biology and Chemistry University of Bremen, Germany
nielsen.matthew@gmail.com

Matthew Nielsen <Matthew.Nielsen@oulu.fi>

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

UCanterbury NZ ComputationalMicrobiology

PhD Position in Computational Microbiology

A scholarship is available to fund a PhD in the computational microbiology research group at Te Whare Wānanga o Waitaha | University of Canterbury (UC) in Christchurch, New Zealand. The available scholarship will cover tuition fees, provide support for research expenses and provide a stipend of \$28,000 per annum for up to 3 years.

The focus of the computational microbiology group is to better understand the diversification and dispersal of microorganisms across environmental gradients and over geological time. To facilitate scientific insights, we are interested in finding ways to improve computational techniques used in the analysis of microbial communities and in organizing microbial data in meaningful ways. We are seeking those who are comfortable with coding and have a strong interest in microbiology.

Example topics include:

* Biogeography of genes and function.

* Phylogeny-assisted functional characterization of genes.

* Improvement of metagenomic binning techniques

* Resolving deep relationships in the prokaryotic tree of life

* Tree-free classification schemes for bacteria and archaea

Successful applicants are expected to draw on their research interests to develop an individualized research plan and will have the opportunity to test computationally generated hypotheses with field sampling and laboratory experiments.

Requirements:

* Completion of a research-focused Honours or Master's degree, at First or Second Class (Division I) Honours or Distinction level (or equivalent) in bioinformatics, molecular biology, microbiology or a relevant field. Please review the Regulations for the Doctor of Philosophy (<https://www.canterbury.ac.nz/regulations/academic-regulations/phd-36/>) and/or use the admission requirements checker (<https://checkwhatyouneed.canterbury.ac.nz/home>).

* Proficiency in scripting (e.g., R, Python, bash) or programming (e.g. C++).

* Experience in processing high-throughput sequencing data

* A desire to present research findings at conferences and publish in scientific journals.

Application Process:

To apply for this position, please submit the following documents:

* A cover letter (2 page max) stating how your research interests fit into the broader goals of the research group and/or topics provided above. Include a link to a Github repository (or equivalent) with examples of code that you wrote or contributed to and describe in the cover letter what the code was used for and your contribution to it.

* A detailed curriculum vitae (CV) highlighting your academic achievements and research experience.

* Contact information for two academic referees who can provide letters of recommendation.

Please email your application as a single PDF file to craig.herbold@canterbury.ac.nz with the subject line "PhD Position in Computational Microbiology." Should you have any further inquiries regarding this position, please contact Dr. Craig Herbold at craig.herbold@canterbury.ac.nz. Screening of applicants

will begin immediately and will continue until a suitable candidate has been identified.

This email may be confidential and subject to legal privilege, it may not reflect the views of the University of Canterbury, and it is not guaranteed to be virus free. If you are not an intended recipient, please notify the sender immediately and erase all copies of the message and any attachments.

Craig Herbold <craig.herbold@canterbury.ac.nz>

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UGroningen EvolAnimalPersonality

UGroningen.EvolAnimalPersonality

content: We are looking for a talented and enthusiastic evolutionary or behavioural ecologist for a fully funded 4-year PhD position. The successful applicant will work on a project aimed at understanding the role of animal personality in mating. The PhD candidate will work in the research group of Dr. Marion Nicolaus which is embedded within the Groningen Institute for Evolutionary Life Sciences, Institute of the Faculty of Science and Engineering of the University of Groningen (The Netherlands).

Description: In most animals, individuals of the same population differ systematically in behaviour. While the proximate and ultimate causation of such animal personalities has received much attention, the consequences of these differences for ecology and evolution have been less studied. Yet, personality variation causes individuals to specialise in different (micro)habitats affecting how behavioural types distribute spatially and interact with each other. Such phenomena could promote personality-based mating (positive or negative correlation between the personality of mated individuals) and, potentially, be a first step towards reproductive isolation and species divergence. The project will address three main questions: What is the prevalence of mating by personality in natural populations? What are the mechanisms underlying mating by personality (active mate choice; spatial/temporal segregation; behavioural plasticity)? What are their associated consequences for ecology and evolution?

These questions will be addressed by experimental studies on three-spined sticklebacks (*Gasterosteus aculeatus*) where populations of migrants were isolated in fresh-

water habitats becoming residents, following habitat fragmentation ~50 years ago. We have previously shown that populations of residents and migrants differ genetically in movement and social behaviour. Because conservation efforts are underway to reconnect the waterways, we need to study the consequences of barrier removal for these populations. The successful applicant will have the possibility to do field work and design experiments in the lab and in a mesocosm system (replicate series of semi-natural ponds connected by corridors) where movement, social and breeding behaviour of tagged individuals can be automatically tracked.

The PhD candidate will receive varied and cutting-edge research training, with ample opportunities for following advanced courses, workshops and conferences, complemented by training in transferable skills and teaching. As a PhD candidate, you are committed to conduct independent and original scientific research, to report on this research in international publications and presentations, and to present the results of the research in a PhD dissertation, to be completed within 4 years. PhD candidates are expected to contribute 10% of their overall workload to teaching

Qualifications

The ideal candidate is highly motivated, ambitious, creative, and has a good affinity with behavioural ecology research. The successful candidate will have the following required qualifications:

- an MSc degree with specialisation in ecology, evolution, animal behaviour or related disciplines;
- the ability to work independently and in a team;
- excellent conceptual capacity;
- excellent command of the English language;
- excellent communication and presentation skills, both in words and in writing;
- some knowledge of advanced statistics and a computer language like R.

Conditions of employment

We offer you in accordance with the Collective Labour Agreement for Dutch Universities:

- a salary of €2,541 gross per month in the first year, up to a maximum of €3,247 gross per month in the fourth and final year - a full-time position (1.0 FTE; based on a 38 hours per week) - a holiday allowance of 8% gross annual income - an 8.3% end-of-the-year allowance
- minimum of 29 holidays and additional 12 holidays in case of full-time employment.

The position offered is for four years. Each successful

candidate will first be offered a temporary position of one year with the option of renewal for another three years. Prolongation of the contract is contingent on sufficient progress in the first year to indicate that a successful completion of the PhD thesis within the contract period is to be expected. A PhD training programme is part of the agreement and the successful candidate will be enrolled in the Graduate School of the Faculty.

The conditions of employment are available at the University of Groningen website under Human Resources: www.rug.nl/about-ug/work-with-us/-information-for-new-staff?lang=eng The preferred starting date is 1 October 2023.

Application

You can submit your application until 30 June 11:59 pm / before 1 July 2023 Dutch local time (CET) on the following website:

— / —

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>

UIIdaho BulltroutGenomics

PhD position Department of Biological Sciences University of Idaho

We are recruiting a Ph.D. student to work on genomics of isolated populations of bulltrout (charr; *Salvelinus confluentus*). The student would work with Drs. James Nagler and Paul Hohenlohe (University of Idaho) and Dr. Alexandra Fraik (USDA Forest Service). This project will characterize patterns of standing genetic variation shared or unique to sub-alpine lake populations in Idaho and Montana, as well as spawning behavior in these unique non-migratory, lake-resident fish. Goals include understanding adaptive genetic variation in an understudied life history form, investigating inbreeding and demographics, and identifying mechanisms of persistence in small, isolated populations, with implications for the conservation of genetic diversity in this species. The research will involve both laboratory (e.g., molecular genomics, bioinformatics) and fieldwork (e.g., fish sampling, remote travel) components.

Qualifications: Bachelors degree in biology, fisheries, or a related field.

Stipend: \$30,000 per year plus tuition and fees; may require working as a teaching assistant in some academic terms.

Start date: August 2023 if available; January 2024 also possible

Contact: Please send a letter of intent and CV with contact information electronically to: Dr. James Nagler, Department of Biological Sciences, University of Idaho at jamesn@uidaho.edu

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

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ULausanne Switzerland PlantEvolution

PhD studentship in plant evolution - Department of Ecology and Evolution, University of Lausanne, Switzerland

A PhD studentship in plant evolutionary biology is available in the research group of John Pannell in the Department of Ecology and Evolution, University of Lausanne. The project will be on one of two topics currently central to the lab's research: (1) the evolution of plant sexual systems; or (2) evolution at and beyond species' range margins. Both projects could use a combination of field work, experimental evolution and genome sequence analysis (depending on the student's particular skills and interests).

The lab's work on plant sexual-system evolution is focused largely on evolutionary transitions between hermaphroditism and dioecy and their implications for the evolution of sexual dimorphism and sex chromosomes. One of three possible PhD projects could be envisaged within this area. First, the project could use phenotype, quantitative genetic and/or genome analysis of a transition of experimental populations from dioecy to hermaphroditism and now, remarkably, back towards separate sexes. Second, the project could involve establishing a new model system for the lab to investigate the ecological and genetic factors responsible for the differential maintenance of hermaphroditism versus dioecy across environmental gradients.

Our work on species range margins aims to test key hypotheses about what prevents populations from becoming locally adapted at the edge of species' ranges. It involves assessing the demographic and evolutionary effects of gene flow on populations across the distribution of an annual plant across its European range. The project is highly collaborative, with replicate populations evaluated by project partners at sites across Europe, from the eastern Mediterranean Basin to Scandinavia, and with modules focussing demographic, quantitative genetic and genomic data.

For details of current research in the lab and a list of publications, see <https://www.unil.ch/dee/pannell-group>. Research scope and skills sought The student's specific research can be tailored to his or her background, interests and personal training objectives. He or she should be able to demonstrate a strong interest in evolutionary ecology and/or population genetics. Experience in working with plants is not essential but could be an advantage. The successful candidate should also have good communication and interpersonal skills, and an ability to work in a team.

Host department and university The Department of Ecology and Evolution at the University of Lausanne hosts a broad range of research groups, and its members enjoy a lively intellectual and social life. Although the University of Lausanne is francophone, the department is highly international, and all its research activity and seminars are conducted in English. The University has seven faculties and approximately 14,300 students and 3,900 researchers from over 120 countries. It is situated on a beautiful campus on the shore of Lake Geneva, and is close to the Swiss and French Alps.

Applications Informal enquiries should be sent to John Pannell (john.pannell@unil.ch). Formal applications should be sent to John Pannell as a single pdf that should include: a cover letter detailing your research interests, experience and motivation for applying; your CV; and the names of two or three referees. In addition, you will also need to upload your application to the University of Lausanne recruitment platform following this link: <https://bit.ly/3ny1TZu>. All applications received by 22 May 2023 will receive full consideration.

University equality policy The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

John Pannell <john.pannell@unil.ch>

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UNottingham EvolutionParasitologyGenomics

Hi all

We have a BBSRC funded PhD project open to students with UK home fees status. Would suit a student in any combination of evolution/parasitology/genomics/snails, particularly someone who is keen to build their skills in both lab and bioinformatics. Of course, training will be provided.

Apply by May 23rd here: <https://www.nottingham.ac.uk/bbdtp/index.aspx>. Note that there is pre-application mentoring available for Black and Black mixed students with home fees status <https://www.nottingham.ac.uk/bbdtp/equality-diversity-and-inclusion/amplify.aspx> If you are interested in applying, and/or would like further information, then certainly worth a chat with either Chris Wade (Chris.Wade@nottingham.ac.uk) or myself (angus.davison@nottingham.ac.uk) before the deadline

Angus

Fully-funded studentship: Evolutionary genomics of trematode parasites and their intermediate snail vectors

Overview: The student will use genome sequencing technologies and population genomic methods to take a key step towards understanding the interactions between snail hosts, schistosomes and other trematode parasites in the natural environment. In establishing this baseline research, the research will prepare the ground for studies that are directly aimed at controlling disease in humans and livestock.

Further information: Molluscs such as slugs and snails are intermediate vectors of important pathogens of humans and their livestock. In an agricultural context, snail-transmitted parasites have a high economic cost, because snails transmit trematodes to sheep and cattle, costing the industry hundreds of millions per annum. There are also direct impacts to human health. For example, schistosomiasis, a major neglected tropical disease of humans, is frequently transmitted to persons from snails when undertaking agricultural work in or around water bodies. In Africa, where the problem is most acute, about 200 million people are infected with *Schistosoma* parasites, causing fever, fatigue and an increased risk of bladder cancer, with tens of thousands dying from schistosomiasis worldwide each year

(WHO estimates 200,000 globally), and incurring the widespread use of toxic molluscicides, which then enter the food chain.

To date, the majority of research on trematode parasites in Africa has tended to focus on the schistosome/human interaction, neglecting both the variety of snail intermediate vector species, and also other trematode parasites that infect livestock. Yet, strategies for both control of agricultural disease and also elimination of schistosomes should consider the intermediate host snail. Of the relatively limited prior work on these snail vectors, molecular genetic research has mainly used species-specific methods to identify parasites in snails, thus limiting the findings to species known to be present. More recently, metabarcoding methods have proved useful in providing a comprehensive catalogue of trematode parasites within a snail. However, while useful, both of these approaches neglect the snails, usually requiring further costly but low-power PCR-based methods to identify the species.

In this study, we will take advantage of advancing genome sequencing technologies and an existing resource of field-collected snails. Population genomic methods will be applied to the snails and the parasites, to take a first step towards understanding interactions between the snails, the schistosomes in the natural environment. Specifically, whole genome sequences of the snails will be used to 1) identify and quantify parasites present within the snail 2) assemble whole snail and parasite genomes from fragmentary information 3) describe the phylogenomic structure and species status of the snails, and 4) synthesise this information, relating parasite presence/absence to underlying genetics and geography of the snail host.

Data from whole genome sequencing will be used to understand whether infection by a particular species of trematode makes snails recalcitrant to infection by other parasites, a finding that would have direct implications for surveillance and control. In a pilot study, we have shown that this approach works, detecting pre-patent trematode infection in snail hosts. A more comprehensive PhD study will prepare the ground for future studies that are directly aimed at controlling these diseases of humans and livestock.

Further reading:

1. Joof E, Andrus PS, Sowunmi K, Onyango VM, Wade CM (2020) Comparing PCR techniques against conventional cercarial shedding methods for detecting *Schistosoma mansoni* infection in *Biomphalaria* snails. *Acta Tropica* 212: 105716
2. Joof E, Sanneh B, Sambou SM, Wade CM (2021a) Species diversity and distribution of schistosome intermediate snail hosts in The Gambia.

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UPadua EvolutionEcolAndConservation

Call for PhD students in Ecology, Evolution and Conservation at Padua University is open. Deadline for applications June 07th, 2023

Scholarship starting date: Oct 1st, 2023

Information about the proposed research topics, the training program and the application procedure can be found at <https://dottorato.biologia.unipd.it/> The board of the curriculum EVOLUTION, ECOLOGY and CONSERVATION of the BIOSCIENCES PhD program at Padua University, invites applications from highly motivated and outstanding students with specific interest for evolutionary and ecological research.

Padua University is top ranked in Italy and among world Universities. Our PhD students have access to first-class facilities at the Biology Department and work within a friendly and strongly international research community under the supervision of experts of the field. Research opportunities are multi-disciplinary, spanning the whole range of ecological and evolutionary research. Interdisciplinary approaches are encouraged as well as the scientific interaction among PhD students (approx. 80 PhD students are enrolled at the Biology Department), post-docs and the about 100 faculty members of the Department.

Proposed research topics in this call include:

- The role of waterbirds in the functioning and services of the Venice Lagoon ecosystem. Contact: Prof. Alberto Barausse, e-mail: alberto.barausse@unipd.it
- Fighting extinction using genomic tools. Contact: Prof. Leonardo Congiu, e-mail: leonardo.congiu@unipd.it
- Biological signals of anthropogenic environmental changes: integrating museums and dissemination into contemporary scientific research. Contact: Prof.ssa Isabella Moro, e-mail: isabella.moro@unipd.it
- Fine-scale interpolation of Eurasian genetic components across time and space. Contact: Prof. Luca Pagani, e-mail: luca.pagani@unipd.it

- Live cool, live long? Exploring longevity and ageing in Antarctic fish. Contact: Prof.ssa Chiara Papetti, e-mail: chiara.papetti@unipd.it

- Mate choice, sexual selection, and chooser fitness in tropical livebearing fishes. Contact: Prof. Gil Rosenthal, e-mail: gil.rosenthal@unipd.it

- Environmental DNA and RNA approaches to monitor biodiversity of the Adriatic Sea. Contact: Prof. Lorenzo Zane, e-mail: lorenzo.zane@unipd.it

Scholarships are competitive and only 3 to 4 of the 7 above projects will be funded according to the curriculum of the applicants. Further details on the research projects are reported at: https://dottorato.biologia.unipd.it/fileadmin/dottorato/-1_Evolution_Ecology_and_Conservation_2023.pdf

Furthermore, 2 additional so-called “priority research grants” will fund two PhD Scholarships on the following topics:

- Linking species richness, community structure and ecosystem function to support biodiversity monitoring in increasingly urbanized marine areas. Contact: Prof. Laura Airoidi, e-mail: laura.airoidi@unipd.it

- Intrinsic and extrinsic factors affecting migratory behaviour of waterbirds. Contact: Prof. Andrea Pilastro, e-mail: andrea.pilastro@unipd.it

Details on the priority research grants are available at: https://dottorato.biologia.unipd.it/fileadmin/dottorato/Priority_Research_Grants_2023.pdf Candidates are encouraged to carefully read the research projects and to send an email to the reference persons for further details. When applying, please also check news at https://dottorato.biologia.unipd.it/fileadmin/dottorato/Important_notices_2023.pdf On behalf of the Evolution, Ecology and Conservation board:

Lorenzo Zane (lorenzo.zane@unipd.it) Professor of Ecology Department of Biology ‘Padua University (IT)

Lorenzo Zane Professore Ordinario di Ecologia Coordinatore della Didattica DiBio

tel: +39 0498276220 mobile: +39 3929495233 skype contact: lolozaup

Secondo Piano Sud Dipartimento di Biologia Università di Padova via U. Bassi/58B I-35121 Padova Italy

lorenzo.zane@unipd.it

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UParma PrimateEvolutionaryGenomics

GraduatePosition:UniParma.PrimateEvolutionaryGenomics.PhD

Three year PhD position to study Primate evolutionary genomics at the Department of Chemistry, Life Sciences and Environmental Sustainability (SCVSA), University of Parma (Italy) (<https://scvsa.unipr.it/en>), under the supervision of Prof. Cristian Capelli.

The project aims at investigating the evolutionary history of primate species using available and newly generated genomic data comprising high and low coverage whole genome sequences. Given the nature of the project applicants will be expected to have previous proven experience in the handling of genomic data (whole genome sequences) within a population genomic context (including reads mapping, variants calling and biostatistical pop gen analyses) and use of high-performance computational clusters.

The call for applicants is expected to open in early Summer 2023 and the PhD will begin in Autumn 2023. Interested candidates fulfilling the indicate criteria are strongly advised to contact Prof. Capelli to discuss the project (email: cristian.capelli@unipr.it).

The PhD is part of the Doctorate program in Biotechnology and Biosciences, which focuses on the study of the function, organisation and regulation of the genomes of microorganisms, animals and plants. The program recruits every year about 10 students and is one of the doctoral programs offered by the SCVSA department.

The SCVSA department has been recognised Department of Excellence by the Italian Ministry of Education, University and Research (MUR), receiving dedicated funding.

University of Parma is one of the oldest in the world, originally founded in 962 by Emperor Ottonian. The University holds 9 Departments, 40 First Cycle Degree Courses, 6 Single Cycle Degree Courses, 46 Second Cycle Degree Courses (7 of which entirely held in English), as well as many Postgraduate schools, Teacher Training courses, several Master Programmes and PhDs. The size of the University (27,000 students, with more than 5,000 graduates per year and about 1,700 faculty and staff members), together with the quality of life in Parma has always attracted a large number of students from all over Italy. More than two-thirds of our registered

students come from outside of Parma and its Province: for this reason the University deserves top ranking for attracting the most non-resident students nationwide.

Many facilities are available to students to enhance the quality of their studies and university life, including, language courses at the Foreign Language Centre, and many sports activities run by the University of Parma CUS, which offers courses in a number of disciplines in a wide range of structures - a swimming pool, athletics tracks, tennis courts, football pitches, a golf course, basketball courts, rugby pitches, etc.

Parma, the hometown of the famous Italian music composers Giuseppe Verdi and Arturo Toscanini, is located in the Emilia-Romagna region, in the North of Italy. The city hosts several famous historical buildings (the Renaissance Teatro Farnese among the others) and is placed within the beautiful Parma valley, also known as the "Food Valley" for its world-wide renowned gastro-nomic products.

Firma il tuo 5xmille all'Universit? di Parma, aiutaci a essere sempre pi? accoglienti e inclusivi verso le nostre studentesse e i nostri studenti - Indica 00308780345 nella tua dichiarazione dei redditi.

Cristian CAPELLI <cristian.capelli@unipr.it>

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UQueensland AntibioticResistance

The Engelstaedter Lab at The University of Queensland, Brisbane, Australia, invites applications for a PhD position in microbial evolutionary biology. The successful candidate will work on projects investigating the evolution of antibiotic resistance in bacteria. Specific projects are flexible and will be arrived at in discussion with the candidate. Our previous research includes work on the evolution of natural transformation, integron evolution, fitness landscapes underlying drug resistance evolution and the predictability of evolutionary dynamics. We use a combination of different approaches in our lab, including mathematical modelling, bioinformatics and experimental evolution. For details about our research and recent publications, see our website at <http://engelstaedterlab.org/>. We are looking for a highly motivated student with a strong background in evolutionary genetics, bioinformatics, mathematics and/or microbiology. Applicants should possess a Bach-

elor's degree with Honours, Master of Science, MPhil or equivalent. Good communication skills, scientific curiosity and enthusiasm for research in evolutionary biology are essential.

The School of Biological Sciences is a large and research-intensive unit at the University of Queensland, one of Australia's most prestigious universities. Brisbane is the third-largest city in Australia and offers mild subtropical climate, vibrant cultural life, plenty of outdoor activities and native wildlife.

Acceptance for this PhD is contingent on successful application for a PhD scholarship. Several PhD scholarships for domestic and international students are available; options will be discussed during the interview.

Interested applicants should send a cover letter (including a brief outline of their research interests), CV, and academic transcript to j.engelstaedter@uq.edu.au. Informal inquiries are also welcome. Please submit your application before 12 June 2023 to be considered for the international scholarships.

Dr Jan Engelstj?dter Associate Professor School of Biological Sciences The University of Queensland Brisbane QLD 4072 Australia

phone: +61 7 336 57959 fax: +61 7 336 51655 <http://-engelstaedterlab.org/> j.engelstaedter@uq.edu.au

j.engelstaedter@uq.edu.au

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UReading

PlantDiseaseEpidemiologyEvolution

PhD studentship, University of Reading, UK, open to applicants with UK fees status. Deadline 19th June 2023.

Title: "Smart control of crop diseases: how can we best combine fungicides and plant resistance genes?"

About the project:

This interdisciplinary PhD project will investigate the epidemiology and evolutionary adaptation of the major fungal pathogen of wheat *Zymoseptoria tritici* (Zt) to control measures – fungicides and disease resistance genes, thereby using evolutionary biology to tackle one of the most urgent problems in agriculture. The methodology combines mathematical modelling,

machine learning and field experimentation.

Zt causes septoria tritici blotch (STB), the most damaging disease of wheat in Europe and one of the largest constraints on wheat production globally. The disease is especially serious in the UK because of conducive climatic conditions. It is becoming increasingly difficult to control STB, because Zt is capable of rapidly evolving resistance to fungicides and adapting to disease-resistant wheat varieties and environmental conditions. It is recognized that no single control measure is durable in the face of the pathogen's notorious adaptive capacity, hence the two key control methods - fungicides and disease resistance genes in wheat - need to be combined in a manner that optimizes not only control efficacy in the short term, but also their sustainability in the longer term. This interdisciplinary project will make a major contribution to this goal using a powerful combination of large-scale field experimentation with novel high-throughput phenotyping techniques, bioinformatic analyses, state-of-the-art machine learning and mathematical modelling approaches.

In the first phase, a field experiment will be conducted during two consecutive years to investigate the STB epidemic development in a large number of different wheat genotypes. The amount of disease will be measured using both the conventional visual assessments and novel digital phenotyping approaches, and the daily weather data will be recorded. The data on epidemic development will be linked to genomic data already available for the wheat population under study, and in this way you are likely to identify new genetic bases of STB resistance in wheat. In the second phase, powerful machine learning techniques will be used to combine the three types of data (disease measurements, weather data and wheat genomic data) and construct a model predicting the seasonal STB epidemic development. Finally, in the third phase of the project, the outcomes of the two previous phases will be incorporated into a mathematical modelling framework (epidemiological/evolutionary model) that describes how the pathogen population changes over time in its interaction with the host population of wheat plants. The model will incorporate the effect of two control measures: fungicides and STB resistance genes in wheat. This will allow you to optimize choices of fungicide treatment programmes and disease-resistant wheat cultivars that maximize net benefit of growers over a short term of a single growing season. You will then be able to compare the outcomes with the predicted net benefit over a longer term of a number of consecutive growing seasons, taking into account disease levels, weather variables and wheat genomes.

Training opportunities:

The student will acquire inter-disciplinary skills in designing and conducting large-scale field experiments with crop pathogens, acquiring large datasets with the help of novel digital phenotyping approaches, use machine learning and mathematical modelling to extract knowledge from data. The student will receive extensive training by the supervisory team in computer programming to handle large and complex data sets and conduct mathematical and computational modelling using Linux, Python and R. The student will have access to advanced computational infrastructures, such as the high-performance computing clusters available at Aberystwyth University, and via Supercomputing Wales, and receive appropriate training in their usage. The student will be embedded within the extensive international collaborative network of the supervisory team that includes plant pathologists, genomics experts, modellers and practice-oriented researchers, enabling the student to make use of these diverse sets of expertise. A three-month placement with Syngenta will provide the student with the industry's perspective on the project's outcomes, expanding the range of possible employment options after the completion of the project. The unique combination of empirical, mathematical and computational skills as well as a valuable professional network developed in the course of the project will increase the student's chances to find a high-profile job in academia, governmental agencies or industry.

Student profile:

— / —

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URennes France ClimateChangeFertility

Fully-funded 3-year PhD position to work on the project "Fertility in a changing world"

(deadline: 25th May 2023)

I am seeking candidates for a PhD project on the evolutionary ecology of reproduction in *Macrostomum* flatworms in connection with the recently-started Chaire de Recherche Rennes Métropole / Chaire de Professeur Junior project "Fertility in a changing world", based in

the ECOBIO lab (UMR 6553 Ecosystèmes, Biodiversité, Evolution) at the Université de Rennes in Brittany, France.

Using an experimental evolution approach, we will investigate plastic and evolutionary responses to altered thermal and salinity environments, with aims including: (1) to measure differential impacts on male and female fertility; (2) to test the additivity of these stressors; and (3) to elucidate the interaction between natural and sexual selection in driving climate change adaptation. The initial focus will be on phenotypic and fitness measures, with possible extension to look at their underlying molecular basis as the project develops. Advantages of the proposed model system - the simultaneously hermaphroditic marine flatworm, *Macrostomum lignano* - include its small size and short generation time for establishing experimental evolution lines; transparency, for efficient in vivo phenotyping of reproductive traits; and the availability of a GFP-transformed line, for tracking sperm and performing large-scale fitness (paternity) assays.

For more information, potential candidates should please contact Steve Ramm (steven.ramm@univ-rennes.fr).

Formal applications through the doctoral school EGAAL are due 25/05/23 via: <https://theses.doctorat-bretagne.fr/egaal/campagne-2023> Dr. Steven RAMM UMR 6553 ECOBIO - Ecosystèmes, Biodiversité, Evolution Université de Rennes Campus de Beaulieu 35042 Rennes Cedex, France steven.ramm@univ-rennes.fr

“Ramm, Steven” <steven.ramm@uni-bielefeld.de>

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UWageningen EvolutionFungalResistance

PhD position: Understanding pan-fungicide resistance in the airborne human fungal pathogen *Aspergillus fumigatus*

Published on May 22, 2023 Location Wageningen End date Fri 23 June 2023

Your job

Are you interested in genetics and understanding how resistance to environmental chemicals can affect reproductive barriers? Are you excited about using CRISPR-

Cas9 and state-of-the-art molecular biology in fungi? Do you want to pursue a PhD? Then we have an excellent opportunity for you in Wageningen, The Netherlands!

Aspergillus fumigatus is a human pathogenic fungus causing serious life-threatening diseases. Antifungal resistance against the azole class is rapidly spreading on a global scale and hampering effective treatment of patients. *A. fumigatus* isolates from patients have not only acquired azole resistance but also resistance to other agricultural fungicides. Recent analysis shows that multiple genes are involved in this pan-fungicide resistance, and these variants may have unforeseen impact on various aspects of the biology of this fungus.

As a PhD candidate you will be employed in the recently funded NWO ENW M1 project “Reaching far and wide: understanding pan-fungicide resistance in the airborne human fungal pathogen *Aspergillus fumigatus*” (the full application is available by e-mailing toeveline.snelders@wur.nl). You will have the opportunity to:

§Gain a deep understanding of the complex pan-fungicide resistance in *A. fumigatus* and characterize the causal genes by using CRISPR Cas9 and sexual crossing experiments.

§Implement and validate a wax moth model to study the fitness cost and compensatory mutations associated with antifungal resistance.

§Utilize genomic data to investigate the consequences of agricultural pan-fungicide-resistant *A. fumigatus* on the population structure of this fungus.

Your qualities

We are seeking candidates who possess:

§A strong interest in genetics and working with fungi.

§Innovativeness and eagerness to use new techniques and models.

§Enjoy working in an international environment and a multidisciplinary team.

§Proficient writing and oral communication skills in English. Additionally, you should have:

§Successfully completed a MSc degree in Biology, Microbiology, Biotechnology or related field.

§Basic bioinformatics skills or the motivation to acquire them.

§Meet the entry requirements of the WUR PhD programme.

For this position your command of the English language is expected to be at C1 level. Sometimes it is necessary to submit an internationally recognized Certificate of

Proficiency in the English Language. More information can be found here.

We offer you Wageningen University & Research offers excellent terms of employment. A few highlights from our Collective Labour Agreement include:

§sabbatical leave, study leave, and partially paid parental leave;

§working hours that can be discussed and arranged so that they allow for the best possible work-life balance;

§the option to accrue additional compensation / holiday hours by working more, up to 40 hours per week;

§there is a strong focus on vitality and you can make use of the sports facilities available on campus for a small fee;

§a fixed December bonus of 8.3%;

§excellent pension scheme.

In addition to these first-rate employee benefits, you will receive a fully funded PhD position and you will be offered a course program tailored to your needs and the research team. The gross salary for the first year is euro 2.541,- per month rising to euro 3.247,- in the fourth year in according to the Collective Labour Agreements for Dutch Universities (CAO-NU)(scale P). This is based on a full-time working week of 38 hours. We offer a temporary contract for 18 months which will be extended for the duration of the project if you perform well.

There are plenty of options for personal initiative in a learning environment, and we provide excellent training opportunities. We are offering a unique position in an international environment with a pleasant and open working atmosphere.

You are going to work at the greenest and most innovative campus in Holland, and at a university that has been chosen as the “Best University” in the Netherlands for the 18th consecutive time.

Coming from abroad Wageningen University & Research is the university and research centre for life sciences. The themes we deal with are relevant to everyone around the world and Wageningen, therefore, has a large international community and a lot to offer to international employees. Our team of advisors on Dutch immigration procedures will help you with the visa application procedures for yourself and, if applicable, for your family.

Feeling welcome also has everything to do with being well informed. Wageningen University & Research's International Community page contains practical information about what we can do to support international employees and students coming to

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UZurich PlantEvolutionaryBiology

THIS IS A READVARTISEMENT, PLEASE APPLY AS SOON AS POSSIBLE!

PhD position or part-time post-doctoral position in plant evolutionary biology, University of Zurich. University of Zurich, Dept. of Systematic and Evolutionary Botany

RESEARCH PROJECT: Whether evolutionary trajectories leading to a particular function/morphology are predictable is a fundamental question of evolutionary biology. Yet, there is little consensus on this issue and experimental evidence is contentious. The phenomenon of convergent evolution, the repeated evolution of traits in independent lineages, provides an ideal framework to test for constraints on the trajectory of the evolutionary processes. Our project investigates the genetic bases of parallel morphological evolution in a closely related group of moss species, the family Funariaceae. In mosses, the dominant haploid gametophyte phase (the leafy shoot) alternates with a diploid sporophyte (spore producing) phase. Fitting the classical example of parallel evolution, the reduced sporophyte phenotype has evolved multiple times independently in the Funariid mosses. The availability of information on the developmental biology of complex and reduced sporophyte phases, the simple structure of the sporophyte phase and the family's amenability for reverse genetic work makes it an ideal system to investigate the genetics basis of parallel evolution.

This project heavily relies on the vast amount of preliminary data produced during the last three years using comparative transcriptomic and genomic analyses on two species (*Physcomitrium* (*Physcomitrella*) *patens* and *Funaria hygrometrica*) representing the end points of sporophyte complexity in the Funariaceae family. The preliminary data encompassing chromosome-scale genome assemblies, comparative transcriptomics and established methods for reverse genetic manipulation already enabled us to identify candidate genes and jump start this project. We envision that the proposed research will contribute to the general understanding of

the molecular processes underlying parallel evolution of morphological traits, a fundamental issue of evolutionary biology.

This project is funded by a Swiss National Science Foundation (SNSF) grant to Peter Szovenyi (<http://peterszovenyi.weebly.com/publications.html>) and will be carried out in collaboration with Bernard Goffinet (UConn) and Joan Coudert (University of Lyon). The Dept. of Systematic and Evolutionary Botany hosts research groups working on the evolutionary and ecological drivers of biodiversity, on the macroevolution of plants, on plant-insect interactions/pollination, on the evolution of mating systems, hybridization and speciation. The Dept. of Plant and Microbial Biology hosts many groups working on plant molecular and developmental biology, epigenetics, community genomics and plant adaptation. Both institutes are housed in the beautiful Botanical Gardens and host a diverse community of researchers in plant biology.

IDEAL CANDIDATES: Ideal candidates will have an MSc in biology with a specialization in evolution, developmental genetics and/or bioinformatics. This position involves expert level bioinformatic work including genome assembly (long-reads, Hi-C) and genome annotation. Furthermore, the project uses comparative transcriptomics (spatial transcriptomics) including gene regulatory network analyses in a phylogenetic context, and high throughput reverse genetic work. Therefore, this position requires advanced skills in handling, analyzing and interpreting high-throughput next-generation sequencing and RNA-seq data. Good skills in assembling vectors, carrying out genetic transformations and microscopy are also required. In case not all these skills are covered, the willingness to quickly acquire them is necessary. The student will closely work together with the postdoctoral fellow on this grant. Students should be willing to work both in the wet lab and in the office doing computational work. The position (if PhD) for four years. Selected candidates will be enrolled in one of the two affiliated PHD schools in evolution or plant sciences.

CLOSING DATE: The position is opened until filled, but all application material including CV, a summary of research experience, a letter of motivation, copies of relevant publications (published or submitted) and names and contact information of three reference persons should be received by 10th June 2023 to ensure full consideration. The position will start at the earliest possible date, but it is negotiable (at the latest in September 2023). Candidates should indicate in a cover letter when they could take up the position and whether they are applying for a phd or postdoc position.

Please send all application material with the following subject line “PhD_sporophyte_evolution” to: Peter Szovenyi, peter.szovenyi@uzh.ch, as a single pdf document. For enquiries, please contact Peter Szovenyi

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Vienna Polygenic Adaptation

REMINDER: Apply by June 04, 2023

PhD positions are available within the *Special Research Program (SFB)* < <https://www.vetmeduni.ac.at/sfb-polygenic-adaptation> >* “Polygenic adaptation: from single selected loci to the infinitesimal model” in Vienna, Austria*. Vienna is on top of the world’s most liveable cities and home to one of the largest communities of evolutionary research in Europe (www.evolVienna.at).

The SFB program is funded by the Austrian Science Fund (FWF) and brings together eight research groups at four institutions in and around Vienna with the common goal of elucidating the evolutionary genetics of adaptation of complex phenotypes: *Neda Barghi* < <https://www.vetmeduni.ac.at/en/population-genetics/research/barghi-lab/group-leader> > *, **Robert Kofler* < <https://www.vetmeduni.ac.at/en/population-genetics/research/kofler-lab> > *, **Christian Schlotterer* < <https://www.vetmeduni.ac.at/en/population-genetics/research/schlotterer-lab> > * (Vetmeduni); **Joachim Hermisson* < <https://www.mabs.at/team/> >*, **Himani Sachdeva* < <https://www.mabs.at/team/> >* (Univ. of Vienna); **Magnus Nordborg* < <https://www.oeaw.ac.at/gmi/research/research-groups/magnus-nordborg/> >*, **Kelly Swarts* < <https://www.oeaw.ac.at/gmi/research/research-groups/kelly-swarts> >* (Gregor Mendel Institute); **Nick Barton* < <https://bartongroup.pages.ist.ac.at/people/group-leader/> >* (ISTA)*. For young scientists, this cluster offers a unique environment for interaction and personal growth.

The SFB aims to develop a framework for understanding polygenic adaptation and to establish new standards for the analysis of adaptive polygenic traits in GWAS and experimental evolution studies. We will

combine model-based conceptual work and data-driven approaches from GWAS and experimental evolution to achieve this goal. The models and methods that will be developed integrate population genetic and quantitative genetic approaches to detect, analyze, and interpret genomic patterns of the “architecture of polygenic adaptation”.

*SFB - a collaborative environment for research and learning: *The theoretical and empirical projects of the SFB are highly synergistic and the collaborative nature of the SFB will provide an inspiring academic environment and promote curiosity-driven research. The interaction between projects of the SFB is strongly facilitated by a long-standing track record of fruitful interactions among the PIs. The PhD students and postdocs in the SFB will benefit enormously from these tight interactions.

To ensure a good integration of experiment and theory, researchers have the opportunity to spend some time in a group from the other “camp”. These regular exchanges will improve the mutual understanding of concepts and problems, ensure that the theoretical work is guided by experiments (and vice versa) and will represent a true added value of the SFB. In addition to the formal supervisor, both PhD students and postdocs will have at least one co-advisor with complementary expertise.

*Courses: *The recruited early-stage researchers in the SFB will have the opportunity to acquire experience beyond their own projects and working groups.

The SFB PIs participate in joint teaching activities and representatives of all institutions are contributing to the Vienna Graduate School of Population Genetics (www.popgen-vienna.at). The PhD students will be integrated in the Vienna Graduate School of Population Genetics, which offers a 5-week introductory course that covers subjects as diverse as statistics, population genetics, Drosophila genetics, programming, NGS data analysis (both DNA- and RNA-Seq) and quantitative genetics.

SFB postdocs will have the opportunity to participate in the teaching in introductory course in their areas of expertise. But at the same time can attend specific modules of the introductory course together with the PhD students. This joint event will have a tremendous impact on team-building and can enable scientists from different host institutions to establish strong ties which can result in research collaborations.

The IST Graduate School offers more advanced courses in evolutionary

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Vienna PopulationGenetics

REMINDER: apply by June 04, 2023

PhD positions in Population Genetics

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

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

Topics include:

Adaptation from reduced genetic variation. Evolution from de novo mutations - influence of elevated mutation rates. Evolution of sex-specific neuronal signaling. Genomic and phenotypic patterns of adaptation in large experimentally evolved populations. Inference of selection signatures from time-series data. Long-term dynamics of local Drosophila populations. Speciation from standing genetic variation. Studying the evolution of gene expression with single cell RNA-Seq.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by June 04, 2023 will be considered. Two letters of recommendation need to be sent directly by the referees.

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

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at Dr. Julia Hosp

Vienna Graduate School of Population Genetics Coordinator

www.popgen-vienna.at <https://twitter.com/PopGenViennaPhD> c/o Institut für Mathematik,

Universität Wien & Institut für Populationsgenetik,
Veterinärmedizinische Universität Wien

T +43 1 25077 4302

Julia Hosp <Julia.Hosp@vetmeduni.ac.at>

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ing@mcmaster.ca)

VirginiaTechU UrbanEvolution

Virginia Tech: Graduate student positions

MS or Ph.D positions available in urban evolutionary entomology:

I am currently accepting applications for graduate positions within the Urban Entomology Research Lab at The Virginia Polytechnic Institute and State University (Virginia Tech). Here, we use genomic tools to understand how organisms adapt and/or evolve in urban environments. Primarily, we use Cimicid insects (bed bugs) as a model system due to the ease of laboratory rearing, availability of samples, and a haplotype resolved chromosome-level genome recently completed within my lab.

Questions we are particularly interested in addressing include, but are not limited to:

- 1)The evolution of target-site associated insecticide resistance; specifically, understanding the role of standing variation vs. novel mutation.
- 2)The genomics of lineage propagation and failure in a highly inbred system. Specifically, at the genomic level,

do we see characteristics associated with lineages that survive vs. those that fail?

3)How does socio-economic status influence the genetic diversity and spread of indoor urban pest insects at city, regional, national, and international scales?

While we work primarily with cimicid insects, we are interested in all urban pest insects.

Applicants should have a strong background in evolutionary biology, genetics, and have undertaken lab-based research. Skills in bioinformatics are preferred but are not essential. However, these skills must be acquired and developed in the early stages of graduate school.

Positions are available starting in the fall of 2023 or Spring 2024.

Interested students should send an email with a concise (2 pages max.) statement of interest that includes questions you might be interested in working on, your long-term goals/interests, and how you believe you would fit in the lab. Include also a copy of your CV, a list of relevant classes/coursework, and any other relevant experience to Dr. Warren Booth by email (warrenbooth@vt.edu). Reference letters for top candidates will be solicited at a later date. Top candidates will be brought in to visit the university, meet with graduate students and faculty, and tour the campus.

Warren Booth, Ph.D Associate Professor Urban Entomology Research Lab Virginia Polytechnic Institute and State University Department of Entomology (MC0390) Steger Hall (204/215C), 1015 Life Science Cir Blacksburg, VA 24061 Departmental website: <https://www.ento.vt.edu/people/Faculty0/Booth.html> Warren Booth <warrenbooth@vt.edu>

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BGE CIBIO Portugal GenomicsLabTech

1. Association BIOPOLIS is opening a call for one Laboratory Technician position (Reference BIOPOLIS 2023-29), in the framework of the project Biodiversity Genomics Europe (BGE; Grant Agreement - project 101059492). BGE is a Horizon Europe collaborative project funded through the Horizon Europe programme that aims to accelerate the use of genomic data for biodiversity genomics endeavours across Europe. The consortium consists of 33 partners, with an overall budget of 21M€, and a duration of 42 months. The successful candidate will develop laboratory work in the fields of molecular biology, carrying out tasks related to the processing of biological samples, genomic library preparation, barcoding, metabarcoding and associated work.

The contracting institution, Association BIOPOLIS, is a private, non-profit organization, which was created in the scope of the project “BIOPOLIS - Teaming to Upgrade Excellence in Environmental Biology, Ecosystem Research, and AgroBiodiversity” (2019-2027), with direct EC funding of 15 M€ and a similar amount by CCDR Norte. BIOPOLIS aims to support the upgrade of the research unit CIBIO - Research Centre in Biodiversity and Genetic Resources to a Centre of Excellence in Environmental Biology, Ecosystem Research, and AgroBiodiversity, through a teaming with a leading scientific institution, the University of Montpellier (France), and with the participation of a business partner, the Porto Business School (PBS - University of Porto, Portugal). CIBIO conducts world-class research in the fields of biodiversity and evolution, hosting more than 30 research groups, which include nearly 200 researchers, and over 100 MSc and PhD students, from across the world. The Centre has state-of-the-art ecology and molecular laboratories and conducts research projects on a global

scale, offering great opportunities for multidisciplinary research. Association BIOPOLIS is an inclusive, equal opportunity employer, offering attractive conditions and benefits.

The Laboratory Technician will be responsible for manipulating and conducting molecular analyses planned within this project. The work plan will involve:

- a. Biological Sample processing and organization.
 - b. DNA extraction and quantification from pollinator insects and mammalian samples, and possibly other source material;
 - c. Preparation of different library types for Whole-Genome Sequencing and Metabarcoding.
 - d. PCR and Sequencing.
 - e. Collaboration in writing technical reports and scientific publications.
2. Applications can be submitted by candidates of any nationality holding a Bachelor (BSc) or a master degree (MSc) in Biological Sciences or equivalent areas.
3. Skills and competences required:
- i) Experience in laboratory procedures of molecular biology (DNA extraction, amplification, and sequencing)
 - ii) Experience in the preparation of different library types for Next Generation Sequencing (DNA PCR free, DNA PCR based, Metabarcoding);
 - iii) Experience in genetics and genomics laboratory procedures;

The candidate should be able to work well within a team and have excellent English and communication skills. Furthermore, the candidate is expected to have strong troubleshooting and problem-solving skills.

4. Application formalization:

4.1 The applications are formalized at the electronic address <http://www.cibio.pt>. The following documents are required in a digital form (PDF format):

- i) Curriculum vitae;

ii) Motivation Letter (including a brief description of research experience and why the candidate is suitable for the announced position);

iii) Qualification Certificates;

iv) Other relevant documentation

4.2. The application period is from 5th May until 26th May 2023.

Expected starting date: 1st July 2023.

Complete description of the job offer: <https://www.euraxess.pt/jobs/103145> For queries, please contact João Pimenta: jpimenta@cibio.up.pt

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Brigham Young U DNA Sequencing Center Manager

Job Title: DNASC Manager, Biology

Job Classification: CFS Professional

Posting close date: May 31, 2023

Start date of this position: July 1, 2023

Required Degree: PhD preferred and/or MS required

Application: https://hrms.byu.edu/-psp/ps/EMPLOYEE/HRMS/c/-HRS_HRAM_EMP.HRS_APP_SCHJOB.GBL?Page=-HRS_APP_JBPST&Action=U&FOCUS=-Employee&SiteId=70&JobOpeningId=122982&PostingSeq=1

Experience: The Department of Biology at Brigham Young University seeks to fill a full-time manager of the BYU DNA Sequencing Center. Applicants with a PhD, post-doctoral experience, and demonstrated expertise in nucleic acid sequencing are encouraged to apply. Applications will also be considered from persons with a MS degree and extensive lab and/or managerial experience in nucleic acid sequencing and analysis.

Duties/Expectations: We seek a colleague who has demonstrated expertise in nucleic acid sequencing technologies to manage the Life Sciences DNA Sequencing Center (<https://biology.byu.edu/dnasc>). This professional faculty, continuing faculty status track (BYU's equivalent to tenure) position has a 70% Administrative and 30% Teaching expectation. We anticipate that the teaching responsibilities will include 1-2 didactic

courses per year and substantial lab-related mentoring of undergraduate and graduate students. The successful applicant will oversee sequencing services, currently including custom PacBio sequencing on Revio and Sequel II instruments, and ABI 3730xl sequencing and fragment analysis. Maintaining expertise with rapidly developing technologies is expected. The candidate will train, supervise and mentor part-time technical staff, including undergraduate students, and provide consultative expertise to life sciences faculty in experimental design, sample preparation, library construction, cost estimates/budgeting, sequencing platform and read depth. Bioinformatics skills sufficient for initiating downstream analyses are also expected. As a department matriculating increasingly diverse students, we encourage applications from women, minorities, and individuals committed to mentoring under-represented demographics in the biological sciences. Teaching responsibilities may include upper division undergraduate and graduate courses in experimental design and analysis of sequencing applications that complement existing research programs in the College of Life Sciences.

Information required at the time of application - Applicants should attach a cover letter describing their professional and academic preparation, and their experience with DNA sequencing technologies and applications. Applicants should also attach a current CV, and a separate statement of management and teaching philosophy. Applicants' statements should detail how their supervisory mentoring experience aligns with the BYU Aims and Mission statements, and can support the success of students from racial, ethnic, and gender backgrounds that are underrepresented in the life sciences. Applicants who have not yet had the opportunity for such experience should note how their work will further the College of Life Sciences and Brigham Young University's commitment to equity and belonging.

Please list the contact information for three recommenders on the faculty application. They may be contacted and required to submit their letters of reference electronically at some point during the selection process.

Document(s) required at the time of application - Please attach your Mission Alignment Statement (full-time faculty only), updated Curriculum Vitae, cover letter to the faculty application, and management and teaching philosophy document.

Questions may be directed to: Dr. Byron J. Adams, DNASC Faculty Search 4102 LSB BYU-Department of Biology Provo, UT 84602, USA (Byron_Adams@byu.edu).

Mission Alignment Statement: BYU is committed to hiring faculty members who enthusiastically embrace

and energetically advance its unique mission. To this end, please include a one-page mission alignment statement as part of your application that addresses how you might, as a BYU faculty member: (1) live a life of loyalty to Jesus Christ and His restored Church and align yourself with doctrines and teachings declared by living prophets, seers, and revelators; (2) demonstrate intentionality in building faith in Jesus Christ and testimony of His restored gospel among students and others in the BYU community; and (3) teach your subject matter with the Spirit of God and strive to keep it “bathed in the light and color of the restored gospel” (Spencer W. Kimball).

Applicants who are not members of The Church of Jesus Christ of Latter-day Saints include a one-page mission alignment statement

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CaliforniaAcademySci LabTech ComparativeGenomics

The Center for Comparative Genomics at the California Academy of Sciences is hiring a Senior Lab Technician. This is a very exciting position that is critical to the biodiversity genomic research we do at CAS.

For details of the position and to apply, please see: <https://californiaacademyofsciences.applytojob.com/-apply/awcUunTO87/Senior-Lab-T> About the Opportunity Under the supervision of the Director of the Center for Comparative Genomics, the Senior Laboratory Technician will: 1) manage the operation and general maintenance of the Center for Comparative Genomics, its activities and related equipment; 2) serve as CCG HAZMAT and Health & Safety monitor; 3) support the training of users of the core molecular laboratory; and 4) manage the Accounting and billing of the CCG Lab. We would like to fill the position as soon as possible (ideally in June), but flexible for a later start date.

Responsibilities In this role you will be required to collaborate with Academy researchers and oversee the daily function of the CCG. General expectations and outline of duties are listed below. Reasonable accommodations

may be made to enable persons with disabilities to perform the essential functions.

LAB MAINTENANCE - Prepare aliquots of reagents and stock solutions for general lab use - Stock lab consumables and maintain/track inventory (tubes, tips, etc.) for general lab use - Assist with operation maintenance of lab equipment - Assist with training students, visitors, and staff in molecular techniques - Trains new staff, students, and visitors when Director is unavailable - Assist with new user orientation - Handle HAZMAT Monitor duties for the CCG under supervision of the Director - Handle Health & Safety Monitor duties for the CCG under supervision of the Director - Takes on responsibilities if Lab Manager or Director is unavailable and is required to

MOLECULAR WORK - DNA and RNA extraction - Library preparation (Sanger, NGS etc.) - Assist with data collection for grant deliverables as needed and under supervision of the Director

COMPUTER WORK - Mange accounting and billing of the CCG lab records and check accounting reports - Order new consumables, supplies, equipment, and sequencing requests as needed with Director’s approval and supervision - Bill lab users (in-house, out-of-house, and visiting researchers) for reagents and consumables under supervision of the Director - Maintain database to manage and oversee purchasing - Oversee administrative duties for the Department, including preparing and maintaining financial records, reserving rooms as needed for workshops and presentations, answering online inquiries about the lab and volunteer/intern opportunities

COLLECTION WORK - Assist with chemical inventory, frozen and refrigerated DNA collections - Assist with database management and data submission to public databases (GenBank, etc.) - Assist with collection duties as needed - cryogenic collections and database management

Qualifications The qualifications listed below are representative of the knowledge, skill, and/or ability required or preferred.

EXPERIENCE: - Bachelor’s degree in biological sciences or equivalent, Master’s preferred - Minimum two years’ experience in Sanger and/or NGS laboratory protocols is highly preferred. - Experience in second and third-generation sequencing techniques and protocols preferred - Able to work independently with minimal supervision/training on specific techniques - Experience working with museum or research specimens preferred - Excellent verbal and written communication skills (English) and a strong background in science communication with diverse audiences’

KNOWLEDGE, SKILLS AND ABILITIES: - Strong interest in biodiversity and ability to communicate that passion - Good communication and organizational skills - Ability to perform standard PCR and DNA sequencing lab work - Familiarity with second and third generation sequencing techniques - Ability to write routine reports and correspondence, perform repetitive work, and demonstrate attention to detail - Experience using relevant DNA analysis programs, Google Suite, and MS Office - Ability to read and interpret documents such as safety rules, operating and maintenance instructions, and procedure manuals

- Committed to working on a team that is striving to be anti-racist in work, interactions, systems, and tools
- Ability to work independently and as a member of interdisciplinary teams on cross-cutting issues

Compensation and Benefits Hourly hiring range: \$30.00-\$32.00 per hour. Hourly rate will vary based on experience and relevant skills/knowledge set. The Academy offers a total compensation package that emphasizes both base salary and comprehensive benefits.

Schedule: Full-Time, 40 hours per week.

APPLICATION DEADLINE:

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George Washington U LabTech Evolutionary Biology

The Zhang Lab at the George Washington University is planning to hire a lab technician to work on host plant adaptation, speciation, and multi-trophic level interactions among herbivore insects. This position will include coordinating and carrying out field work, molecular experiment, general lab maintenance and administrative tasks, and data management & analysis. This position also provide opportunities to conduct independent research projects. Zhang lab addresses fundamental questions in adaptation and speciation, including the cause and maintenance of phenotypic, behavioral, and genomic divergence across the speciation spectrum. We apply interdisciplinary approaches including field surveys, natural history, behavior observation, manipulative experiments, simulations, and genomic techniques.

- Field work include: driving across the country to collect gall forming insects and their associated host plants.

- Lab activities include: plant and insect maintenance and care, phenotypic measurement of galls and galling insects, DNA and RNA sample preparation.

- Experiment and data management duties include, 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.

- General laboratory duties include ordering and restocking supplies, organizing the lab, ensuring laboratory compliance for lab safety

- Research team duties include, providing assistance and training for incoming trainees, coordination of projects involving collaboration between lab members, participation in lab and research meetings.

- Other job duties and tasks as assigned.

*To apply for the job, use the link below: * <https://www.gwu.jobs/hr/postings/102524> Linyi Zhang <linyizhangecnu@gmail.com>

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Holden Arboretum Ohio LabTech Plant Microbe Symbiosis

Plant-Microbiome Symbiosis Research Specialist

Position Title: Research Specialist Institution: Holden Forests and Gardens Department/Division: Research City: Kirtland, Ohio, United States of America

General Information: The Science & Conservation: Research department at Holden Forests & Gardens (HF&G) is looking for a Research Specialist to join the Evolutionary Ecology team. The team is interested in the ecological and evolutionary mechanisms that influence plant adaptation to rapid environmental change, through the lenses of ecology, genomics, and microbiome. The team is currently funded by National Science Foundation and state grants.

The Research Specialist will contribute to a project on plant-microbiome symbiosis that leverages robotic and phenotyping platforms to advance our understanding of the rules that govern microbe-microbe and microbe-plant interactions under changing climates. The Re-

search Specialist will conduct field sampling, maintain cultures of plants and microbes, perform manipulative experiments and microbiome sequencing, and prepare scientific results for presentation and publication. The Research Specialist will have opportunities to travel to collaborators' labs, perform outreach, mentor undergraduate and high school students, and present at meetings and conferences.

We are looking for a motivated member who is curious to understand how symbiosis works, passionate to work at the interface of plant biology, ecology, evolution, microbiology, computer science, statistics, and environmental science, dedicated to share findings with communities, and willing to do meaningful work in an organization that values diversity of thoughts and perspectives. Holden Forests & Gardens connects people with the wonder, beauty and value of trees and plants, to inspire action for healthy communities. HF&G strives for a welcoming workplace where everyone feels that they belong.

Position Details: - Non-Exempt Position - 32-40 hours a week flexible - Starting date flexible but preferably August 1, 2023 - Salary commensurate with candidate's qualifications - One year appointment at minimum with reappointment contingent upon satisfaction of performance

Key Responsibilities: - Manages and executes field work such as sampling plants and microbes across states - Manages and executes laboratory work such as microbial culturing and assays, maintaining cultures of plants and microbes, DNA/RNA extraction, PCR, genomic sequencing, and growth chamber experiments - Leads data management and protocol creation for research projects - Assists in experimental data analyses, preparation for publication in scientific journals, and presentation to agencies or the public - Practices generally accepted ethical standards in research and scholarship - Assists and mentors interns, students, volunteers with data collection, independent projects, and other coursework as needed - Performs K-12 STEM outreach - Contributes to internal and external publications for Holden Forests & Gardens - Collaborates with various cross-departmental initiatives at Holden Forests & Gardens

Qualifications and Skills: - A bachelor's degree in biology, ecology, evolution, genetics, microbiology, molecular biology, or related field, required - Master of Science or higher, preferred - Experience with field work, preferred - Experience with laboratory work including but not limited to microbial culturing and assays, aseptic techniques, DNA/RNA extraction, and PCR, required - Experience with data management prac-

tices - Using Microsoft 365, Dropbox, OneDrive, and Google Drive, required - Experience with statistical data analyses - Using R, programming, bioinformatics, or related skills, preferred - Experience with scientific writing, preferred - A valid Driver's License and acceptable driving record, required

Application Instructions (submission methods, etc.): Holden Forests & Gardens values an authentic sense of belonging at all levels of the organization, including staff, volunteers, Board of Directors, and visitors. HF&G believes that working toward an equitable culture that values all perspectives enriches the work environment, helping achieve our goal to build a greener and healthier Northeast Ohio. We are working to create and sustain a supportive environment and sense of belonging for people of all backgrounds. HF&G also provides regular DEAI training for staff, managers, volunteers and Board to create a welcoming and accessible environment.

Research shows that women and individuals from underrepresented backgrounds often apply to jobs only if they meet 100% of the qualifications. We recognize that it is highly unlikely that an applicant meets 100% of the qualifications for a given role. Therefore, if much of this job describes you, then you are highly encouraged to apply for this

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KU Leuven EcolBiodivSustdev

Assistant/Associate Professor in Ecology, BIODIVERSITY and/OR SUSTAINABLE DEVELOPMENT at KU Leuven, Belgium

The Division 'Ecology, Evolution and Biodiversity Conservation' at the Department of Biology at the KU Leuven (Belgium) is scouting candidates for a faculty position in Ecology, Biodiversity and/or Sustainable development starting 1 October 2024. Current position is linked to the Division's research theme on global change ecology, where we study responses to human-induced environmental change.

We encourage applications by outstanding candidates with a research program at the intersection of Ecology,

Biodiversity and/or Sustainable development which addresses fundamental research topics with a focus on aquatic environments. We especially want to encourage female candidates to apply. The successful candidate will be expected to build her/his own independent research group and further integrate and strengthen collaborations across research groups within the Division. The new faculty member will also gradually have responsibility for part of the teaching in ecology, biodiversity and/or sustainable development.

After a pre-selection step by the Division, the successful candidate will be expected to continue a competitive selection procedure at the university level (hence across disciplines) for one of the two 'BOFZAP' categories of research professorships: junior BOFZAP for a researcher with high research potential proven by internationally recognized scientific publications, or Senior BOFZAP for a highly internationally recognized researcher in the field. Key selection criteria for BOFZAP positions is excellence in research reflected in both the scientific achievements (publications at the highest scientific level in top 5% journals of her/his research field), and the research plan for the next five years. We aim for candidates with a research profile at the level of successful ERC applicants. Candidates are expected to teach students at all academic levels, including supervision of PhD students and postdocs. Candidates will be appointed in an academic staff position (ZAP) with a rank depending on the candidate's qualifications. BOFZAP researchers receive a BOF start-up grant < https://www.kuleuven.be/-onderzoek/gedocumenteerd/index_en.html#details/-ac6a8115c765a8699ea4db628cd50a1dd0f61bed > of 100,000 euro. In addition, the department of Biology provides a PhD fellowship of 4 years.

Information about the Division 'Ecology, Evolution and Biodiversity Conservation' can be found at <https://bio.kuleuven.be/research>. KU Leuven is a research-intensive, internationally oriented university that was elected Europe's most innovative university by Reuters and consistently ranks and features in Europe's top-15 universities within the Times Higher Education ranking < <https://www.timeshighereducation.com/world-university-rankings/ku-leuven#ranking-dataset/-589595> >. Leuven is a historic, dynamic and lively city located in the heart of Belgium, within 20 minutes from Brussels, the capital of the European Union, and less than two hours from Paris, London and Amsterdam.

For the pre-selection step by the Division please submit a motivation letter (max. 1 page), short CV (max. 2 pages, including orcid), a scientific achievements track-record (max. 2 pages) including a list of five most important publications, and a first outline of a research

plan for the coming 5 years (max. 2 pages). Please refer to potential collaborations within the Division in your research plan.

Questions can be directed to the Head of the Division, Professor Robby Stoks (robby.stoks@kuleuven.be). The application must be sent as a single PDF by email to Conny.coeckelberghs@kuleuven.be with as subject 'BOFZAP faculty position'. The closing date for applications is June 16th 2023.

Robby Stoks <robby.stoks@kuleuven.be>

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Leiden Biodiversity Systematics

Naturalis Biodiversity Center in Leiden is the Dutch national research institute for biodiversity and systematics. With our collection of 43 million specimens, one of the world's largest natural history collections, and our state-of-the-art research facilities we offer the (inter)national research infrastructure for species, identification and monitoring (for example in ARISE and DiSSCo). We closely collaborate with many Dutch universities, research institutes, industry, and government. We host over 120 researchers including 16 academia embedded professors and 50 PhD students. We present the history of our planet, and the diversity of life on Earth, through permanent and temporary museum exhibitions, educational programmes, and online presence, with more than 400,000 visitors per year. All in all, a unique combination of science and culture in the Netherlands and elsewhere in the world!

Naturalis is looking for a Group Leader for the research group Tropical Botany 32-36 hours a week

About us

Biodiversity drives the fundamental ecosystem processes that we depend on. Biodiversity is a multidisciplinary and multi stakeholder topic. So we do not cover all biodiversity research ourselves. Naturalis is about species. About discovering and identifying species. About the evolution, the interaction and monitoring of species. We combine our knowledge of species with promising novel technologies such as metagenomics, artificial intelligence, data science and 3D imaging.

We aim to accelerate the discovery of species and their interactions in ecosystems. For this, we create exciting

new multidisciplinary lines of research and we train scientists, students and experts to become world-leading in this new frontier of research.

Ever since the 16th century, taxonomists have been naming and describing the plants, animals, fungi and microorganisms that share our planet today and in the past. Although about 2 million species are now known, research suggests there are at least 10 and probably more than 20 million species on Earth, meaning that 80-90% of our world's biodiversity is still undiscovered! At the same time, we are witnessing alarming biodiversity declines. Reports indicate that 1 million species are currently threatened with extinction. It is increasingly recognized that biodiversity loss is one of the most significant threats to the environment and to our ability to transition to a sustainable future. These circumstances call for transformational scientific progress and serious action. We believe that we, as Naturalis, can play an important role in this transformation by:

Fostering excellence in science and innovation in the field of biology and earth sciences

Training scientists, students and experts to provide sustainable capacity building in the field of taxonomy

Providing a vibrant scientific environment for early-stage and mid-career researchers and foster their academic career

Providing and maintaining a sustainable state-of-the-art (inter)national research infrastructure

Further supporting and strengthening the national research community in the field of biology

Further developing an extensive (inter)national network that connects academia, society, government, industry and the general public

Extending our outreach to the general public by not only focussing on our visitors, but also by engaging with new audiences outside the museum, and by using citizen science

Expanding our role in Dutch national science policy by calling for an ambitious biodiversity strategy in societal and political agendas.

Find out more about our research, labs and collection.

Position The research group Tropical Botany focuses on describing species, understanding their distributions, evolutionary and ecological relationships and recognizing their role in human societies in the tropics. The group consists of 7 (senior) researchers, 2 postdoctoral fellows, 8 PhD students and 9 guest researchers and several students.

We are seeking an enthusiastic, ambitious, innovative

senior scientist to fulfill the role of Groupleader for the research group Tropical Botany. A strong representative within and outside Naturalis with a worldwide (scientific) botanical network (incl. herbaria). An inspiring and stimulating leader and team player with a clear (long term) vision. An excellent experienced senior researcher with a strong scientific background in taxonomy/ systematics in Southeast Asia, who brings innovative technologies to improve taxonomy (e.g. phylogeny and state-of-the-art techniques such as DNA, image recognition, infrared scanning) and has field work experience. We are looking for someone with experience in teaching and fundraising, who can attract PhD students and Postdoctoral Fellows and is able to train them. Someone who values the importance of our collections.

The concrete assignment for this group leader is to strengthen and renew the research field of tropical botany and taxonomy within Naturalis,

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MaxPlanckInst Leipzig LabManager

The Max Planck Institute for Evolutionary Anthropology unites scientists with various backgrounds (natural sciences and humanities) whose aim is to investigate the history of humankind from an interdisciplinary perspective with the help of comparative analyses of genes, cultures, cognitive abilities, languages and social systems of past and present human populations as well as those of primates closely related to human beings.

We are looking for an experienced lab manager (f/m/d, full-time or part-time) to support wet lab research and wet lab-field site coordination in the Department of Primate Behavior and Evolution.

YOUR TASKS. You will support the scientific staff of the Department in tasks related to wet lab management and data generation. The labs in the Department of Primate Behavior and Evolution encompass work in molecular ecology, functional genomics, and cell culture-based experimentation, both in Leipzig and in the field. The lab manager will help coordinate activities, space use, and equipment across these groups; contribute to molecular genetic/genomic data generation; help orga-

nize experimental and lab safety protocols; and manage sample archiving and tracking, including contributing to biological sample permitting, import, and export. You will report directly to department Director Professor Jenny Tung. You will also contribute significantly to departmental lab organization and purchasing for work in Leipzig and at departmental field sites, and may support student training in molecular techniques.

YOUR PROFILE. We expect a committed, collaborative, and detail-oriented person who enjoys providing expert support for scientific projects and takes the lead within a collaborative team of technicians and PIs. Duties include learning and executing new lab techniques, managing extensive sample archives, and coordinating research activities between the field and the lab. The ideal candidate will have previous wet lab management experience and experience with DNA and RNA extraction, high-throughput sequencing library preparation and other molecular genetic techniques, mammalian cell culture, and development and optimization of wet lab protocols. The ideal candidate will also have experience coordinating complex sample shipments, managing lab supply, equipment, and biological sample inventories, and monitoring lab safety requirements and compliance.

We require a completed university education (B.Sc., B.A., M.Sc., M.A.), or demonstration of comparable training and corresponding professional experience and skills. In addition, we require you to be fully conversant with the MS Office package, have excellent written and spoken mastery of English, and have strong communication skills. Other important traits include the ability to work independently, the ability to multi-task, and a strong work ethic in a fast-paced environment. Attention to detail and careful record keeping are essential.

OUR OFFER. We offer a stimulating job in a young, scientifically oriented international team. The Max Planck Society offers its employees a comprehensive training program and social benefits in accordance with the regulations of the public service.

The position is available from June 2023, though an earlier or later start may be negotiated. The position is initially limited to 2 years. Following that, a permanent contract is possible, subject to a successful review. The position is funded according to the collective agreement of the public service (TVi_ü¹/₂D Bund). **YOUR APPLICATION.** Please apply online at <https://recruitingapp-5112.de.umantis.com/-Vacancies/567/Application/New/2>. Only complete submissions via this link will be taken into consideration. The Max Planck Society is committed to employing individuals with disabilities and especially encourages them to apply. Additionally, we seek to increase diversity of

our workforce in areas where it is underrepresented and therefore explicitly encourage women and members of underrepresented groups to apply. For queries, please contact: primevo_sec@eva.mpg.de

Susann Walters

Department Administrator Primate Behavior and Evolution

Max Planck Institute for Evolutionary Anthropology

Deutscher Platz 6

04103 Leipzig Germany

Phone +49 341 3550-200

susann_walters@eva.mpg.de

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Potsdam Germany ResAssoc AnimalBehaviouralEvolution

The University of Potsdam is seeking to fill the following position by October 1st 2023:

Research Associate (m/f/d) (salary 13 TV-L)

Animal Ecology/Behavioural Ecology The animal ecology group lead by Jana Eccard works on the connection of individual difference in behavior with ecology, interspecific interactions, biological invasion processes, adaptation to urban environments, to predation risk, and on reproductive behaviour, mainly on wild small mammals (but also insects). Facilities include a behavioural lab, large scale outdoor enclosures, field equipment including automated telemetry, technical support and an international team.

The candidate is expected to conduct research complementing our profile. We expect a strong publication record, the continuation of publishing, the potential to acquire research grants, an interest in joined research, enjoyment of teaching and supervision, and an affinity to experimental work and advanced statistics. Candidate should be able to work both independently and as part of a team. Research topics with native small mammals as model organisms due to existing infrastructure is favourable. Teaching language is English on the master level, knowledge of German is advantageous for teaching and dealing with administration.

Candidates hold an excellent doctoral degree in the

field of animal/behavioralecology /behavioural ecology. Teaching requirements include 4 semester hours (SWS) in the study program Biowissenschaften or Master Ecology, Evolution and Conservation (MEEC).

This is a temporary position limited to 3+3 years in accordance with Section 2 subsection 1 of the Academic Fixed-Term Contract Law (WissZeitVG). The position is suited for qualification on the habilitation level. The contract will be issued for an initial period of three years. After positive evaluation and the fulfilment of the legal requirements, the position can be extended for a maximum of another three years. We are looking forward to receiving your application including a motivation letter, a research, CV, links to relevant publications, account of teaching experience, and certificates and the contact details of 2 referees. Please send this all in one PDF until 1. Juli 2023 to eccard@uni-potsdam.de use "Research Associate" as subject line

Jana Eccard <eccard@uni-potsdam.de>

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QatarU ResAssoc PDF MarineGenomics

Marine Genomics Research Associate Job Offer

Job Title: Research Associate or Postdoctoral Location: Qatar University, Doha, QATAR Department Name: Biological and Environmental Sciences College/Department Profile: College of Arts and Sciences, Qatar University, Qatar

Background and Role:

Qatar University is seeking a highly motivated candidate with a background in Molecular Ecology, Population Genetics and preferentially Marine Biology with emphasis on Fish and/or Coral communities. The position is for a Research Associate or Postdoctoral Researcher (commensurate to previous experience and expertise), funded by a 3-year project (QNRF-NPRP and TotalEnergies), dealing with connectivity and genetic diversity and flow in coral and artificial reefs. The candidate is also expected to collaborate with the other members of the research team in developing these lines of research in the framework of related projects and supporting (under)graduate students. The position will involve maintaining several national and international collaborations (e.g. University of Copenhagen, California State

University, the National Biotechnology Centre and other industrial and governmental stakeholders).

The Marine Restoration and Conservation Research Group (MARESCO) recently started carrying out genomic projects in the Persian/Arabian Gulf focusing on both model and non-model species, such as corals, bony fishes and whale sharks. The Gulf is unique marine environment, where summer sea temperatures is often 34 °C, though it remains relatively unstudied.

Qatar University Profile: Qatar University is the national institution of higher education in Qatar. It provides high quality undergraduate and graduate programs that prepare competent graduates, destined to shape the future of Qatar. The university community has diverse and multicultural committed faculty that teaches and conduct research, which addresses relevant local and regional challenges, advances knowledge, and contributes actively to the needs and aspirations of society. Qatar University is a leading research institution in the Middle East (QS World University Rankings 2023: #208), with 18 interdisciplinary research centers, over 133 research collaborations with leading institutions across the world.

Duties & Responsibilities The candidate will be mainly responsible for the following duties: 1. DNA extraction from corals and other marine habitats associated fauna for Genotyping by sequencing (GBS) 2. Connectivity: Combine Isolation-by-Distance and effective density to estimate dispersal scales in both coral and bony fish. 3. Whale shark population structure: Every summer Qatari waters receive the world's largest whale shark aggregation to feed on tuna eggs. We want to use high throughput sequencing to investigate the population structure of both whale sharks and tunas.

And potentially collaborate in the following tasks:

- Collection and processing of samples for environmental DNA (eDNA) - Collaborating with external and international partners for the execution of collaborative research tasks - Contribute to project management activities, such as progress reports. - Participate in the publication of research results in peer-reviewed journals - Support students' supervision inserted in the MARESCO group - Participation in field survey of coral and artificial reefs habitats

Qualification & Experience Requirements - PhD (desirable) or MSc (with proven experience) in Molecular ecology and genomics or related field from a recognized University. - Extraction, purification and amplification of DNA from (marine) organisms and preparation of DNA samples for sequencing and genotyping - Background in population genetic data analysis - Phylogenetic and genetic diversity analyses - Bioinformatics

pipelines and downstream genomics analyses of RAD sequencing (Experience in analyzing RAD-seq data using command line programs) - Genomics analyses include F-statistic, Admixture, Principal component analysis ??? PCA and Isolation by Distance - IBD - A strong record of relevant research experience backed by relevant research publications - Fluent in English - Ability to work effectively in a multi-cultural environment. Optional: - Scientific diving (highly valued) - Previous research experience in coral and/or fishes genomics are desirable.

Salary and Benefits - A one-year renewable contract (up to 3 years). - Highly competitive and Tax-free salary. - Housing, transport and children education allowances in accordance with QU HR policies. - Annual round trip air tickets, in accordance with QU HR policies (for candidate, spouse and children). - Private health care and health insurance in accordance with QU HR policies (for candidate, spouse and children). - Annual leave of 35 days.

Documents required to Apply Interested candidates should submit by email to Dr. Radhouane Ben Hamadou (benhamadou@qu.edu.qa):

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St Andrews Scotland Genetic Breeding Manager

Job Title: Breeding Programme Project Manager (aquaculture genetics) Location: Xelect, St Andrews, Scotland

Background and role:

Xelect is a leading aquaculture genetics services provider, based in St Andrews, Scotland. After a sustained period of rapid growth we are looking to recruit an additional Project Manager to join our growing team of aquaculture breeding programme managers. Our Breeding Programme Project Managers are experienced aquaculture professionals who are responsible for developing, and managing genetics-backed breeding programmes and carrying out consultancy for our global portfolio of customers.

With the support of our highly experienced laboratory, bioinformatics and genetics teams you will:

- Co-ordinate the design of new programmes and communicate them to our customers - Manage the day-to-day running of our programmes, co-ordinating our internal resources whilst acting as a virtual member of our customers' team - Ensure that programmes are well managed, run efficiently and are delivered on budget and on time - Prepare annual reports and other briefings for customers, demonstrating performance against their commercial objectives - Proactively identify opportunities for improving our service and efficiency - Travel to support our customers on site at key times, providing practical support to implement their breeding programme - Report to the Head of Project Management

Essential skills:

- A minimum of a MSc relating to aquaculture, quantitative genetics, fish reproduction or animal breeding - Excellent written and spoken English - Knowledge and experience of hatchery and broodstock management, including aquaculture operations more widely for finfish and / or shellfish species - Experience working within the aquaculture industry - Excellent data management and computer literacy skills - Willing to travel and experience working in other countries - Basic knowledge of statistics and programming platforms.

Desirable skills:

- PhD relating to aquaculture, fish reproduction or animal breeding - Proficiency with programming platforms R and / or Linux - Advanced statistical skills including multivariate analysis - Proficiency in other languages - Peer reviewed publications in the field of aquaculture, reproduction or genetics.

Salary and Location: Salary ??36,000 - ??47,000 per year. We currently operate a ???hybrid??? working pattern, combining office days and working from home. The position will be based in St Andrews, Scotland.

About Xelect:

Xelect is a leading aquaculture genetics service provider with a global portfolio of clients, including some of the biggest names in the industry. We employ a team of 17 staff, including a multidisciplinary technical team with 13 PhDs in aquaculture, quantitative genetics, bioinformatics, molecular biology and physiology. There are three business streams: breeding programme management, BioAudit & due diligence services and laboratory services. The business has its headquarters in the medieval university town of St Andrews on the East coast of Scotland some 80 km from Edinburgh airport. The company occupies modern office and laboratory facilities

with 2 Illumina DNA sequencing machines. Breeding programme management is the largest business segment contributing 80% of revenues from customers in 20 countries dealing with 19 species of fish, shrimp and oysters.

The company has developed sophisticated industry-leading genetic and bioinformatic analysis pipelines including advanced mate selection software. The breeding service involves strategic partnerships with customers on rolling long-term contracts with a high level of project management support delivered from the UK and through customer visits. Revenues are in excess of £2million/year and are growing at around 30% per annum. The company is profitable with good levels of cash flow. The shareholders in decreasing order of holding are Genus plc, Prof. Ian Johnston FRSE (current CEO and co-founder), the University of St Andrews, Dr Tom Ashton (Operations Director and co-founder) and the EOS Technology Investment Syndicate.???

Further information:

To apply please send a current CV and a covering letter to hello@xselect.co.uk, along with contact details of two referees. References will only be contacted after a successful interview. If you would like to make any enquiries about the role please email hello@xselect.co.uk. Closing date 9th June.

Rachael Wilbourn <rachael.wilbourn@xselect.co.uk>

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UBath UK EvolutionCentre Director

Director of the Milner Centre for Evolution (MCE)

KH10561 Director of the Milner Centre - Jobs at Bath
bath.ac.uk

We are looking for a new Director to continue and expand the work of the MCE, specifically to provide leadership and vision for the Milner Centre for Evolution. You will be appointed to the position of professor within the Department of Life Sciences and will take on the role of Director of the Milner Centre.

About the Role:

Reporting to the Head of Department of Life Sciences, the Director will be tasked with enabling its members to continue to achieve excellence in all aspects of our remit,

including world-class fundamental and applied evolution research and outreach activities. You will develop and enhance the relationships with our funders and other stakeholders that made the Centre possible, and to seek further support for the members of the Centre. You will work with other members of the Leadership Team to further the operation and strategic development objectives of the Department of Life Sciences, The Faculty of Science, and University at large.

About you:

We are seeking a professor with an elite research program in evolutionary biology, in addition to a high-profile record of outreach and public engagement. The successful candidate will have a record of excellence in research and leadership, proven track record in science communication and outreach, and the academic and interpersonal skills needed to drive the strategic direction of the core objectives of the Centre.

You will lead the strategic goals of the department which are:

to deliver outstanding research and develop our current excellent reputation, to deliver innovative and effective evolution research programmes to produce influential post graduates with excellent career prospects, to expand our capacity and capability by investment in new infrastructure, facilities and people, to foster a positive, balanced and enthusiastic working culture with a sense of common purpose, to enhance the impact of research and knowledge through increasing our industry-facing and engagement activity and to become the hub for evolutionary research and engagement.

Your application:

Please ensure you attach a CV and covering letter to your application.

For an informal discussion about the position, please feel free to contact: Duncan Craig, Dean, Faculty of Science, dqmc21@bath.ac.uk, or Philip Ingham FRS, Head of Department of Life Sciences, pwi20@bath.ac.uk.

What we can offer you:

a very generous employer contributory pension scheme generous annual leave allowance with an additional 5 discretionary days so that you can enjoy a positive work life balance we are a family-friendly University and with an increasingly agile workforce, are open to flexible working arrangements an excellent reward package that recognises the talents of our diverse work force a wide range of personal and professional development opportunities a number of support options available for new and existing staff to help with the cost of some immigration expenses which you may be eligible for: Relocation

allowance, Visa Reimbursement, Interest-Free Loan.

We aim to be an inclusive university, where difference is celebrated, respected and encouraged. We have an excellent international reputation with staff from over 60 different nations and have made a positive commitment towards gender equality and intersectionality receiving a Silver Athena SWAN award. We truly believe that diversity of experience, perspectives, and backgrounds will lead to a better environment for our employees and students, so we encourage applications from all genders, backgrounds, and communities, particularly from under-represented groups, and value the positive impact that will have on our teams.

We are very proud to be an autism friendly university and are an accredited Disability Confident Leader; committed to building disability confidence and supporting disabled staff.

Find out from our staff what makes the University of Bath a great place to work. Follow us@UniofBath and @UniofBathJobs on Twitter for more information.

Email details to a friend

Further details:

JobDescription&PersonSpecificationBrochure

Terms of employment Visa information If you think you may require a visa to work in the UK, you should refer to our guidance on the Skilled Worker Visa before embarking on a job application to ensure you understand the requirements for sponsorship. You may be eligible to work in the UK via other alternative visa routes such as the Global Talent Visa or by having Settlement / Indefinite Leave to Remain ??? please refer to our Staff Immigration web pages for further details.

Update to our application process We are constantly seeking to reduce the unconscious bias that enters any assessment process, with the goal of creating an inclusive and equal assessment process. To support this, personal details will be removed from application forms at the initial shortlisting stage.

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UConnecticut Storrs Program Coordinator Genomic Novelty

The EEB Department at the University of Connecticut is seeking a program coordinator for—a new postbaccalaureate training program in phenotypic and genomic novelty. —This position could be a career stepping stone for a recent PhD or MS—graduate (MS requires at least 1 year of additional experience) who would like a research-adjacent career focused on mentorship of a diverse cohort of new scientists.—This—NSF-funded RaMP program—offers immersive research training, along with professional development and networking opportunities to a cohort of 8-12 trainees annually. —The trainees—are motivated recent college graduates who did not have the opportunity for sufficient research experience as undergraduates. —The program coordinator would have the opportunity to—develop training materials and teach workshops on genomics, bioinformatics and professional development topics, coordinate a cohort project involving genome assembly and—annotation, and provide close mentorship to trainees as they explore career and graduate school opportunities. —The position is in-person at the University of Connecticut, Storrs—campus, beginning this summer.—The application deadline is May 31, 2023.—(Note: submission of a CV rather than a resume is acceptable.)

Useful links:— Full position description and application information: <https://jobs.hr.uconn.edu/en-us/-job/497466/ramp-program-assistantcoordinator-ed-program-assistant-2-or-ed-program-coordinator> UConn RaMP website:—<https://genome-postbac.biology.clas.uconn.edu/> NSF RaMP program information: <https://new.nsf.gov/funding/opportunities/-research-mentoring-postbaccalaureates-biological> I'm happy to answer inquiries about the position.

Elizabeth Jockusch elizabeth.jockusch@uconn.edu Professor & RaMP Program Director Ecology and Evolutionary Biology University of Connecticut, Storrs

“Jockusch, Elizabeth” <elizabeth.jockusch@uconn.edu>

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UCSantaCruz AssistRes GlobalChange

The Global Change Lab in the Department of Ecology and Evolutionary Biology (<https://www.eeb.ucsc.edu/>) at the University of California Santa Cruz (UCSC) invites applications for a Global Change Assistant Researcher. The Researcher will assist with population and historical genomics research, develop and apply bioinformatic pipelines, analyze large datasets with scientific computing, maintain and promote open science practices, help with research group administration, and assist with maintaining a collaborative and supportive research environment for all members.

In the Global Change Lab, we use population genomics and data science to study biodiversity change from genes to communities, locally and around the world. Much of our research is focused on climate change and conservation in coastal marine environments. We offer a dynamic and collaborative work environment, involvement in a wide range of research projects, extensive learning and professional development, and many opportunities for co-authorship on scientific manuscripts. We value a healthy work-life balance and pursue actively inclusive and anti-racist practices.

The work environment will primarily be a population genomics lab on the beautiful Coastal Science Campus at UCSC within a short walk of the ocean and easy access to mountains and open space. The EEB department offers a diverse, exciting, and supportive environment for learning and research and is complemented by colleagues at the Institute for Marine Science, the Coastal Science and Policy Program, NOAA Fisheries, the Center for Coastal Climate Resilience, and others. Fieldwork will be infrequent but may be diverse, remote, physically challenging, or involve international travel. Sample collection could involve SCUBA diving or hiking. Work may require lifting 30 pounds.

Laboratory and field research (30%)

- Perform DNA and RNA extractions, DNA and RNA library preparations for next-generation sequencing, and other molecular ecology procedures to support research. Maintain contamination-free work environment for research on historical specimens. Assists students and other researchers in learning field and laboratory skills.

Bioinformatics & Data Science (30%)

- Data entry and analysis with bioinformatic and scientific computing for contribution to research papers, articles, and professional journals. Maintain meticulous analysis records. Lead training within the group to improve data science and open science practices.

Open science and administrative (20%)

- Lead open science practices and training in the group across data, code, and samples; lead purchasing, record-keeping, organization of supplies and equipment, laboratory compliance with safety regulations, and maintenance of budgets and related paperwork. Contribute to improvement and efficiency of research group operations.

Outreach and community building (20%)

- Maintain research group and related websites - Assist with building a collaborative and supportive research environment for all members and guests of the research group

Benefits

This is a full time position with benefits. Pay will be \$56,600-\$59,800. Start date is 9/1/2023 or other mutually agreed upon date.

Knowledge and Experience

- Bachelor's degree or higher (or equivalent foreign degree) in population genomics, molecular ecology, or related scientific field at time of application.
- Experience building population genomic libraries, developing bioinformatic pipelines, and conducting population genomics analyses.
- Computer literacy in R and a commitment to open science practices.
- Excellent written and oral communication skills.
- Ability to solve diverse technical and organizational challenges with exceptional creativity and collaboration
- Exceptional organizational skills and strong ability to accomplish tasks independently
- Evidence of community-building skills and ability to foster inclusion

Application

To apply, please submit a cover letter that describes your interest in and qualifications for the position, a curriculum vitae, and the contact information for three references to mpinsky@ucsc.edu. Review of applications is ongoing and will continue until the position is filled.

Please contact Malin Pinsky (malin.pinsky@ucsc.edu) with questions.

Malin Pinsky <malin.pinsky@gmail.com>

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UGlasgow UK ComparativeGenomics

Professor/Senior Lecturer in Comparative Genomics
The School of Biodiversity, One Health and Veterinary
Medicine has an exciting opportunity to appoint a Pro-
fessor/Senior Lecturer in Comparative Genomics.

Applications are invited from candidates of international standing with an appropriate record of academic achievement in comparative genomics and associated omics technologies. We are looking for a candidate who will complement our existing strengths in clinical veterinary medicine, evolutionary biology, and animal physiology, with a demonstrable interest in using domestic mammals among their study systems. We are particularly interested in applications from candidates with a track record of studying health related traits and their underlying genomic basis in companion animals. Traits of specific interest include those related to metabolism, ageing, and disease (e.g. cancer, autoimmune diseases, neuromuscular disorders).

Job Purpose To make a substantial and positive contribution to the strategic direction of the School/College through leading and contributing to research of international standard, high quality teaching at both undergraduate and postgraduate level, securing research funding, and providing academic leadership and management within the School/College. To actively engage in relationships with external stakeholders that advance knowledge exchange, public understanding and outreach.

Main Duties and Responsibilities 1. Undertake a leading role in the development and implementation of individual and/or joint research projects of international standard, participating actively in the development of College/School research strategy in the area of comparative genomics of domesticated animals. 2. Act as principal investigator or project leader on major research projects with a portfolio of research activity and publications of high quality and impact. 3. Take a lead in major funding bids and related activities, including Knowledge Exchange, which develop and sustain support for the subject area and recognised excellence for the University. 4. Undertake academic management and leadership roles and responsibilities to ensure high quality course/programme administration, setting and monitoring standards and lead on the development of

policy and practice across research and teaching teams (beyond subject/school level). 5. Create and develop effective networks with students, veterinary clinicians and other staff across the University, as well as external stakeholders to oversee the embedding of key University priorities such as graduate attributes, professional requirements, work-related learning, transitions support, student mobility and quality enhancement within credit bearing and non-credit bearing activities. 6. Lead the development of inclusive and innovative approaches to teaching, learning and assessment that recognise the needs of a diverse student cohort, taking appropriate responsibility for managing associated cultural changes and staff support and development. 7. Regularly attend and participate in appropriate activities to effectively contribute to the subject specialism, through learned societies, professional bodies, broader review, and editorial processes. Disseminate research findings locally, nationally and internationally to enhance learning within the discipline and to represent the University externally. 8. Supervise individual student projects at both undergraduate and postgraduate level to ensure their effective development and assisting with difficulties e.g. learning support/problems. 9. Actively engage with clinicians in the University's Small Animal Hospital, and other areas, to support clinical research and develop joint research projects in areas of shared interest and high potential for impact. 10. Engage in continuing professional development activities as appropriate. 11. Undertake any other reasonable duties as required by the Head of School. 12. To contribute to the enhancement of the University's international profile in line with the University's Strategic Plan, Inspiring People Changing The World.

For appointment at Professorial level We would expect all of the above criteria, but to be undertaken in line with 13. More academic management and senior leadership roles in a manner that enhances the student and clinical staff experience, ensures programmes are internationally benchmarked and of international standing, and that values and supports a culture of enhancement. 14. Sustained internationally leading high-quality research activity, seeking and securing funding for a portfolio of research projects through grant applications to external funding bodies, e.g. charities and UK Research Councils and mentoring early career staff to support their development in securing funding.

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UKansas GenomicDataScientist

The Kansas-INBRE (<https://www.k-inbre.org/>) and the University of Kansas Research Rising in Genomics (<https://research.ku.edu/research-rising/growing-kus-interdisciplinary-strengths-genomics>) programs are jointly hiring a genomic data scientist. We are seeking a colleague to work with members of the life sciences community in Kansas at several levels. First, the researcher will conduct genomic analyses as a service (e.g., RNA-sequencing analysis for differential expression, SNP calling, genome assembly). Second, they will teach genomic analysis approaches to the community (mostly postdocs and graduate students) in informal sessions or workshops. No formal classroom teaching is expected. Finally, they will work with experienced researchers in the application of more sophisticated genomics analyses, and assist in the design and implementation of new software/algorithms. We anticipate the successful candidate will also have ample time to conduct their own research, and the position includes a modest budget to support that research.

Job Description: 50% - Collaborate with, and assist, KU and KINBRE-affiliated faculty, postdocs and students to facilitate and support their genomic research. Duties will include, but are not limited to conducting genomic analyses as a service (e.g. RNA-sequencing analysis for differential expression, SNP calling, Genome assembly). 25% - Conduct training in genomic data analysis in the format of informal courses and/or workshops and one-on-one training. This training will involve teaching genomic analysis approaches to mostly graduate students and postdoctoral researchers. 25% - Conduct independent and/or collaborative primary research on a genomics-related project using sophisticated genomics analyses, and/or the design and implementation of new software/algorithms using Python, R and other coding languages. Other duties as assigned.

Required Qualifications: (1) PhD in the life sciences or a related field and postdoc or work experience in genomics. (2) Demonstrated excellence with oral and written scientific communication as evidenced by application materials. (3) Demonstrated excellence in scientific research as evidenced by publications and preprints, fellowships, etc. (4) Demonstrated excellence in computational genomics as evidenced by publications and research experience. (5) Demonstrated experience with computing languages

(e.g. Python) and applications (e.g. High Performance Computing clusters) as evidenced by application materials. (6) Demonstrated commitment to diversity, equity, inclusion and belonging as evidenced by application materials.

Contact Information to Applicants: Dr. Stuart Macdonald sjmac@ku.edu

Application: For a complete announcement and to apply online, go to: employment.ku.edu/staff/25152BR

A complete online application includes the following: (a) Cover letter that includes a discussion of both the applicant's vision for training in genomic data science and competencies with scripting languages, high performance computing clusters and data management. (b) Statement of research interests and how they would integrate with the current genomics community at KU. Specifically, the applicant is expected to outline a primary research project and they will accomplish the goals of that project at KU (collaborators, core labs, etc). (c) Curriculum Vitae with complete background/history. (d) Contact information for 3 professional references.

Review of applications will begin on June 13th, 2023 and will continue until a qualified applicant pool has been identified.

Advertised Salary Range: \$90,000-\$110,000

Anticipated Start Date: 01-Sep-2023 (although this is flexible)

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

Dr. Stuart J Macdonald he, him, his

University of Kansas (785) 864-5362

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UMainz Germany Evolutionary Biology

The Institute of Organismic and Molecular Evolution (iomE) at the Faculty of Biology, University of Mainz (Germany), invites applications for the position of a University Professor of Evolutionary Biology (Salary grade W 3 LBesG / Civil servant (tenured)), beginning at the earliest date possible.

We are seeking an internationally renowned scientist in the field of evolutionary biology whose research will complement our existing and emerging strengths in quantitative and theoretical aspects of evolutionary research. The successful candidate's research builds a bridge between theoretical and empirical approaches to evolutionary processes, with a research program that develops and/or applies quantitative methods to address evolutionary questions in extant animals preferably vertebrates (including humans) in natural populations. Research topics should include at least one of the following: population genetics, evolutionary genomics/epigenetics, evolution of life histories, biotic interactions, eco-evolutionary dynamics, long-term population field studies, or anthropology.

The successful candidate will receive departmental positions and start-up funds and will be expected to establish an independent and internationally visible research program sustained by third party funding. Our new colleague should work with our recently established international community of evolutionary biologists at the iomE to develop new collaborative research initiatives and participate in existing ones.

Examples of cooperation opportunities include: the Institute of Quantitative and Computational Biosciences, which is currently being established, the Institute of Molecular Biology (IMB) as well as collaborative research centers (e.g. CRC 1361 DNA Repair & Genome Stability; CRC 1551 Polymer Concepts in Cellular Function), the Research Training Group GenEvo (Gene Regulation in Evolution), and profile areas such as ReALity (Resilience - Adaptation - Longevity) or the Centre of Healthy Aging (further details: <https://www.blogs.uni-mainz.de/fb10-biologie-eng/research/>). The Sencken-

berg Biodiversity and Climate Research Centre and the LOEWE Centre for Translational Biodiversity Genomics offer further collaboration opportunities within the Rhine Main region.

Finally, the successful candidate will teach courses in evolutionary biology, quantitative biology, and human biology at JGU, including the planned master's program in Evolutionary Biology. We seek to increase the number of courses taught in English. Participation in academic service is expected.

For a full set of requirements and instructions see <https://karriere.uni-mainz.de/university-professor-of-evolutionary-biology/> Please upload your complete application information and documents (CV, references, diplomas and certificates, as well as lists of publications and teaching activities, funding record, current research and future research plans, teaching concept) no later than June 28, 2023 via our portal with the following link: <https://berufungsportal.uni-mainz.de/-ausschreibungsportale/stellen> The interview symposium is tentatively planned for September 2023. For questions and further information, please contact the chairperson of the search committee Prof. Hanna Kokko (hkokko@uni-mainz.de).

Hanna Kokko

Prof. Hanna Kokko

Institute of Organismic and Molecular Evolution (iomE)
Johannes Gutenberg-Universität Mainz
Hanns-Dieter-Hüsch Weg 15 55128 Mainz Germany

Email: hkokko@uni-mainz.de

"Kokko, Hanna" <hkokko@uni-mainz.de>

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UMaryland Chair Dept Entomology

Professor and Chair

The University of Maryland, College Park, invites applications for Chair of the Entomology Department. We are seeking candidates with outstanding records in research and education, along with administrative skills and vision to lead the unit.

The University of Maryland at College Park is a diverse and vibrant institution of research and higher learning that serves as the Flagship campus for the University of

Maryland system. The Department of Entomology at University of Maryland is committed to 1) advancing scientific knowledge through basic and applied research, 2) providing science education in Entomology and broader areas of the biological sciences at the undergraduate, graduate, and postgraduate levels, and 3) fulfilling the University land grant mission to provide research-based information and solutions to serve Maryland communities. Department members have broad disciplinary interests, spanning molecular, evolutionary, and developmental biology, genetics and genomics, systematics, ecology, conservation and restoration biology, toxicology, pathology, and population management, with shared focus on insects and their relatives. Faculty collaborate extensively with NIH, the U.S. Department of Agriculture, the Smithsonian and other local agencies. The University's proximity to Washington, D.C. offers diverse opportunities for partnerships with governmental and non-profit organizations and research groups.

The Chair is the chief administrative officer of the Department and is expected to foster a culture of excellence in research, teaching, mentorship, extension, and service in the following ways:

1. Develop and implement a compelling vision for the future of the department.
2. Provide leadership in planning and supervising programs relevant to the department's mission within the land grant university system, manage departmental budgets and other financial matters, and assist in generating extramural support for department activities.
3. Evaluate, counsel, and promote professional development of faculty, staff, and students.
4. Ensure recruitment and retention of outstanding faculty, staff, and students, while also fostering a diverse and inclusive working environment within the department.
5. Communicate effectively with faculty, staff, students, university administrators and stakeholders, including appropriately seeking and applying feedback.

The appointee will have a Ph.D. in Entomology, Biology or other Life Sciences- related field (disciplines above), at the rank of Professor. Candidates should submit the following materials to <https://ejobs.umd.edu/postings/105230>: 1) Cover letter describing qualifications,

- 2) Curriculum vitae,
- 3) Statement on leadership experience and vision, and
- 4) Contact information for 4 people from whom letters of recommendation can be requested.

For best consideration, apply by June 1, 2023. Ques-

tions may be submitted to the search committee chair, Dr. Kevin McIver, at entmsearch@umd.edu.

The University of Maryland, College Park, actively subscribes to a policy of equal employment opportunity, and will not discriminate against any employee or applicant because of race, age, sex, color, sexual orientation, physical or mental disability, religion, ancestry or national origin, marital status, genetic information, or political affiliation. Minorities and women are encouraged to apply.

Megan Fritz

Assistant Professor Department of Entomology Institute for Advanced Computer Studies University of Maryland
4291 Field House Dr. Plant Sciences Bldg. Rm. 3126
College Park, MD 20742 Office Phone: 301-405-3945
Website: <https://sites.google.com/view/megan-fritz-lab>
Twitter Handle: @MosquitoDoc she/her

mfritz13@umd.edu

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UPittsburgh ResTech PlantPloidy

Dr. Tia-Lynn Ashman and I (U. of Pittsburgh) are recruiting a research technician to study the consequences of plant polyploidy in a model plant system.

The technician will help create and maintain colonies of polyploid duckweed which are small aquatic fast growing plants. They will help conduct experiments exploring the ecological and evolutionary impacts of whole genome duplication such as challenges to various biotic and abiotic stressors and conduct genetic analyses. They will collect and help interpret data as well as help with ordering materials. The work will be conducted in the lab or greenhouse. They will be integrated in both the Turcotte and Ashman lab and give presentations of their work at lab meetings and sometimes help other lab members with their experiments. They will also have an opportunity to conduct their own supervised research project. The technician needs to be organized and prioritize duties, be detail oriented, and communicate issues.

Full details and application link: <https://t.co/J6g38yTp4f> Martin Turcotte, Ph.D.
at www.martinturcotte.net Assistant Professor,
Department of Biological Sciences University of

Pittsburgh

“Turcotte, Martin” <TURCOTTE@pitt.edu>

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US NatlCenterScienceEducation ExecutiveDirector

Dear Evoldir,

The National Center for Science Education is hiring a new Executive Director: https://pub.marq.com/-morrisberger_2223 <https://morrisberger.com/-position.php?id=3D2223> National Center for Science Education (Remote or Hybrid Position, San Francisco-Oakland Bay Area, CA) Title: Executive Director

[View Position Brochure Here](#)

THE ORGANIZATION

The National Center for Science Education (NCSE) is the nation’s leading independent organization fighting for integrity and accuracy in science education. NCSE works with teachers, parents, scientists, and concerned citizens at the local, state, and national levels to ensure that evolution, climate change, and other scientific matters are taught accurately, honestly, and confidently. Established in 1982, NCSE has successfully championed against efforts to insert creationism into the science classroom, to water down the teaching of evolution, and compromise the teaching of climate science. NCSE serves as a public advocate for sound, effective science education, conducts research on science education and science-education policy, and supports science educators with activities that include teacher training, curriculum development, and professional mentorship.

For additional information, please visit www.ncse.ngo .

THE OPPORTUNITY

With a mission to promote and defend accurate, effective science education, NCSE is well-positioned to benefit from a forward-thinking, persuasive, and passionate leader as its next Executive Director.

Through a collaborative approach in partnership with the staff and Board of Directors, the Executive Director will help shape the future of NCSE to achieve its goals and objectives, as outlined in its Strategic Plan, which include:

Ensuring that all efforts to interfere with the teaching

of accurate science are detected and blocked. Becoming a nationally recognized and trusted provider of high-quality professional learning. Building a community of skilled and confident K-12 teachers of evolution, climate change and the nature and practice of science, focusing on communities where societal acceptance is limited. Establishing a national reputation for expertise in teaching on climate change, evolution and the nature of science by conducting, publishing, and communicating peer-reviewed research and developing effective ways to improve teaching practices. Increasing and diversifying NCSE’s reach to and support from people whose deeply held values are aligned with NCSE’s mission. As NCSE grows, ensuring operational resilience through structure, culture, and processes that seamlessly support its work. **THE POSITION**

In addition to serving as primary spokesperson and champion on behalf of NCSE, the Executive Director is responsible for the strategic, programmatic, and financial health of the organization. Through cooperation with the Board of Directors, the Executive Director upholds the organization’s mission and vision, sets priorities, evaluates programmatic outcomes, establishes and adheres to an annual budget, and ensures compliance with the organization’s bylaws.

The Executive Director manages the day-to-day operation of the organization, including personnel management, program guidance and oversight, fiscal oversight, fundraising, and communications. The Executive Director is responsible for ensuring that NCSE remains focused on fulfilling its mission and for leading fundraising and outreach initiatives to reinforce the financial stability and strength of the organization.

Reporting to the Board of Directors, the Executive Director supervises the 11-member NCSE staff and is responsible for the annual operating budget of approximately \$1.6 million.

THE IDEAL CANDIDATE

Above all, the Executive Director must demonstrate a compelling passion for the mission of NCSE and the ability to convey the vital importance of basic scientific literacy to all members of society.

NCSE is seeking a strategic and facilitative coalition builder who can work at multiple levels and in multiple sectors with staff, board, supporters, the scientific community, the science education community, and members of local communities to advance the organization’s mission. The Executive Director will have exceptional communication skills and be a persuasive and motivating leader who will represent NCSE to a broad audience. A demonstrated ability to reach out, form effective re-

relationships, and work collaboratively in a diversity of communities is important, as is the ability to build bridges, foster dialogue, and build trust. As such, the successful candidate should be conversant around issues of Diversity, Equity, Inclusion, and Access (DEIA) and have experience working productively across lines of difference, effectively incorporating DEIA into all aspects of their work.

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USussex EvolutionaryBiology

The University of Sussex is looking to appoint a lecturer (equivalent to an assistant professor) within the Evolution, Behaviour and Environment subject group. The University of Sussex has a long history of research in evolutionary biology starting with John Maynard Smith who founded the school of life sciences. Current areas of activity include molecular evolution, the evolution of plants, pollinators, social insects, behaviour and visual systems. The position is open to applications across the field of evolutionary biology. Further details of the department can be found at <http://www.sussex.ac.uk/lifesci/ebe/> and the official job advertisement can be found at <https://www.sussex.ac.uk/about/jobs/lecturer-in-biology-education-research-ref-20493> including how to apply; the closing date is June 30th 2023. Informal enquiries can be made to Professor Daniel Osorio (d.osorio@sussex.ac.uk) or Professor Adam Eyre-Walker (a.c.eyre-walker@sussex.ac.uk).

Adam Eyre-Walker <a.c.eyre-walker@sussex.ac.uk>

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UWisconsin StevensPoint LabManager FisheriesGenetics

This position is responsible for directing laboratory and research functions as well as coordinating research projects and student staff activities to ensure quality control and compliance within the Molecular Conservation Genetics Laboratory (MCGL) of the WI Cooperative Fishery Research Unit (WICFRU). As such, this position provides research support for WICFRU, the Wisconsin Department of Natural Resources, and faculty and staff of the College of Natural Resources. MCGL research typically relies on techniques such as RAD-seq, sequencer-based microsatellite genotyping, GT-seq, whole genome resequencing, eDNA (qPCR and metabarcoding), and RNA-seq. Protocol-specific training will be available as needed.

Required Knowledge, Skills, and Abilities: Master's degree in genetics, zoology, biology, molecular biology, microbiology, or other field with expertise in genetic techniques and protocols, Experience in research and development of genetic techniques and protocols, Experience in management/implementation of instrumentation and workflow in a genetics laboratory, Experience with experimental design and data analysis

Preferred Knowledge, Skills, and Abilities: Good interpersonal skills, Good verbal and written communication skills, Fisheries and aquatic science sampling and field experience

Expected start date: Sept 1, 2023

Apply by: May 21, 2023

Salary: \$48-60K depending on experience

More information, including how to apply available at: <https://www3.uwsp.edu/hr/jobs/Pages/AcademicJobView.aspx?UWSPJobsCode=3D19634>

Questions can be directed toward:

Jared Homola Assistant Unit Leader USGS, Wisconsin Cooperative Fishery Research Unit Director, Molecular Conservation Genetics Lab jhomola@uwsp.edu

"Homola, Jared" <jhomola@uwsp.edu>

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Vairao Portugal ResTech TreeGenomics

We are seeking a research technician to support the research group BIODESERTS at the BIOPOLIS/CIBIO - Research Centre in Biodiversity and Genetic Resources, Campus de Vairão, Vairão, Portugal.

This is a full-time 12-month position with the possibility of an extension. The work will include several tasks within the ongoing research project on evaluating tree disease causes, particularly studying invertebrate, vertebrate, fungi and bacteria communities associated with trees. The tasks to be accomplished involve i) DNA extraction of invasive and non-invasive samples; ii) DNA amplification and library preparation for Sanger and Illumina sequencing, iii) bioinformatic analysis, including data processing, barcoding and metabarcoding and statistical analysis; and iv) reporting activities on laboratory and data analysis.

For more information and position requirements see <https://www.cibio.pt/?p=2731> Application deadline: 15 May 2023 “

Bárbara Santos <barbarasantosbio@gmail.com>

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VirginiaStateU Technician GenomicsBioinformatics

Research Technician Position in Genomics/Bioinformatics at the Virginia State University

We are seeking a skilled and motivated research technician with interest and experience in genomics/bioinformatics to join the NSF-funded Virginia State University (VSU) Genomics and Bioinformatics Program, which is part of the newly founded VSU Center for Biotechnology, Genomics, and Bioinformatics (VSU CeBiGeBi) under the direction of Dr. Xianfa Xie. The lab space is located in a recently renovated building and well equipped with instruments for DNA sequencing (including Illumina MiSeq, NextSeq 500, and Nanopore

sequencers), other related molecular biology instruments, and a Linux server for bioinformatic analysis.

The research technician will be able to join a variety of research projects in genomics and bioinformatics, including microbiome study for termite and soil, comparative genomic study of bioluminescent fungi, cancer epigenomics, among others, besides managing the instruments, supplies, and lab space for the projects. There will also be opportunities to train students and explore independent research.

A strong background in molecular biology and genomics/bioinformatics and excellent organizational and communication skills are essential. The applicant should have a strong work ethic and is expected to develop creative solutions that promote current research and educational goals of the VSU Genomics and Bioinformatics Program. The VSU CeBiGeBi also has a strong commitment to maintaining an inclusive environment that is welcoming to anyone who wants to experience research, thus applicants should share this commitment to diversity and inclusion.

Required qualifications: * A minimum of Bachelor of Science degree in biology, biochemistry, bioinformatics, or related fields * Strong wet-lab skills in molecular biology, including DNA/RNA extractions and assessments, PCR, etc. * Strong organization, time management, and communication skills * Ability to work effectively and collegially with colleagues and be a productive member of a research team

Preferred qualifications: * Extensive and successful experience in library preparation and sequencing with Illumina, Nanopore, and/or PacBio technologies * Successful experience with cell culture * Experience in bioinformatic analysis of genomic data * Interest and experience in field study

The position is funded by a grant from the U.S. National Science Foundation and available for a minimum of one year as a full-time 12-month appointment, with renewal possible. The compensation includes competitive salary and full benefits. Anticipated start date is July 10, 2023, but is flexible depending on the candidate. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment. Women and minorities are strongly encouraged to apply.

The university is located in central Virginia, a great location with nice weather. It is about two hours' drive from the Appalachia mountains and the Shenandoah National Park, the ocean, Washington DC, and the Research Tri-

angle in North Carolina. The “River City” Richmond is very close by and the annual Richmond Folk Festival has been attracting performers and audience from across the world. There are great opportunities for sightseeing (particularly historic sites), water activities, hiking, camping, other outdoor activities and sports, arts, etc. Plus, living in this area is much more affordable than many other places in the U.S. and the area is generally safe as well.

If interested, please submit your application at the following site: <https://www.jobs.virginia.gov/-jobs/research-technician-charles-city-virginia-united-states-chesterfield-colonial-heights-dinwiddie-emporia-fredericksburg-hopewell-north-chesterfield-petersburg-prince-george> Review of applications will be on a rolling basis and continue until a suitable applicant is found.

Xianfa Xie, Ph.D. Associate Professor, Department of Biology Director, Center for Biotechnology, Genomics, and Bioinformatics Virginia State University xxie@vsu.edu

Xianfa Xie <xxie@vsu.edu>

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WageningenU Evolutionary Population Genomics

Scientist in Evolutionary and Population Genomics

Link:

<https://www.wur.nl/en/vacancy/scientist-in-evolutionary-and-population-genomics.htm>

description:

Your job

Human activities have greatly impacted freshwater and marine ecosystems. As a scientist you will contribute to explore insight in how this has affected the genomic architecture of aquatic species is a prerequisite for their ecological restoration and genetic management.

At Wageningen University and research we have an challenging position for you if you have with a clear interest in one or more of the following research fields: functional genomics, population genomics, evolutionary biology, aquaculture, animal breeding, and bioinformatics.

You will as scientist contribute to population genomics

of aquatic species this within the chair group Animal Breeding and Genomics.

Your duties and responsibilities include:

participate in research to enable the genetic management and genomic monitoring of aquatic species in the wild and in aquaculture. initiate innovative initiatives in this domain participate in teaching related to functional and population genomics.

Your qualities

a PhD degree in a relevant biological field (Genomics, bioinformatics, developmental biology or evolutionary biology). Further preferred skills and experience: Experience in analyses of whole genome sequence data for functional genomic analysis Experience in population and evolutionary genomics Ability to work in a multidisciplinary team. Scientific track record of working with aquatic species.

You also have:

A strong interest in comparative biological analysis and computational biology. A strong interest in population genetic concepts and population conservation management. A strong interest in fundamental and applied research. A clear interest in aquatic animal species. A creative and innovative mindset. Good organisational and (written and spoken) communication skills in English, as well as a proven ability to collaborate with others. In our international working environment there is an increasing amount of communication in English. For this position it is about language level C1. If you do not yet have this level, we will of course help you and you can go to our language center Wageningen into Language.

You can see that there are plenty of challenges ahead of you. These challenges can also be seen as development opportunities. So if you do not yet have the track-record required in the vacancy, but do have solid work experience, we would also like to invite you to apply.

We offer you Wageningen University & Research offers excellent terms of employment. A few highlights from our Collective Labour Agreement include:

sabbatical leave, study leave, and partially paid parental leave; working hours that can be discussed and arranged so that they allow for the best possible work-life balance; the option to accrue additional compensation / holiday hours by working more, up to 40 hours per week; there is a strong focus on vitality and you can make use of the sports facilities available on campus for a small fee; a fixed December bonus of 8.3%; excellent pension scheme.

In addition to these first-rate employee benefits, you will of course receive a good salary. Depending on your

Job

experience, we offer a competitive gross salary from a minimum of euro 2.960,- for a full-time working week of 38 hours, in accordance with the Collective Labour Agreements for Dutch Universities (CAO-NU) (scale 10). At first, we offer you a one-year contract, with the possibility to be extended to a tenured position upon mutual enthusiasm. Of course, we would be happy to discuss this with you if you have any questions.

Wageningen University & Research encourages internal advancement opportunities and mobility with an internal recruitment policy. There are plenty of options for personal initiative in a learning environment, and we provide excellent training opportunities. We are offering a unique position in an international environment with a pleasant and open working atmosphere.

You are going to work at the greenest and most innovative campus in Holland, and at a university that has been chosen as the “Best University” in the Netherlands

for the 18th consecutive time.

Do you want more information? For more information about this position, please contact prof. Martien Groenen (martien.groenen@wur.nl; +31317483747) or Dr Hendrik-Jan Megens (hendrik-jan.megens@wur.nl +31317482469) For more information about the procedure, please contact Ine van't Land, corporate recruiter, recruitment.asg@wur.nl

- H-J Megens, PhD, - Assistant Professor - Animal Breeding & Genomics - Wageningen University, - Wageningen, The Netherlands - LinkedIn: <http://nl.linkedin.com/pub/hendrik-jan-megens/24/536/2b8>

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Other

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AncientBiomolecules AMNH NewYork

Dear colleagues,

We would like to present the recently opened Ancient Biomolecules Lab (abLab) at the American Museum of Natural History in New York, New York! This is a lab dedicated to the extraction of DNA and proteins from ancient tissues stored at the AMNH, other collec-

tions facilities, or obtained directly from paleontological/archaeological sites. This facility serves as a shared, training space for users both experienced and new to the fields of paleogenomics and paleoproteomics. There is no facilities fee to use the lab.

We invite those who have interests in completing their own funded paleogenomic or paleoproteomic project(s) within our state-of-the-art laboratory to start an application by first completing the Contact Form. Following submission, our team will follow-up regarding whether your project is suitable, who will complete the wet lab work (as we are not a paid-for service facility), and how we can best proceed to complete your project in a timely

fashion.

Please also consider that, currently, we do not support projects that intend to extract biomolecular data from human remains.

If you have questions about the application process, please do not hesitate to contact our lab manager (lclark@amnh.org).

We look forward to hearing from you.

Thanks!

Lauren T. Clark Research Assistant | Ancient Biomolecules Lab Institute of Comparative Genomics American Museum of Natural History 200 Central Park West, New York, NY e: lclark@amnh.org

p: +1 212-313-7602

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BiodiversityGenomicsEurope CallForInterest

Call for Expression of Interest for financial support for: Sampling reference genomes of eukaryotic species from biodiversity hotspots in Europe to support the mission of Biodiversity Genomics Europe

Global environmental change is causing a massive biodiversity loss, with an estimated 25% of species threatened with extinction worldwide. A coordinated global effort is crucial to fight biodiversity decline. Of particular interest are the so-called biodiversity hotspots, biogeographic regions that have the richest and most endangered endemic reservoirs of eukaryotic species. A better understanding of the biodiversity hotspots species composition is crucial in order to protect them.

The Biodiversity Genomics Europe (BGE, <https://biodiversitygenomics.eu/>) consortium has the goal of advancing the use of genomic science to improve our understanding of biodiversity, monitor biodiversity change, and guide interventions to prevent its decline. To achieve this goal, BGE brings together two newly formed networks: BIOSCAN Europe (<https://www.bioscaneurope.org/>) that focuses on DNA barcoding, and the European Reference Genome Atlas (ERGA: <https://www.erga-biodiversity.eu/>) that focuses on reference genome generation and is the Eu-

ropean node of the Earth BioGenome Project (<https://www.earthbiogenome.org/>).

BGE is eager to involve partners outside of the project consortium that are interested in contributing with specimens needed to achieve its goals. BGE is therefore calling for Expressions of Interest for parties to organise BioBlitz events (i.e., field campaigns aiming at collecting as many species as possible in a specific area over a short period of time) in biodiversity hotspots within Europe. The goal is to collect species of a broad taxonomic range that can be submitted for full genome sequencing and/or reference barcode generation. We ask for Expressions of Interest for projects that can include scientific activities (mainly related to species collection, taxonomic identification and proper sample preservation for reference genome sequencing) as well as citizen science activities related to the topic. All Expressions of Interest must include (i) DNA barcoding as a taxonomic confirmation of the species intended for reference genome sequencing, or if focused on the barcode reference library, proof of the lack of representation in Barcode of Life Data Systems (BOLD); (ii) preservation of fresh specimen samples suitable for reference genome sequencing (e.g., dry ice, liquid nitrogen, or similar) or DNA barcoding (e.g., 96% ethanol); (iii) plan for vouchers, metadata collection suitability and permission clearance for sampling and sample export; and (iv) shipping of samples to the designated coordination hub (CSIC, Barcelona, Spain). All eukaryotic species collected from biodiversity hotspots will be considered for genome sequencing, as long as they have not been previously sequenced or are nominated to be sequenced by any of the initiatives that are part of the Earth BioGenome Project. Projects with a focus on species groups that are poorly represented in BOLD will have priority.

BGE will provide SOPs with guidelines on how the samples need to be collected and stored to ensure good preservation of the specimen samples and the ability to extract HMW-DNA of good quality for reference genome sequencing. Priority will also be given to Expressions of Interest for projects aiming to organise the BioBlitz events in Eastern European Countries and widening countries*, as well as for areas considered as blind spots for barcode data. The goal of this call for Expressions of Interest is to build capacity in biodiversity genomics in the priority countries. Therefore, local engagement is crucial. The organising teams should be from the same country where the expeditions will take place, but the expedition team can include experts from any nationality.

*List of eligible widening countries: Bulgaria, Croatia, Cyprus, Czechia, Estonia, Greece, Hungary (except public interest trusts established on the basis of the

Hungarian Act IX of 2021 or any entity maintained by such a public interest trust that are not eligible under EU Council Implementing Decision 2022/2506), Latvia, Lithuania, Malta, Poland, Portugal, Romania, Slovakia, Slovenia and all Associated Countries with equivalent characteristics in terms of Research & Innovation performance (Albania, Bosnia & Herzegovina, Kosovo, Montenegro, North Macedonia, Serbia, Turkey, Armenia, Georgia, Moldova, Morocco, Tunisia, Ukraine, Faroe Islands).

Requirements:

- The applicants must be ERGA members. Non-ERGA members interested in applying should become members before the application deadline. - The Expression of Interest for project leadership should be from an

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Cogent GenomicDataWrangling Survey

Hi all!

I'm a developer of the open source software tool cogent3 for genomic data wrangling and molecular evolutionary analyses. (cogent3 is a direct descendant of PyCogent, of which I was co-lead developer with Rob Knight.)

I'm running a survey to evaluate what the major computational challenges being faced by our community are in terms of getting data ready for phylogenomic analyses.

If this is of interest to you, you can fill out the survey at <https://forms.gle/VSt8TKdWtzUfe5A99> It will take 2 minutes.

Please forward to any colleagues who you think might be interested!

thank you! Gavin

Professor Gavin Huttley, Convenor, Masters in Quantitative Biology and Bioinformatics, Research School of Biology, ANU College of Science, RN Robertson Building, 46 Sullivans Creek Road, The Australian National University Canberra ACT 2600 Australia +61 2 6125 5308 CRICOS #00120C

Gavin A Huttley <Gavin.Huttley@anu.edu.au>

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Europe DevelopingBiodiversityGenomicsApplications

Call for Expression of Interest for financial support for: Developing biodiversity genomics applications for species in Europe to support the mission of Biodiversity Genomics Europe

Genomics, anchored on the analysis of high quality reference genomes and additional genome-wide data, is a key component of biodiversity research, conservation efforts and bioeconomy. This is particularly relevant today when global environmental change is causing a massive biodiversity loss, with an estimated 25% of species threatened with extinction worldwide. A coordinated global effort is crucial to fight biodiversity decline. The Biodiversity Genomics Europe (BGE, <https://biodiversitygenomics.eu/>) consortium has the goal of advancing the use of genomic science to improve our understanding of biodiversity, monitor biodiversity change, and guide interventions to prevent its decline. To achieve this goal, BGE brings together two newly formed networks: BIOSCAN Europe (<https://www.bioscaneurope.org/>) that focuses on DNA barcoding, and the European Reference Genome Atlas (ERGA: <https://www.erga-biodiversity.eu/>) that focuses on reference genome generation and is the European node of the Earth BioGenome Project (<https://www.earthbiogenome.org/>). To achieve its goals, BGE intends to involve institutions outside of the project consortium, who are interested in developing Case Studies that build genomic biodiversity applications. BGE is therefore calling for Expressions of Interest for parties to develop case studies focused on European species that (1) demonstrate the application of reference genomes and genomic data to the conservation of species affected by anthropogenic changes in climate, habitats and ecosystems, or (2) demonstrate the application of reference genomes and genomic data for species of economic importance or disease control, thus contributing to the sustainability of ecosystem services. All submitted projects must include (i) focus on a biological system in Europe, suitable to develop one of the two application types; (ii) genomic analyses based on at least one high quality reference genome and additional

downstream data; (iii) a plan for sampling, genomic data collection and data analysis; and (iv) a plan for stakeholder engagement.

Priority will be given to Expressions of Interest for projects implemented in Widening Countries*, to increase and diversify participation in European biodiversity genomics endeavours and the targets of biodiversity genomic application studies. The goal of this call for Expressions of Interest is to extend the reach of genomic applications developed by BGE and build capacity in biodiversity genomics in the priority countries. Therefore, local engagement is crucial. The Case Study Teams should include researchers from the country or countries of provenance of the target genomic resources and fulfil requirements for access and benefit sharing.

*List of eligible widening countries: Bulgaria, Croatia, Cyprus, Czechia, Estonia, Greece, Hungary (except public interest trusts established on the basis of the Hungarian Act IX of 2021 or any entity maintained by such a public interest trust that are not eligible under EU Council Implementing Decision 2022/2506), Latvia, Lithuania, Malta, Poland, Portugal, Romania, Slovakia, Slovenia and all Associated Countries with equivalent characteristics in terms of Research & Innovation performance (Albania, Bosnia & Herzegovina, Kosovo, Montenegro, North Macedonia, Serbia, Turkey, Armenia, Georgia, Moldova, Morocco, Tunisia, Ukraine, Faroe Islands).

Requirements:

- The applicants must be ERGA members. Non-ERGA members interested in applying should become ERGA members before the application deadline.
- The responsible researcher of the Expression of Interest should be from an official institution in the country or one of the countries where the model species are sampled, and should be responsible to comply with all local and EU regulations. We will consider applications of collaborative nature if the incentive of capacity building in the country of sample origin is clear.
- The delivery of projects should allow completion before August 2025.
- Applicants should have all the required collection permits and Nagoya authorization for collecting and exporting species before the start of the project. The permits need to allow for open access deposition of the sequencing data, as all sequencing data generated within the project will be automatically deposited in ENA after their completion. Protected specimens will not be collected unless with permission.
- Applicants should adhere to the open data and FAIR principles

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InMemoriam DrNei

In Memoriam - Dr. Masatoshi Nei

It is with great sorrow that I share the news of the passing of Prof. Masatoshi Nei. He died peacefully on May 18, 2023, after a brief overnight illness. His demise marks a huge loss to the global scientific community and us in the evolutionary community.

Dr. Masatoshi Nei was a pioneer in evolutionary genetics and a laureate of the prestigious Kyoto Prize. His extraordinary life, which spanned 92 years, was marked by transformative contributions to evolutionary genetics, molecular evolution, phylogenetics, and evolutionary biology. Over the last few years, I have had the privilege of visiting and interacting with him. He was always in high spirits, constantly working on scientific and personal book projects. It often felt like nothing had changed in the last decade, except there were physical age-related health challenges.

Please visit Temple University's announcement (<https://igem.temple.edu/nei>) to learn about some of his remarkable accomplishments.

Our heartfelt thoughts and prayers are with Dr. Nei's family in this difficult time.

Sudhir

Sudhir Kumar, PhD Carnell Professor (kumarlab.net)
Institute Director (igem.temple.edu) Temple University

Sudhir Kumar <s.kumar@temple.edu>

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Montreal EvolutionaryBiology Jul26-30 CallForSymposia

We are pleased to issue this call for symposia proposals for the Third Joint Congress on Evolutionary Biology, which will take place in Montreal, Canada, July 26-30, 2024!

The Congress merges the traditions of the participating societies: ESEB, the European Society for Evolutionary Biology; ASN, the American Society of Naturalists; SSB, the Society for Systematic Biology; and SSE, the Society for the Study of Evolution. The sextennial Congress takes the place of the ESEB and Evolution Meetings in 2024, and it builds on the success of the previous Congresses in Ottawa in 2012 and Montpellier in 2018.

The structure of this Congress will be unique. Roughly 40% of talks will be structured into symposia, following the traditional ESEB format. The remaining 60% of talks will be structured into general sessions according to topic, following the traditional Evolution meetings format. The success of the joint meeting therefore depends on the strength and range of the symposia complementing the standard sessions.

We are now asking members of all four participating societies to submit symposium proposals. This is an opportunity to create a session that pushes your field forward and draws new researchers into its orbit. Symposia play a special role in bringing together researchers from disparate disciplines and backgrounds and generating new integrative perspectives. Symposia should transcend the conventional themes of standard meeting sessions. The deadline for proposals is September 1, 2023.

In contrast to the usual ESEB format, no funding will be provided for symposia and consequently they will not feature formally invited speakers (though organizers can solicit submissions). Instead, symposium organizers will select talks and posters from submitted abstracts, and presentations not selected for a symposium will be assigned to the general sessions. Symposium talks will generally be 14 minutes (including questions), as in typical Evolution meetings.

Each symposium should have two organizers with a vision for an exciting and timely scientific session. We welcome proposals from researchers at all career stages, and our goal is to assemble a collection of symposia that encompass a broad diversity of researchers and research topics. The Joint Congress Scientific Committee, with members from all four societies, will select symposia from the proposals, with decisions announced in November 2023. Abstract submissions for the symposia and general sessions will close in the spring of 2024, not long before the meeting. Symposium organizers will then select talks for their sessions from the submitted abstracts. We ask organizers to ensure diversity among their session speakers, with attention to gender, career stage, geography, and other axes. We are particularly interested in symposia that draw themes from the disciplines of multiple participating societies.

To submit a symposium proposal, you will be asked to provide the following components: 1. The names, e-mail addresses, and society affiliations of two organizers who are committed to attend the whole meeting in person. If you are not a member of any of the participating societies, please join! Find links below, and note that the societies have membership assistance programs for researchers from many parts of the world.

2. The proposed symposium title.
3. A scientific abstract of up to 200 words explaining the theme of the symposium. This is the text that will attract submissions to your session.
4. An account of up to 200 words explaining how your symposium is timely and of broad interest, how it will facilitate integration and synthesis across the boundaries of the scientific societies, and how it will benefit from its status as a symposium as opposed to having the same talks distributed into general sessions.
5. Optionally, provide names and affiliations for two speakers that you believe would be a good fit for your symposium. It is not required that these speakers have agreed to submit abstracts for your symposium. Note that we are interested in symposia that will contribute to the diversity of the conference participants, across career stage, gender, nationality, and other dimensions.

Submit proposals at <https://forms.gle/-GEy3jvXr6y83u2wFA> by September 1, 2023. Each organizer can submit a maximum of one proposal.

Join the societies: SSE: <http://www.evolutionsociety.org/membership.html> SSB: <https://www.systbio.org/membership.html> ASN: <https://amnat.org/membership/beamember.html> ESEB: <https://eseb.org/society/eseb-membership/> Alex Wong <alex.wong@ag.tamu.edu>

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NewCaledonia AvianFieldAssistants

Field assistants ??? Avian behavioural ecology New Caledonia

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

When: up to 2-3 months between October - December 2023, exact dates and duration to be agreed.

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

Duties: nest searching and monitoring, mist-netting and banding, data collection and analysis, maintenance of field equipment.

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

Working conditions: 8-10 hours daily for 5 days a week on average, up to 10-12 hours and 6-7 days a week during the peak of the breeding season. Early morning start. Selected applicants will need to arrange their own travel to and from New Caledonia. The project will provide free accommodation and a monthly wage to cover food costs and living expenses.

How to apply: send a single PDF named `NC2023_Assistant_NameSurname.pdf` with CV, cover letter (max 1 page) describing relevant experience and contact details of 2 referees to `aattisano@miiz.waw.pl` by the 18/06/2023. Prospective postgraduate candidates should also include a brief preliminary research proposal (max 1 page). Only selected applicants will be contacted and invited for an online interview.

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

Alfredo Attisano <`aattisano@miiz.waw.pl`>

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Online NCBI Codeathon Population Genomics Jul31-Aug4

Hi EvoBio Community,

NCBI and NIAID are excited to announce our codeathon, `i2VCF Files for Population Genomics: Scaling to Millions of Samples`, `i2` to be held virtually from July 31st `i2` to August 4th, 2023 (1-5 PM ET). `i2VCF`, or Variant Call Format Files, are a widely used file for storing information about genetic variations across multiple samples. This event aims to bring together experts in viral evolution, molecular epidemiology, and population genomics to explore methods for computing on the scale of millions of records using VCF files as inputs, with `i2SARS-CoV-2 VCFs` `i2` serving as a case study. `i2`

Codeathon Webpage: <https://ncbiinsights.ncbi.nlm.nih.gov/event/vcf-for-population-genomics-codeathon/> Direct Application Link: https://nlmenterprise.co1.qualtrics.com/jfe/form/SV_cOpigxaqhdZ7AmG Contact E-mail: `codeathons@ncbi.nlm.nih.gov`

We invite both programmers and non-programming subject matter experts to apply for this event. During the week-long codeathon, teams of 5-10 people will collaborate virtually to design visualizations and write software to address the following objectives: `i2`

- Explore the use of `i2SARS-CoV-2` variant call format (VCF) files `i2` as input to downstream applications such as viral classification, characterization, and phylogenetic tree construction. `i2`
- Estimate intra-host sequence diversity and predict emerging new variants of SARS-CoV-2 using VCFs as input. `i2`
- Streamline processes to assess the current therapeutic and preventative options using VCFs. For example, assessing genome-scale responses to vaccines or therapeutics. `i2i2`
- Enhance and facilitate the data clustering process and modeling for predictions using VCFs. `i2`

The codeathon will be cooperative rather than competitive, and teams will share ideas and technical expertise. At the end of the event, teams will present their work to each other and representatives across the National Institutes of Health (NIH). `i2` After the codeathon, we

will make the team products publicly available through the NCBI Codeathons GitHub Organization. We encourage participants to co-author a joint manuscript, share their work online, and/or at conferences.

If you are interested in participating, pitching an idea for a team project, and/or serving as a team leader, please apply or email us at codeathons@ncbi.nlm.nih.gov. Please note that participation may be capped due to technical limitations and the total number of accepted projects. We look forward to hearing from you and working together to explore methods for computing on the scale of millions of records.

Thanks, NCBI Education Team

“Chang, Sally (NIH/NLM/NCBI) [C]”
<sally.chang@nih.gov>

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Reminder Call Applications PostDocFellow

Dear Colleagues,

Reminder that applications for our training program to navigate the faculty job process are due next week, May 15th! Please see below for details and remind your networks to apply!

Best,

Lisa

—

Dear Colleagues,

We are excited to invite applicants for a new professional development program: 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 underrepresented 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 2023-2024 academic year (see more details on eligibility at the link below). For this first 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/zNWfktVM1tpDUUW7>. The deadline for applications is May 15th, 2023.

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 would greatly appreciate your assistance circulating this message to your networks, and any questions about the program can be directed to lkomoroske@umass.edu.

Respectfully,

Lisa Komoroske & the UNVEIL Steering Committee

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/> Lisa Komoroske <lkomoroske@umass.edu>

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SMBE Call Best Graduate Student Paper 2022 Nominations

Call for Best Graduate Student Paper of 2022 Nominations

Dear SMBE Members,

SMBE is calling for nominations for Best Graduate Student Papers of 2022. These awards provide recognition for outstanding papers in both our SMBE journals, Molecular Biology & Evolution (MBE) and Genome Biology & Evolution (GBE). There will be one Best Graduate Student Paper award for each journal. Like

last year, each journal may also name up to 3 'honorable mentions' for outstanding runners-up.

All articles published in the calendar year 2022 are eligible for nomination. This corresponds to papers published in the printed volume 39 in MBE and volume 14 in GBE. Please see below for additional information on eligibility.

Winners will receive a prize each of US\$ 500, runners up a prize each of US\$ 100.

Best Regards, Kateryna Makova President, SMBE

Eligibility & Nomination 1. All articles published in the two SMBE journals, Molecular Biology & Evolution and Genome Biology & Evolution (one prize for each journal), in the calendar year 2022 are automatically eligible if the final publication date of the nominated paper is not more than two years later than the date of the nominee's Ph.D.

2. The nominated graduate student must be the first author or joint first- author of the nominated paper.

3. An article and its first author can be nominated by anyone; self- nominations are acceptable.

4. A signed letter from the Ph.D. advisor, MSc advisor, or equivalent, confirming that the paper was part of the nominee's thesis or graduate work is required.

5. The deadline for submitting nominations is June 1, 2023.

How to Enter Please send the name of the nominee, a scan of the signed advisor letter, and the name of the paper for which the award is to be considered as a SINGLE PDF to smbe.ks@kwglobal.com.

Please use the email subject line "MBE/GBE Best Student Paper Nomination", deleting journal name as appropriate.

smbe.contact@gmail.com

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SSB Mentorship Program enrollment

The Society of Systematic Biologists is launching a new Mentorship Program. The program will help create mentorship pairs between junior and senior members of the systematics community. The program will pair

graduate students and postdocs (junior members) with more-established members of the systematics community that include faculty, curators, teachers, researchers, etc. (senior members). Junior members will receive guidance (e.g., scientific, professional, etc.) from senior members located at different institutions, while senior members nurture growth in the next generation of systematists.

We will announce the first 20 mentoring pairs in mid-May, 2023. Enrollment does not require SSB membership. We are especially looking to enroll more Mentors (senior members) to support the next generation of systematists and biodiversity researchers.

Please carefully read the contents of the SSB Mentorship Program Overview & Expectations page before enrolling.

Program information:

- Overview & Expectations link: <https://www.systbio.org/mentoring-program.html> - Enrollment link: <https://forms.gle/mc2gPDwaTGYvcR1k7>
- Comments and questions: mentorship@systematicbiologists.org

- Coordinators: Michael Landis, Laura Kubatko, Alonso Delgado, Ixchel Gonzi, $\frac{1}{2}$ lez-Ramiz $\frac{1}{2}$ rez

Mentorship Program <mentorship@systematicbiologists.org>

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StudentNetwork AmphibianPathogenSurveillance

Subject: Join the Student Network for Amphibian Pathogen Surveillance

SNAPS (Student Network for Amphibian Pathogen Surveillance) is an experiential learning network of students, educators, and scientists, sponsored by the USGS, ARMI, and Environment & Climate Change Canada. Our mission is to mobilize students to lead the search for emerging amphibian pathogens in North America, with a focus on early detection of the salamander pathogen *Batrachochytrium salamandrivorans* (Bsal).

We provide all the materials that educators need to guide their students in testing their local amphibian populations for emerging diseases, including field sampling supplies, protocols, diagnostic testing, and optional lesson plans that complement field sampling. These dis-

eases are simple to test for and do not pose any risks to humans.

For more information, see <https://snaps.amphibiandisease.org/>. With three seasons behind us, SNAPS is expanding! We are seeking undergraduate educators in the U.S. interested in incorporating SNAPS into their courses in 2023. We encourage participation across academic disciplines (e.g., biology, herpetology, statistics, and beyond) and welcome new lesson plans to the program. We are open to all types of academic and academic-affiliated institutions with the capacity to incorporate Bsal surveillance into undergraduate education (all types of colleges, universities, and field stations). We are especially interested in bringing on partners with diverse perspectives and an interest in contributing to the growth and vision of the program.

We invite expression of interest through this 5-minute form:

<https://forms.gle/a2ndzq61YTn6AqMu8> While capacity is limited, we will keep all interest forms on file for future openings!

For questions, please email Sasha Greenspan at sasha.greenspan@gmail.com

Sasha Greenspan <sasha.greenspan@gmail.com>

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UFlorida Internships BehavioralEvolution

Applications are invited for post-graduate interns to work on the behavioral ecology of insects at the University of Florida in Gainesville. Positions will start September 1, 2023, and continue for 6 to 12 months. Shorter internships are not available at this time.

Position description: The Miller Lab at the University of Florida welcomes applications from recent or soon-to-be graduates with B.A., B.S., or M.S. degrees in the biological sciences. Paid internships are designed to provide interns with opportunities for their own career advancement while also producing high-quality scientific research in our laboratory. Activities, including research design, execution, and analysis, will help the successful applicants prepare for Ph.D. programs in ecology, evolutionary biology, and behavior. This work will

be engaging, challenging, and will help direct future research. Interns will work closely with numerous lab members including students, staff, and the PI.

Job responsibilities:

Designing and conducting experiments in collaboration with members of the research team; working as part of a team to maintain insect colonies and provide plant care; engaging with our extended team to provide scientific outreach including interfacing with classrooms and uploading videos for online engagement; and contributing to a positive and supportive working atmosphere.

Qualifications: Well-qualified candidates will have a B.A., B.S., or M.S. degree in the biological sciences, with coursework in ecology, evolution, and/or animal behavior; evidence of excellent communication skills; excellent organizational skills and attention to detail; previous research experience in the biological sciences.

Desirable (though not necessary) qualities include:

Possession of a drivers license; Comfort conducting field work in hot, humid Florida conditions on occasion;

In-depth research experiences as demonstrated through the presentation of posters or talks at scientific meetings or peer-reviewed publications.

Interested applicants can learn more about this position, including how to apply, at: www.millerlab.net. Click through to “Opportunities.” Applications are due on June 1st, 2023. Positions are open to U.S. and international applicants.

Diversity and inclusion are more than just words for us. These are central in guiding how we come together as a research team, cultivate excellence, and go forth into the world to share our discoveries and our love of our work.

Information about Gainesville, Florida:

Situated in the rolling countryside of north central Florida, Gainesville, is close to world-class fishing, snorkeling, canoeing, tubing and kayaking. On land, those so inclined may enjoy birding, hiking, biking, and fishing. Home of the University of Florida, seat of Alachua County’s government and the region’s commercial hub, Gainesville is progressive, environmentally conscious, and culturally diverse. The presence of many students and faculty from abroad among its 99,000-plus population adds a strong cross-cultural flavor to its historic small-town Southern roots. Its natural environment, temperate climate and civic amenities make Gainesville a beautiful, pleasant, and interesting place in which to learn and to live.

Christine W. Miller (she/her) Associate Professor

Email: cwmiller@ufl.edu

Entomology & Nematology Department University of Florida

2022-2023 On sabbatical at the University of Cambridge,

UK

"Miller, Christine W." <cwmiller@ufl.edu>(to subscribe/unsubscribe the EvoDir send mail to golding@mcmaster.ca)

PostDocs

BielefeldU TheoreticalEvolutionaryEcol	62	UChicago MacroevolutionPhylogenetics	83
ColoradoStateU PlantMutationEvolution	62	UCollege London GeneticsEvolution	83
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LinkopingU Sweden DrosophilaEvolGenomics	67	ULausanne PlantEvolution	88
MarianU PolyploidGenomicsEvolution	68	ULausanne Switzerland ExpEvolutionDrosophilaPhysiology	89
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Munich Germany AncientPathogens	70	UMarburg 9Phd 3Postdoc Oak-microbiomeInteraction	90
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OhioStateU ConservationGenomics	72	UMontpellier Three SociableWeaverEvolution	92
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Job announcement

Bielefeld University, Department of Evolutionary Biology

Postdoc position in Theoretical Evolutionary Ecology

Application deadline: 09.06.2023

The Faculty of Biology offers a full-time research position in Theoretical Evolutionary Ecology

The position can start on January 1, 2024 and is funded until the end of the year 2025 by the German Research Foundation (DFG) within the collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3). The aim of the Postdoc project is to develop ecological and evolutionary theory to contribute towards a better understanding of intra-species niche variation. The project is entitled "Armament, hunger, and mating: how competition can drive individual variation" (sub-project D04 of the collaborative research centre, with Klaus Reinhold). This theoretical project will explore the conditions that favour the evolution of between-individual variation in behavioural niches. The aim is to focus on competition for food, territories and mates and examine to which extent phenotypic variation can be maintained based on genetic differences or variation in adaptive phenotypic plasticity.

The collaborative research centre: The postdoc will be embedded within a larger collaborative research centre (SFB) comprising about 20 principal investigators and more than 20 postdoc and PhD students based at Bielefeld University, the University of Münster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology, and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange, and early career support programs. Full details of the SFB can be found at www.uni-bielefeld.de/biologie/-crc212. For further information on the projects and the involved departments, please contact Klaus Reinhold (klaus.reinhold@uni-bielefeld.de) with any informal inquiries.

Main responsibilities: research tasks (95 %): - development of eco-evolutionary models, including - mathematical analysis of models - implementation in a programming language, e. g. in R, C++, Python - simulation studies - writing scientific publications for international journals

organizational tasks in the research group and collabora-

tive research centre (5 %)

Your Profile We expect - completed university degree in a relevant discipline, e. g. biology, mathematics, physics or bioinformatics - completed PhD in theoretical ecology, population genetics, behavioural ecology or evolutionary ecology - experience with mathematical modelling of evolutionary processes - programming skills in at least one programming language (e. g. R, C++, Python) - interest in biological and mathematical questions - ability to work both independently and as part of a team - very good oral and written communication skills in English

Preferable qualifications - papers in peer-reviewed international journals - experience in collaborations between empiricists and theoreticians - experience with high-performance computing

We offer - salary according to Remuneration level 13 TV-L - fixed-term employment limited until 31.12.2025 - fulltime 100 % contract - internal and external training opportunities - variety of health, consulting and prevention services - flexible working hours - collegial working environment - open and pleasant working atmosphere - exciting, varied tasks

Application Procedure: We are looking forward to receiving your application. For full consideration, your application should be received via either email (a single PDF document is required) sent to klaus.reinhold@uni-bielefeld.de or post (see postal address). Please mark your application with the identification code: Wiss23198.

application deadline: 09.06.2023 Postal Address Bielefeld University, Biological Faculty, Evolutionary Biology Prof. Dr. Klaus Reinhold P.O. Box: 10 01 31, 33501 Bielefeld Germany

Phone: +49 521 106-2721 Email: Klaus.Reinhold@uni-bielefeld.de

"Reinhold, Klaus" <klaus.reinhold@uni-bielefeld.de>

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ColoradoStateU
PlantMutationEvolution

The Sloan Lab at Colorado State University is looking for a postdoctoral researcher with experience in plant molecular genetics and/or biochemistry to investigate

the mechanisms responsible for extreme variation in mutation rates and genome stability in plant mitochondria and plastids. These plant organelles maintain exceptionally low point mutation rates, while exhibiting rapid rates of rearrangements and structural evolution. Our collaborative project to understand the mechanistic basis of these unusual genome properties. This project fits into the broader focus of our research, which is on the evolution of organelle genomes and their coevolution with the nucleus. More information about our research projects and publications is available at our lab website: <https://sites.google.com/site/danielbsloan/> We seek someone who is excited about addressing evolutionary questions at the molecular level and wants to contribute to a positive and collaborative intellectual environment. Start date is flexible but preferably in summer or fall 2023.

Applicants should have expertise in plant biology and one or more of the following areas:

-Genetics, transformation, and genome editing - Mechanisms of mutation and DNA damage/repair - Protein and nucleic acid biochemistry -Mitochondrial and chloroplast biology -Library construction for next-generation sequencing -Comparative genomics and bioinformatics

Our lab is in the Department of Biology at Colorado State University, which is housed in a state-of-the-art research facility that opened in 2017. The department includes numerous labs in the fields of both plant molecular biology and evolutionary biology, so there are ample opportunities for collaboration outside the lab group. The university is in Fort Collins, Colorado, which routinely ranks among the top locations in the country in terms of overall quality of life.

Interested researchers should e-mail Dan Sloan (dan.sloan@colostate.edu) and include a CV, along with a brief statement of research/career goals and how they pertain to the position. Review will begin June 23, 2023, but inquiries are still very much encouraged after that date.

“Sloan,Dan” <Dan.Sloan@colostate.edu>

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CornellU FishMetagenomics

Postdoc Opportunity at Cornell University: Metagenomic Reconstruction of Feed Composition to Support Aquaculture Sustainability Certification

OVERVIEW: Aquaculture is the fastest growing sector of the global food system, creating an enormous demand for feeds that themselves contain fish. The associated supply chains are largely unregulated and invisible, yet have far-reaching implications for ecosystems and human health. We are seeking a postdoctoral researcher to join our project team to examine the species composition and geographic sources of fish products used in aquaculture feeds worldwide.

The position will offer important leadership opportunities in two regards. First, building on earlier metabarcoding work, the postdoctoral associate will explore the potential for leveraging shotgun sequencing approaches to better assess the taxonomic composition and relative abundance of fish species within aquaculture feeds collected worldwide. The resulting species lists will be used to assess the global geography of connections between the harvest of wild fish and the production of farmed fish. Second, the postdoc will constructively engage with aquaculture industry and NGO representatives to pave the way for integrating metagenomic tools into standards for sustainability certifications. Thus, we seek a combination of hard and soft skills that will foster success in both of these major goals.

This project is a collaborative effort, and will require a team-oriented approach as the postdoc works closely with a group of Cornell researchers as well as our NGO partners (Environmental Defense Fund; WorldFish). We anticipate a roughly equal split of time investment between the molecular ecology and sustainability framework goals of the project. The primary tasks will include 1) working with our team to design, optimize, and validate a shotgun sequencing approach for inferring species compositions in sample mixtures, 2) leading bioinformatic data processing and reporting overall results, and 3) communicating project findings to a broad audience while working with NGO, industry, and trade association partners to develop a strategy for incorporating DNA-based ingredient tracing into the next generation of sustainability certifications. The postdoc will be expected to lead the preparation of both scientific publications and outreach materials, with support

and collaboration from other team members.

DESIRED QUALIFICATIONS: In keeping with the dual goals of the project, our ideal candidates would have the following credentials: - Strong computational and genetics lab skills based on metabarcoding, metagenomics, and/or bioinformatics experience - Experience in fisheries, aquatic conservation, and/or sustainable food systems, including stakeholder engagement, is preferred but not required - Evidence of ability to work both collaboratively and independently - Evidence of ability and motivation to publish research results in peer-reviewed journals - A Ph.D. in molecular ecology, bioinformatics, fisheries, or a related field must be completed prior to starting the appointment.

TERMS OF APPOINTMENT: This postdoc position is a full-time appointment, starting in summer 2023 or as soon as possible thereafter. Residency in Ithaca, NY is encouraged, but we have some flexibility. The postdoc will be jointly supervised by Pete McIntyre (<https://mcintyrelab.weebly.com/>) and Nina Overgaard Therkildsen (<https://www.therkildsenlab.org/>) in the Department of Natural Resources & the Environment, which is home to a vibrant community of sustainability scientists at Cornell University. We will support a variety of professional development opportunities within and beyond the project, including engaging with fellow postdocs from other projects funded by the Cornell Atkinson Center for Sustainability.

Salary will be commensurate with experience and competitive, following the National Institutes of Health National Service Awards (NIH NSRA) scale. We have assured funding for an initial 18-month appointment, and anticipate opportunities for extension dependent upon satisfactory performance and availability of funds.

Cornell University and our team embrace diversity and seek candidates who will contribute to a climate that supports students, faculty, and staff of all identities and backgrounds. We strongly encourage individuals from underrepresented and/or marginalized identities to apply.

TIMELINE & APPLICATION PROCESS: Review of applications will begin on May 29, 2023, and continue until the position is filled. To apply, please create a single PDF containing a 2-page cover letter detailing your interest, a complete CV, names and contact information for 3 references, and reprints of your 2-3 most relevant and compelling publications. Applications should be emailed to both Pete

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mcmaster.ca/~brian/evoldir.html

CzechRepublic GenomicsAsexualReproduction

POSTDOCTORAL RESEARCH POSITION IN EVOLUTION OF ASEQUAL REPRODUCTION A postdoctoral position for up to 2.5 years is available in comparative genomics, population genomics, transcriptomics and / or cytogenetics at the Czech Academy of Sciences. (details to be found also here: <https://euraxess.ec.europa.eu/jobs/-101298#additional-information>; and here: <https://meritcb.eu>) The postdoctoral fellow will join the research team of Dr. Karel Janko at the Institute of Animal Physiology and Genetics, which studies how and why multicellular organisms deviate from canonical sex and switch to non-Mendelian inheritance. By studying these phenomena, we strive to unravel the implications of non-sexual reproduction for the evolutionary processes and rise of polyploidy. As a postdoctoral fellow, you will have the opportunity to shape your research within the framework of our ongoing studies in the Laboratory of Non-Mendelian Evolution. This autonomy allows you to explore your own research interests while contributing to our collective understanding of this captivating field.

Research Focus: Our research areas encompass a range of intriguing topics, including (but not only):

- 1) Life history traits and ecology of organisms with non-Mendelian, or clonal, reproduction.
- 2) Genomic, epigenomic, and cellular changes associated with aberrant reproductive strategies and asexuality.
- 3) The role of interspecific hybridization and asexual reproduction in speciation and the emergence of evolutionary novelties.
- 4) Identification of genetic sex-determination systems and their role in hybrid sterility and asexuality.
- 5) Assessing how restricted recombination impacts on adaptive potential to changing environment.
- 6) Linking non-Mendelian reproduction with evolution of polyploidy.

Lab website: <https://www.iapg.cas.cz/en/laboratories/-Laboratory-of-Non-Mendelian-Evolution/Research/>
 Google Scholar: <https://scholar.google.cz/>

[citations?user=azHnMBgAAAAJ&hl=cs&oi=ao](#)

Research Infrastructure: Our state-of-the-art research infrastructure enables interdisciplinary investigations from various angles, including phylogeography, population genomics, genotype-by-environment interactions, gene and allele expression, epigenomics, cytogenetics, and meiotic analyses. A list of representative publications from our lab is provided below.

Collaboration Opportunities: Our team actively collaborates with scientists from Europe and the USA. As a postdoctoral fellow, you will also have the chance to participate in a secondment at one of our collaborating institutions, or another institution of your choice, broadening your research horizons and establishing valuable connections.

Candidate Requirements: We are seeking an individual who possesses a solid publication track record in peer-reviewed journals given his/her career stage. Depending on particular research topic chosen by the applicant, it would be good to have the additional knowledge or experience in some of the areas like programming languages, Genome Wide Association Studies, statistical methods applied to biological data, cytogenetics and/or reproductive physiology. We are looking for an individual who is enthusiastic, creative, highly motivated, willing to work both independently and as a part of a team, and having good written and oral communication skills in English. Location and Accommodation: Our institute is situated in proximity to two beautiful historic towns, Melnik and Prague, where finding accommodation is convenient and enjoyable.

Application Process: For inquiries and information about this position, please email to: janko@iapg.cas.cz. Official information about the position, application process, and eligibility criteria are listed below (<https://meritcb.eu/>).

Representative publications of the lab:

Bartoš O, Röslein J, Kotusz J, Paces J, Pekárik L, Petr M, Halačka K, Četková Kašparová E, Mendel J, Boroň A, et al. 2019. The Legacy of Sexual Ancestors in Phenotypic Variability, Gene Expression, and Homoeolog Regulation of Asexual Hybrids and Polyploids. *Mol Biol Evol* 36:1902-1920.

Choleva L, Janko K, De Gelas K, Bohlen J, Člehtová V, Rábová M, Ráb P. 2012. Synthesis of Clonality and Polyploidy in Vertebrate Animals by Hybridization Between Two Sexual Species. *Evolution* 66:2191-2203.

Dedukh D, Majtánová Z, Marta A, Páleníková M, Kotusz J, Klíma J, Juchno D, Boron A, Janko K. 2020. Parthenogenesis as a Solution to Hybrid

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FederalU SaoPaulo MyxozoaEvolution

Postdoc: Federal University of São - bioinformatics, genome, transcriptome Fellowship provided by São Paulo Research Foundation - FAPESP

The Department of Ecology and Evolutionary Biology of the Federal University of São Paulo-UNIFESP offers a post-doctoral fellowship position (for 24 months) to contribute to the development of the thematic project FAPESP “ Myxozoa - cnidarians adapted to parasitism - integrating different tools to investigate the diversity, evolutionary history, development, and host-parasite interactions”. The selected candidate will work at the Federal University of São Paulo in Diadema (address: Prof. Artur Riedel 275, 09972-270, Diadema, São Paulo State, Brazil) where he/she will develop research on genomes of South American freshwater myxozoan parasites (Cnidaria: Endocnidozoa: Myxozoa). This opportunity is open to candidates of any nationality. The selected candidate will receive a FAPESP’s Post-Doctoral fellowship in the amount of R\$ 8.479,20 monthly and a research contingency fund, equivalent to 10% of the annual value of the fellowship which should be spent on items directly related to the research activity. For more information see <https://fapesp.br/en/postdoc>. The minimum requirements: 1) Experience in designing and processing next-generation sequencing (NGS) data; 2) Communication and writing skills in English; 3) Good history of scientific publications as lead author. 4) According to FAPESP rules, the candidates for post-doctoral fellowships should have completed their doctoral programs no more than seven years prior to application (<https://fapesp.br/en/postdoc>).

Work Location Instituto de Ciências Ambientais, Químicas e Farmacêuticas, Universidade Federal de São Paulo-Unifesp, Street Professor Artur Riedel, 275, Diadema, São Paulo, Brazil. Postal Code 09972-270.

Application must be done by E-mail to adriano@unifesp.br

Application Deadline 10 Jun 2023

Prof. Dr. Edson A. Adriano

Professor of Parasitology Department of Ecology and Evolutionary Biology Federal University of São Paulo-UNIFESP

Diadema - SP - Brazil

Professor de Parasitologia Departamento de Ecologia e Biologia Evolutiva Universidade Federal de São Paulo - UNIFESP Diadema - SP - Brasil

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 É obrigatória a utilização do e-mail @unifesp em todas as correspondências oficiais, institucionais e no acesso aos equipamentos e sistemas da Universidade Federal de São Paulo, conforme a portaria Reitoria n. 1182/2022 que define a Política de e-mail institucional da Unifesp.

“edapadrano@gmail.com” <adriano@unifesp.br>

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Hampton Virginia MarineMammalPopGen

POST DOCTORAL POSITION IN MARINE MAMMAL GENETICS (24 months)

Description The Hampton University Department of Marine and Environmental Sciences (Dr. Carolina Bonin Lewallen’s Lab) invites applications for a post-doctoral researcher in marine mammal genetics beginning September 2023 (24-month position).

Founded in 1868, Hampton University is a leading historically black university (HBCU) located on the Virginia Peninsula in the City of Hampton. It is a privately endowed, co-educational, nonsectarian institution.

Duties and Responsibilities We are seeking a motivated, enthusiastic individual to join Dr. Carolina Bonin Lewallen’s team as a post-doctoral researcher on an NSF-funded project “Move, adapt, or change: Examining the adaptive capacity of a Southern Ocean apex predator, the leopard seal”.

The postdoctoral researcher will be primarily responsible for data generation and data analyses for a global population genetics study of leopard seals. The candidate will work collaboratively with an international team of scientists, assist the PI with mentorship for undergraduate and graduate students, provide support on grant

and laboratory management/upkeep, and participate in Departmental and University academic activities. We value diversity in all forms and welcome applicants from all backgrounds to join us.

Qualifications Minimum Qualifications. The candidate must have the following:

* PhD in Biology, with emphasis in ecology, evolutionary biology, wildlife genetics, or a related field. ABD PhD candidates will be considered. * Experience (1-2 years) analyzing genetics data for non-model organisms (e.g., RADseq and mitogenomes) * Outstanding writing and communication skills

Preferred Qualifications. The candidate will ideally have some or all of the following:

* Ability to customize analytical packages already available (mostly in R) to analyze large genetic datasets * Laboratory skills (e.g., DNA/ RNA extractions; PCR; RT qPCR) * Familiarity with large mammal biology/ecology

How to Apply Review of applications will begin immediately and will continue until the position is filled. Please send the documents listed below to Dr. Carolina Bonin Lewallen, Hampton University carolina.lewallen@hamptonu.edu

* Full CV * Brief cover letter (2 pages max.) detailing your qualifications and experience relative to the position * A separate file listing three recommenders and their full contact information Note: This position may not be able to sponsor work visas of candidates not eligible to work in the United States at the time of the appointment.

Carolina Bonin Lewallen, PhD Assistant Professor Marine and Environmental Sciences Department 3 Shore Rd. Hampton, VA 23668 Office: Marine Science Building # 113 Office phone: (757) 728-6044

CAROLINA.LEWALLEN@HAMPTONU.EDU

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IndianaU EvoGenomics

A postdoc position is available in the Bracewell Lab at Indiana University, Bloomington. We are looking for a colleague to help study functional genomics and chromosome evolution in the most species-rich group of animals on the planet. This position will primarily be

focused on helping generate, analyze, and interpret various types of datasets (e.g., RNA-seq, Hi-C, Nanopore, and PacBio) to understand genome evolution at multiple evolutionary timescales. With this position, there is room to develop projects based on personal interest and research strengths. For more information about the Bracewell lab or the Biology Department, visit <https://ryanbracewell.com> and <https://biology.indiana.edu/>. A Ph.D. in Biology or a related field with previous research experience in evolutionary genetics, genomics, or bioinformatics is required. The ideal candidate will have some programming experience using both R and python and familiarity with large-scale genomic analyses on high performance computing clusters. Excellent communication skills and the ability to work independently as well as part of a team are expected. Salary will be commensurate with experience and will be highly competitive for the right person. Best consideration date is May 31st, 2023. The expected start date is negotiable but may be 8/1/23. 100% remote work is not available. Please submit a cover letter describing interest and previous experience, a curriculum vitae, and the names of at least three references (including email addresses and phone numbers) to <https://indiana.peopleadmin.com/postings/18364>. For questions about the position and additional details about the research, please contact Dr. Ryan Bracewell (rbracewe@iu.edu). The Bracewell Lab is located on the beautiful Indiana University campus. The city of Bloomington is in the rolling hills of southern Indiana and provides ample outdoor recreation in an affordable mid-sized city.

The College of Arts and Sciences is committed to building and supporting a diverse, inclusive, and equitable community of students and scholars.

Indiana University is an equal employment and affirmative action employer and a provider of ADA services. All qualified applicants will receive consideration for employment based on individual qualifications. Indiana University prohibits discrimination based on age, ethnicity, color, race, religion, sex, sexual orientation, gender identity or expression, genetic information, marital status, national origin, disability status or protected veteran status.

“Bracewell, Ryan Russell” <rbracewe@iu.edu>

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LinköpingU Sweden DrosophilaEvolGenomics

Postdoctoral opportunity in Evolutionary Genomics/Bioinformatics - Sweden

We are looking for a highly motivated postdoctoral fellow in Evolutionary Genomics/Bioinformatics for a two-year position at the Department of Physics, Chemistry and Biology, Linköping University in Urban Friberg’s research group (<https://liu.se/en/research/friberg-lab>).

Our research group primarily focuses on the evolution and genetics/genomics of ageing and sex differences. Ongoing projects involve the transcriptomics of ageing, condition dependence of sex-biased gene expression, and factors that influence the penetrance of deleterious mutations. All these projects utilize *Drosophila melanogaster* as a model organism. The postdoctoral fellow will be expected to contribute to these projects, as well as to develop a new line of research on factors that govern the germline mutation rate. Recent advances have revealed unexpected variation between species and individuals with respect to the occurrence of de novo mutations, but our understanding of the causes to this variation is yet limited.

The ideal candidate holds a PhD in evolutionary biology (with substantial experience in bioinformatics - RNA-seq and/or analysis of whole genome sequence data) or in bioinformatics. Proficiency in handling large-scale next-generation sequence data is particularly welcome. Competence in statistics and evolutionary genomics, as well as experience of fruit flies or other insect systems, is a merit. The working language at the department and in the lab is English. A high standard of spoken and written English is required.

Linköping University is a modern university with a vibrant and growing biology division. The university attracts some 27 000 students from all over the world, offering an international and stimulating research environment as well as providing a multitude of opportunities for collaboration and social interactions. Linköping is situated in central Sweden, conveniently located only a couple of hours by train/car from Stockholm and have beautiful and easily accessible surroundings.

Applications should be written in English and include i) a cover letter detailing earlier research, a list of skills,

and a motivation to work on above mentioned projects (max 3 pages), ii) a complete CV, and iii) the names and email addresses of 2-3 independent referees. Applications should be sent as one PDF to urban.friberg@liu.se. Applications will be reviewed continuously, but for full consideration please apply by June 19. The position will remain open until filled. The expected starting date is between September and November 2023.

Urban Friberg <urban.friberg@liu.se>

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MarianU Polyploid Genomics Evolution

As a part of a diverse community of faculty and staff who represent many faith systems and worldviews, the College of Arts and Sciences at Marian University-Indianapolis seeks qualified applicants for a Postdoctoral Scholar. The Postdoctoral Scholar will work alongside Dr. Rob Denton in the Department of Biology and participate in NSF-funded research on the mitonuclear conflict and co-evolution within polyploid salamanders. Preference will be given to those with a record of conducting scientific research in evolutionary biology and genomics and the potential for excellent teaching and leadership. The Postdoctoral Scholar will promote our Catholic Franciscan mission and identity by working closely with other faculty in Biology and teach ~1 course per academic year. The position will be funded up to three years pending satisfactory yearly performance evaluations. The salary will be \$55,000 and includes benefits.

The Department of Biology at Marian University is a collaborative and growing academic community committed to fostering student engagement, problem solving, and communication. Marian University believes that to grow stronger it is essential to recruit and retain a diverse faculty and staff to build an inclusive community. Thus, we welcome and encourage applications across the intersections of diverse races, ethnicities, religions, sexual orientations, gender identities, ages, socio-economic backgrounds, political perspectives, cultures, and national origins.

Essential Duties and Responsibilities: - Collect data, lead analyses, and communicate results (presentations, peer-reviewed manuscripts) on projects related to NSF

CAREER grant #2045704 - Teach approximately one Biology course per year - Mentor undergraduate researchers as they develop and implement independent research projects - Assist in the caretaking of live research animals - Participate in career development programming offered through the PI and Marian's Center for Teaching and Learning - Join the PI in building a respectful, welcoming academic environment in which students from all backgrounds can develop and make progress towards their goals - Actively engage the Catholic Franciscan mission and identity of Marian University by modeling the Franciscan Sponsorship Values, honoring the legacy of the founding congregation, promoting unity in diversity, and integrating the Catholic Franciscan intellectual traditions in programs and services.

Required Qualifications: - A PhD in a related field (Evolutionary Biology, Genomics, Integrative Biology, etc) to be awarded prior to the official start date - Experience in bioinformatics (Examples may include but are not limited to evolutionary genomics analyses, whole genome sequencing of non-model species, RNAseq and comparative transcriptomics). - Potential for excellence in teaching and leadership - Demonstrated ability to work with colleagues and students of diverse backgrounds.

Review of applications will begin immediately and continue until the position is filled. Applications require a cover letter, a current CV, contact information for two professional references, and responses to the supplemental mission questions.

Application link: <https://marian.peopleadmin.com/postings/2368> Contact: Rob Denton Website: dentonlab.org

Dr. Rob Denton (he/him) Assistant Professor of Biology Marian University

Phone: (317) 955-6198 Email: rdenton@marian.edu

063 Marian Hall 3200 Cold Spring Rd Indianapolis, IN 46222

www.dentonlab.org As a part of a diverse community of faculty and staff who represent many faith systems and worldviews, the College of Arts and Sciences at Marian University-Indianapolis seeks qualified applicants for a Postdoctoral Scholar. The Postdoctoral Scholar will work alongside Dr. Rob Denton in the Department of Biology and participate in NSF-funded research on the mitonuclear conflict and co-evolution within polyploid salamanders. Preference will be given to those with a record of conducting scientific research in evolutionary biology and genomics and the potential for excellent teaching and leadership. The Postdoctoral Scholar will promote our Catholic Franciscan mission and identity

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Morton Arboretum Oak Population Genomics

The Morton Arboretum's Plant Systematics Lab and Herbarium (<http://systematics.mortonarb.org>) seek a highly motivated individual to conduct population-level genomic and phylogenomic research on bur oak (*Quercus macrocarpa*) and related oaks of eastern North America. The research is part of a US-China international collaboration funded by the US NSF, investigating the effects of genomic diversity, functional diversity, phylogenetic diversity, and introgressive hybridization on oak symbiont communities. In addition to interacting with the collaborative team in the Center for Tree Science at The Morton Arboretum, the postdoctoral researcher will also be supported by a diverse network of partners at Duke University, Fort Collins Science Center, U of MN, and U of OK; and have opportunities to work with collaborators at South China Botanical Garden and Institute of Botany, Chinese Academy of Sciences.

NSF project summary: https://www.nsf.gov/awardsearch/showAward?AWD_ID=2129281&HistoricalAwards=false The Postdoctoral Researcher will be based in the Herbarium / Systematics Lab and Center for Tree Science of The Morton Arboretum (<https://mortonarb.org/science/center-for-tree-science/>). The Arboretum is a 100 year-old, world-renowned nonprofit botanic garden dedicated

to the study, growth, and conservation of trees. The Herbarium / Systematics Lab is a vibrant research community focused on plant biodiversity of the northern temperate zone, with a strong focus on trees and forested ecosystems. The Center for Tree Science (CTS) is a research center based within the Arboretum. CTS advances tree science expertise, builds collaborative scientific networks and resources, and trains the next generation of tree champions. Both the Herbarium and CTS work in collaboration with many other divisions of the Arboretum, including Chicago Region Trees Initiative, Global Trees Campaign, Living Collections, Learning and Engagement, Plant Clinic, Plant Health Care, and Natural Resources. The Center for Tree Science also acts as a hub for scientific collaboration, bringing together tree scientists from around the world to catalyze integrated, multidisciplinary tree science research to benefit trees and people.

The Postdoctoral Researcher will also have opportunities to connect with the broader evolutionary biology community of the Chicago Region, including potential colleagues at The Field Museum, University of Chicago, University of Illinois at Chicago, and Chicago Botanic Garden.

This position begins as early as August, 2023. Beginning salary is \$60,000 to \$62,000 commensurate with experience. The position comes with full benefits.

Please apply online at: <https://careers.hireology.com/-themortonarboretum/1244052/description> .Applications will be reviewed until the position is filled.

The Morton Arboretum is a champion for diversity, supporting a culture of inclusion that attracts, inspires, and engages people to achieve success. The Arboretum is committed to hire and develop employees based on job-related qualifications irrespective of race, religion, color, national origin, sex, sexual orientation, gender identity, age, disability, or veteran status. To increase diversity in professions related to the public garden realm, we encourage applications from underrepresented minorities, persons with disabilities, and veterans.

Please send all inquiries to ahipp@mortonarb.org.

Andrew Hipp, Director of the Herbarium and Senior Scientist in Plant Systematics

The Morton Arboretum

4100 Illinois Route 53

Lisle, IL 60532-1293

<http://systematics.mortonarb.org> *Andrew Hipp, PhD
*| Director of the Herbarium and Senior Scientist in Plant Systematics Lecturer, Committee on Evolutionary Biology, University of Chicago The Morton Ar-

boretum | 4100 Illinois Route 53 | Lisle Illinois 60532
T 630 725 2094 | ahipp@mortonarb.org | systematics.mortonarb.org

ahipp@mortonarb.org

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Munich Germany AncientPathogens

Dear all,

The Palaeogenomics group of the Department of Veterinary Medicine, at the Ludwig-Maximilians-Universität Munich, is looking to appoint a Postdoctoral Researcher at the earliest possible date.

About us: The Palaeogenomics group, led by Prof. Laurent Frantz, is part of the Institute of Palaeoanatomy, Domestication and the History of Veterinary Medicine, within the Department of Veterinary Medicine. Our group is broadly interested in evolutionary genomics, archaeology, conservation biology and sustainable agriculture. We exploit the power of ancient and modern genomics to contrast current patterns of genetic diversity to those in the past: this allows us to track evolutionary processes including artificial selection, extinction, speciation and domestication through time.

We are looking for you: Postdoctoral Researcher (m/f/x) in Munich

Your tasks and responsibilities: We are looking for a postdoctoral researcher to analyse genomic data from ancient domestic animal pathogens. Our team has already identified key archaeological and historical specimens from across Eurasia, which possess traces of highly interesting pathogens species (e.g. Marek's disease virus in chickens). The goal of the postdoc is to assist with the generation of pathogen genomes from these samples, and to (primarily) analyse the resulting genomic data. The overarching goal is to compare modern and ancient genomic data set to identify genetic variability that differentiates strains before and after the intensification of farming in second half of 20th century that can be functionally validated in collaborations with other labs at LMU and beyond. The work will be primarily computational, but the post-holder will be expected to assist with the logistic of sampling and data generation in our ancient DNA laboratory (e.g. programming robotic platforms). The postdoctoral researcher will be a part of a larger team comprising several postdocs and PhD

students investigating the evolutionary history of domestic animals using palaeogenomics and zooarcheological methods.

- Analyse pathogen both modern and ancient genomic data - Assist with the development of laboratory methods to improve the recovery of ancient pathogen DNA

Your qualifications: - PhD in Genomics or equivalent - Experience with analyses of Next Generation Sequencing data - Experience with bacterial, viral or metagenomics - Experience with analysing palaeogenomic data (desirable) - An interest in Evolutionary biology and/or Archaeology (desirable) - Experience with lab techniques related to ancient DNA (desirable) - Experience with training others in lab techniques (desirable) - Proficiency in English (prerequisite) and German (desirable) Benefits: The Ludwig-Maximilians-Universität Munich is one of the largest and most prestigious research institutions in Germany and offers a wide range of training and development opportunities. The workplace is in a central location in Munich that can be easily reached by public transport. The contract is for an initial 2.5 with potential for extension. The salary will be based on TV-L 'Entgeltgruppe' E13. The University of Munich is interested in increasing the number of female faculty members and encourages women to apply.

Services and offers from the LMU

Pages for employees of the LMU

Also possible in a part-time capacity.

People with disabilities who are equally as qualified as other applicants will receive preferential treatment.

Contact: To apply, please send a C.V, including contact of two referees, and a cover letter to Laurent.Frantz@lmu.de For enquiries or further questions please contact Prof. Laurent Frantz: Laurent.Frantz@lmu.de

Where knowledge is everything. LMU researchers work at the highest level on the great questions affecting people, society, culture, the environment and technology supported by experts in administration, IT and tech. Become part of LMU Munich!

In the course of your application for an open position at Ludwig-Maximilians-Universität (LMU) München, you will be required to submit personal information. Please be sure to refer to our LMU Privacy Policy. By submitting your application, you confirm that you have read and understood our data protection guidelines and privacy policy and that you agree to your data being processed in accordance with the selection process.

Prof. Dr. Laurent Frantz Professor of Palaeogenomics Department of Veterinary Sciences, Ludwig Maximilian

University of Munich

Senior Lecturer in Molecular Genetics/Informatics Department of Organismal Biology, Queen Mary University of London www.animal-palaeogenomics.com
Laurent Frantz <Laurent.Frantz@palaeo.vetmed.uni-muenchen.de>

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NordU Bod MSCA

Dear colleagues,

We are looking for colleagues who are interested in applying for a MSCA Postdoctoral Fellowship (<https://marie-sklodowska-curie-actions.ec.europa.eu/calls/msca-postdoctoral-fellowships-2023>) to join the Landscape Genomics Group at the Faculty of Biosciences and Aquaculture, Nord University, Bodø, $\frac{1}{2}$ (Norway).

The Landscape Genomics Group (LGG; <https://site.nord.no/landscapegenomics/>) studies local adaptation and adaptive potential in natural, human-disturbed, and exploited populations. To do so, we study the ecology and evolution of (mostly) aquatic organisms across large and ecologically diverse landscapes. LGG belongs to the Faculty of Biosciences and Aquaculture (<https://www.nord.no/en/about/faculties-and-centres/faculty-biosciences-and-aquaculture>), which has a strong focus on ecology, evolution, molecular biology, aquaculture, animal sciences, and microbial biotechnology. At 68 degrees north, Bodø, $\frac{1}{2}$ is a vibrant city lying within an area of magnificent nature. Bodø, $\frac{1}{2}$ is the perfect base for outdoor activities and exploration of Northern Norway.

We are primarily interested in candidates who want to gain more experience in evolutionary biology, population/landscape genomics, genome biology, or bioinformatics. We offer training in research, teaching, supervision, project management and proposal writing both through the MSCA fellowship and a customized project. Four members of LGG have received an MSCA fellowship in the past and will guide the candidates throughout the application process.

We welcome researchers who either wish to pursue their own project ideas, or who can contribute to our ongoing research lines. Possible directions of projects include:

- Analysis of climate change and harvesting impacts on the pelagic fish community of Lake Tanganyika;
- The analysis of the relative contribution of population-level structural and sequence variation to freshwater adaptation in three-spined and nine-spined stickleback fishes;
- The analysis of species-level structural variance in vertebrates in order to determine the molecular and evolutionary drivers of genome architecture and size.

The project work may be purely informatic, but can also include fieldwork, experiments, and sequencing, facilitated by our genomics division. You can find more general information about the MSCA Postdoctoral Fellowships below. Please send your CV and a short motivation letter to joost.raeymaekers@nord.no by 19th of June 2023 if you are interested in applying.

Best regards,

Joost Raeymaekers, Anja Westram, Konstantinos Sagonas, Roksana Majewska and Lars Martin Jakt

— About MSCA PF: The goal of MSCA Postdoctoral Fellowships is to enhance the creative and innovative potential of researchers holding a PhD, wishing to acquire new skills through advanced training, and international, interdisciplinary, and inter-sectoral mobility. MSCA Postdoctoral Fellowships are open to excellent researchers of any nationality, including researchers wishing to reintegrate in Europe, researchers who are displaced by conflict as well as researchers with high potential aiming for a career restart in research. The scheme also encourages researchers to work on research and innovation projects in the non-academic sector.

Eligibility: - Experience: in possession of a doctoral degree. At the call deadline, a maximum of 8 years full-time equivalent experience in research, measured from the date of award of the doctoral degree. - Nationality: any - Mobility: the researchers must not have resided or carried out their main activity (work, studies, etc.) in the country of the host organization (in this case Norway) for more than 12 months in the 36 months immediately before the call deadline.

More information: <https://marie-sklodowska-curie-actions.ec.europa.eu/> <https://marie-sklodowska-curie-actions.ec.europa.eu/calls/msca-postdoctoral-fellowships-2023> Joost Raeymaekers Faculty of Biosciences and Aquaculture Nord University N-8049 Bodø, $\frac{1}{2}$ Norway Tel: +47 75 51 78 46 Web: www.nord.no/no/Sok/_layouts/15/UiN.Internet/-UserProfilePage.aspx?pid=NORD%5C06023338

ResearchGate: www.researchgate.net/profile/Joost_Raeymaekers Google Scholar: scholar.google.be/citations?user=EZdjfbYAAAAJ&hl=nl&oi=sra

OhioStateU ConservationGenomics

POSTDOCTORAL POSITION IN SNAKE CONSERVATION GENOMICS

Gibbs Lab (<https://u.osu.edu/gibbslab/>), Department of Evolution, Ecology and Organismal Biology, Ohio State University

I am recruiting a Postdoctoral Research Associate to lead a project on the population genomics of endangered Massasauga Rattlesnakes (*Sistrurus catenatus*). The postdoc will use existing whole genome sequences from 100s of individuals from multiple populations to address a variety of fundamental questions in conservation/population genomics such as using measures of functional genomic variation to define management units, using theoretical and empirical approaches to understand the interaction between levels of functional genomic variation and genetic drift in small isolated populations of this snake, and identifying and assessing levels of variation in putative disease resistance genes. The candidate will have flexibility to develop independent research questions compatible with the primary project.

Recent manuscripts from the lab include:

Ochoa, A., Broe, M., Moriarty Lemmon, E., Lemmon, A.R., Rokyta, D.R., and Gibbs, H. L. 2020. Drift, selection and adaptive variation in small populations of a threatened rattlesnake. *Molecular Ecology* 29: 2612-2625.

Ochoa, A. and Gibbs, H.L. 2021. Genomic signatures of inbreeding and mutation load in a threatened rattlesnake. *Molecular Ecology* 30:5454-5469.

Mathur S., Haynes, E., Allender, M., Gibbs, H.L. 2022. Genetic mechanisms and biological processes underlying host response to ophidiomycosis (Snake Fungal Disease) inferred from tissue-specific transcriptome analyses. *bioRxiv*, 2022.03. 25.485740.

Mathur, S., Mason, A., Bradburd, G., Gibbs, H.L. Functional genomic diversity is correlated with intensity of genetic drift in an endangered rattlesnake. *PNAS* (in review).

The position is funded through the Ohio Biodiversity Conservation Partnership (<https://obcp.osu.edu>) and the selected candidate will gain experience interfacing with government agencies like the Ohio Division of Wildlife personnel. The postdoc will have the oppor-

tunity to be involved in other long-term ongoing research projects such as the evolutionary genomics studies of Brazilian snakes in collaboration with researchers at the Instituto Butantan in Sao Paulo, Brazil.

MINIMUM QUALIFICATIONS: - PhD in evolutionary biology, conservation genetics, bioinformatics or a related field - Expertise in population/conservation genomics or evolutionary genetics - Fluency in a programming language such as Perl or Python - Publication record

DESIRED QUALIFICATIONS: - Experience with analysis of whole genome data - Experience with demographic modeling using high performance computing resources

START DATE AND DURATION The position is available 1 September 2023. The initial appointment is for one year with the strong possibility of reappointment for one additional year pending satisfactory performance. Salary is \$60K with full benefits. The Ohio State University offers an exceptional benefits package.

APPLICATION PROCESS General inquiries and/or applications should be sent to H. Lisle Gibbs (gibbs.128@osu.edu). Interested candidates should send the following: 1) a CV, 2) Statement of research interests and how current professional abilities match possible project goals, 3) Names and contact information for three references. Review of applications will start 15 June 2023 and will continue until the position is filled.

ABOUT COLUMBUS The Ohio State University campus is located in Columbus, the capital city of Ohio. Columbus is the center of a rapidly growing and diverse metropolitan area with a population of over 1.5 million. The area offers a wide range of affordable housing, many cultural and recreational opportunities, excellent schools, and a strong economy based on government as well as service, transportation and technology industries (see <http://liveworkplaycolumbus.com/>). Columbus has consistently been rated as one of the Top U.S. cities for quality of life, and was selected as one of the Top 10 cities for African Americans to live, work, and play by Black Enterprise magazine. Additional information about the Columbus area is available at <http://www.columbus.org>. The Ohio State University is an equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation or identity, national origin, disability status, or protected veteran status.

H. Lisle Gibbs Professor, Department of Evolution, Ecology, and Organismal Biology Director, Ohio Biodiversity Conservation Partnership 318 W. 12th Ave, Ohio State University Columbus, Ohio USA 43210-1293 P: (614)

688-3861

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OhioU FloralEvolution

POSTDOCTORAL RESEARCH POSITION IN FLORAL EVOLUTION

The Schenk Lab at Ohio University is looking for a Postdoctoral Researcher to start an NSF Funded project in the summer/fall of 2023. The position will be in person in Athens, Ohio for two years and includes travel support for research and conferences.

Brief Project Overview: Flowers have experienced extraordinary morphological changes through evolutionary time that includes multiple origins of novel, non-fertile structures. Because flowers are a complex network of interconnected parts, they provide an ideal system for studying integrated-trait evolution in response to functional cooption. We are investigating coopted floral structures called staminodes, which are sterile stamens that can perform novel functions, such as nectar production, pollinator attraction, or enhanced pollen dispersal or deposition. Staminodes provide an exceptional opportunity for revealing the evolutionary consequences of functional cooption in an integrated system. The project will study staminodes in *Mentzelia* (Loasaceae) to answer the question: Is there an evolutionary response to compensate for the loss of reproductive function when a structure is coopted to perform a novel function?

Research tasks: The postdoctoral research associate will be expected to conduct experiments, including genomic library preparation and sequencing, phylogenomics, phylogenetic comparative approaches, morphological characterization of floral traits, floral manipulation experiments with natural pollinators, and field work in the western U.S. The successful candidate will have the opportunity to attend and present work in national and international meetings and publish research results. The postdoctoral research associate will co-mentor undergraduate students and collaborate with a Ph.D. student, research associates, and the PI.

Qualifications: The Postdoctoral Scholar must have earned their Ph.D. in Botany, Biology, or a closely re-

lated field before August 2023. Successful candidates are preferred to have research experience in plant evolution, phylogenetic comparative approaches, floral morphology and evolution, and/or pollinator ecology.

Application process: Please submit a cover letter that outlines your previous research experiences, CV, contact information (name, phone number, email, and mailing address) for three professional references, and one publication that best represents your qualifications to <https://www.ohiouniversityjobs.com/postings/41476>. Applications received by July 9th, 2023 will receive full consideration; however, applications will be reviewed until the position is filled. Please see the above link for additional information about applying and qualifications.

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=2117446 Application link: <https://www.ohiouniversityjobs.com/postings/46192>

Ohio University is proud of its rich history, diverse campuses, international communities, and beautiful Appalachian settings. As part of our ongoing efforts to provide and support a transformative learning experience, we affirm our commitment to fostering a welcoming, respectful, diverse, and inclusive workforce and community. All qualified applicants are encouraged to apply and will receive consideration free from discrimination on the basis of race, color, religion, age, ethnicity, national origin, national ancestry, sex, pregnancy, gender, gender identity or expression, sexual orientation, military service or veteran status, mental or physical disability, or genetic information. Ohio University is an equal access/equal opportunity and affirmative action employer.

John J. Schenk, Ph.D. Assistant Professor Department of Environmental and Plant Biology Ohio University 401 Porter Hall Athens, Ohio 45701-2979 Office phone: (740) 593-0716 E-mail: schenk@ohio.edu Lab website: <https://schenklab.weebly.com> “Schenk, John” <schenk@ohio.edu>

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QuebecCity EvolutionarySystemsBiology

Postdoctoral position in evolutionary systems biology

We are seeking creative candidates for a postdoctoral position in evolutionary systems biology. The specific project will be developed with the selected candidate around the themes of interest in our group, which include the evolution of protein interaction networks, evolution of gene regulation and of gene duplication.

See recent papers from the lab on these topics:

<https://www.science.org/doi/full/10.1126/-sciadv.add9109> <https://www.nature.com/articles/s41559-022-01846-4> <https://www.biorxiv.org/content/10.1101/2022.05.24.493236v2.abstract> <https://www.nature.com/articles/s41467-021-21873-2> <https://www.pnas.org/doi/abs/10.1073/pnas.2014345118> <https://www.embopress.org/doi/full/10.15252/-msb.20198871> <https://www.nature.com/articles/s41467-020-15796-7> <https://www.science.org/doi/abs/10.1126/science.aai7685> We use both computational and experimental approaches (genome editing, deep mutational scanning, experimental evolution), and the ideal candidate would be able to combine both, but this is not a strict requirement.

The Landry lab is located at the Institut de Biologie Intégrative et des Systèmes (IBIS) of Université Laval in Québec City and is part of the Quebec Network for Research on Protein Function, Engineering, and Applications (PROTEO). The lab is an international team of 20+ students, postdoctoral fellows and research associates from diverse backgrounds (microbiology, biology, bioinformatics, biochemistry) addressing questions in evolutionary cell and systems biology. Québec City is an affordable and lively city that offers an excellent quality of life.

https://en.wikipedia.org/wiki/Quebec_City Requirements:

PhD in biology, biochemistry, bioinformatics, or any related and relevant field, obtained after 2022. No formal background in the study of evolution is needed but interest in studying evolution is required.

Publications relevant to the field.

Starting date: September 2023 or January 2024 (flexible)

Duration: 2 years with possibility of extension

The application package (1 single PDF file) should include a motivation letter demonstrating the interest of the candidate for the field and a short summary of specific interests, a CV and the contact information of three people who can be contacted for reference. The single file should be sent to landrylaboratory@gmail.com

The position will remain open until a candidate is selected.

Christian Landry

Christian Landry, PhD Professeur/Professor

Canada Research Chair in Cellular Systems and Synthetic Biology

<http://landrylab.ibis.ulaval.ca/> T: 418-656-3954 Poste interne: 403954 T: 418-656-7176

Christian Landry <Christian.Landry@bio.ulaval.ca>

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StellenboschU ElasmobranchEvolution

“Genomic adaptation and distribution modelling of elasmobranchs in Southern Africa” funded by the NRF Marine and Coastal Research call.

Host: Aletta Bester-van der Merwe (Stellenbosch University) We offer a two-year contract, at a starting value of 250000 ZAR/year.

Summary: On a global scale, climate change and the over-exploitation of marine species are placing severe pressure on marine ecosystems. Elasmobranchs (sharks and rays) are among the most depleted marine animals and the loss of keystone species from ecosystems has profound effects on the entire food-web. To understand the vulnerability of populations to global change, it is crucial to identify unique genetic populations adapted to specific habitats and environments. Genomic studies provide a means not only to assess the degree of connectivity and differentiation between different regions but also to allow the identification of regions involved in genomic adaptation by comparing relative differentiation among genome-wide loci. A better understanding of how environmental changes will impact suitable habitats for these vulnerable elasmobranch populations is

therefore of fundamental importance to guide effective, regional, and global management and conservation initiatives. The project will therefore aim to improve knowledge on sharks and rays impacted by fisheries and environmental changes in coastal waters of Southern Africa through the identification of unique genetic populations adapted to vulnerable habitats and/or possible shifts in distribution ranges brought on by climate change. The project will build on previous genetic work conducted on elasmobranchs in Southern Africa. This will allow the development of an integrative framework of comparative genomics, genotype-environment interactions and evaluating species distribution patterns using species distribution modelling crucially needed to develop effective management strategies for vulnerable elasmobranch populations.

Work tasks: The postdoc will conduct both laboratory and computational work involving genomic assessment and distribution modelling of key shark and ray species including. The more specific aims are to 1) test for signatures of selection through outlier differentiation methods) perform genotype-environment analysis (GEA) (selection driven by environmental variables) and 2) to assess the current and future suitability of habitat for vulnerable shark and ray populations along the Southern African coast and more widely depending on species range.

Minimum requirements: PhD in genetics, molecular biology, bioinformatics or related disciplines obtained in the last 5 years.

First-author or co-author of at least three peer-reviewed manuscripts published in the field.

Ability to work in a multi-disciplinary, international team.

Excellent time and project management skills.

Previous experience with genomics data analyses, in particular low coverage genomes.

Experience with genome assembly and/or species distribution modelling.

Additional requirements: Knowledge of marine ecosystems and species.

Proficiency in wet lab analyses related to molecular markers and DNA sequencing.

Experience in working with R and other programming software Excellent ability to communicate and write in English.

The lab and research group: The Elasmobranch Genetics Research Group, based in the Department of Genetics at Stellenbosch University, South Africa, is currently

collaborating with various governmental and wildlife conservation based organizations on the application of genetic and genomic tools for enhanced fisheries management, monitoring and conservation. The group also contributes to marine conservation and fisheries management in Africa through education, research, community interaction, business development and services.

Postgraduate students and early-career researchers are given an equal opportunity to be trained in the basic and more advanced fields of genetics, genomics, bioinformatics, and integrated ecosystem modelling with application to biodiversity conservation and management. All major facilities and laboratory equipment are available in the Department of Genetics, including several DNA sequencing platforms that are accessible from the Central Analytical Facilities situated in the same building.

To apply: Please send a motivation letter, comprehensive CV and the contact of two references to: aeb@sun.ac.za Ideally, candidates should start as soon as possible, but latest July 2023.

The position will remain open until a suitable candidate is found.

Thank you

Aletta Bester-van der Merwe

PhD Genetics Associate Professor | Mede Professor Agri-sciences | Agriwetenskappe Office number +27 21 808 5835

Rm222, JC Smuts Building, Van der Bijl Street

Stellenbosch Campus | South Africa

“Van der Merwe, AE, Prof [aeb@sun.ac.za]”
<aeb@sun.ac.za>

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TarletonStateU PopulationEcologyEvolutionOfReptiles

TarletonStateU.ReptileEvolutionaryMorphology

Job Title: Postdoctoral Research Scholar

Department: Biological Sciences

Location: Stephenville Campus, Stephenville, TX

Position Overview:

Characterization and Evolution of Morphology in Rep-

tiles. A major research focus in our lab is to understand morphology and evolution of complex phenotypes from developmental to macroevolutionary scales. General interests in this area include the evolution of body size and sexual size dimorphism, developmental constraints on morphospace, phenotypic evolution on islands, and evolution of the squamate body plan—mostly through analysis of skulls, body elongation, and limb loss. Several ongoing projects with great potential for postdoctoral collaboration include evolution and variation in dipsadine snake skulls, improved use of multivariate methods to characterize complex phenotypes (including use of morphology in systematic studies), and pioneering ways to extract complex shape information from photos to evaluate variation in turtle cephalic markings (and in the process, 'hopefully' understand aspects of skin patterning development). Another area for potential research partnership is to understand phenotypic segregation and expression in hybrids, and we are currently developing natural hybrid systems with rattlesnakes and map turtles to further understand the genomic basis of complex traits.

The candidate's start date is expected to be between May 1, 2023 and September 1, 2023. This full-time position is on a renewable twelve-month contract with a maximum appointment of two years. This is a non-faculty research staff appointment.

Job Duties:

This postdoctoral position involves performing and managing scientific research projects, generating and/or vetting data as well as organizing compiled databases, analyzing data using statistical modeling techniques, participating in writing follow-up grants, presenting research at national meetings, and leading the development of high-quality peer-reviewed scientific papers.

Knowledge, Skills, and Abilities:

Basic knowledge of statistical concepts and methods and their application to either population ecology or multivariate morphological research; research methods, principles, techniques, and philosophies. Preferred candidate should be willing to conduct extensive field research and be skilled in using statistical and (preferably) GIS software, primarily in the R environment. Applicant should have the ability to plan, organize, and oversee research projects in conjunction with faculty mentor, interpret and publish research findings, and communicate effectively.

Minimum Qualifications:

The successful candidate will have earned a PhD or equivalent research doctorate at the time of appointment (i.e., start date); will have received their doctoral

degree no more than 4 years before the start of the financial support; and will be able to begin employment at Tarleton State University between May 1 and September 1, 2023.

If the degree has not been conferred at the time applicant applies for the postdoctoral scholar position, a letter needs to be attached from the school's official Graduate Office and/or Registrar's Office certifying that all requirements for the degree have been met and stating the degree conferral date.

The selected candidate for the position must be able to meet eligibility requirements for work in the United States at the time appointment is scheduled to begin and continue working legally for the proposed term of employment, be able to communicate effectively in English, and be trained in or able to obtain training in the responsible and ethical conduct of research.

Preferred Qualifications:

Preferred qualifications include but not limited to the following:

PhD in Biology, Ecology, Evolutionary Biology, or related field
 Experience in field research in aquatic systems with reptiles (turtles and/or snakes) or with morphological data (museums, databases, etc.)
 Skills in statistical concepts and methods and their application to research analysis, including knowledge of a statistical program such as R; experience with linear mixed model analysis, multivariate analysis, and (depending on interests) geometric morphometrics
 Some experience with GIS programs such as ArcGIS (or spatial analysis in R)
 Ability to plan, organize, and assist in directing research projects, including field work, data management, analysis, and report writing/effective communication of results

Salary:

\$60,000/yr

Application Materials:

Cover letter, curriculum vitae (including relevant publications), summary of research experience, contact information for at least three references. Please send initial materials and inquiries to Dr. Jesse Meik (meik@tarleton.edu).

Application Deadline:

The position will be open until filled; however, to guarantee full consideration please submit application materials no later than Monday, June 12, 2023.

Applications must be submitted online at

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To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

TexasAMU Two AvianEpigeneticsMigration

TexasAM.Epigenetics.StructuralVariants.Migration
TWO FULLY FUNDED POSTDOCTORAL POSITIONS AVAILABLE

Delmore lab (delmorelab.com)

Department of Biology, Texas A&M University

Position 1: Epigenetics, seasonal migration, and conservation.

We are seeking one Postdoc to lead a project examining epigenetic signatures related to migration. The main species for this project is the Purple martin, a songbird with both short- and long-distance migrants where the relative importance of plasticity in migratory timing likely varies. Aerial insectivores like martins are in steep decline and their inability to modify their migratory behavior may be partly responsible; a question we will address here. Extensions to a second system - a hybrid zone between Swainson's thrushes that differ in their migratory behavior - are also possible. This project will involve both molecular and bioinformatic work, generating epigenetic libraries and analyzing the subsequent data. There is also potential to contribute to fieldwork although we do already have a large dataset of individual-level tracking data that can be used, allowing the successful applicant to dig in immediately!

Collaboration: The main supervisor is Dr. Kira Delmore but this is part of a large, international collaboration with Dr. Kevin Fraser (University of Manitoba) and Dr. Pierre deVillemereuil (École Pratique des Hautes Études). This project is highly collaborative with team meetings and opportunities to visit both collaborators. The project is also supported by partnerships with government agencies (e.g., the US Fish and Wildlife Service and Committee on the Status of Endangered Wildlife in Canada).

Position 2: Structural variants, seasonal migration, and speciation.

We are seeking a second Postdoc to lead a project linking structural variants to both seasonal migration and speciation. The main study system for this project is a

hybrid zone between Swainson's thrushes that differ in their migratory behavior. This is largely a bioinformatic project; we already have individual-level tracking data for hundreds of birds. We are looking for someone to design a sequencing strategy, call and analyze structural variants. We also have quite a few additional '-omic' datasets that can be used to complement results from structural variants. There is considerable flexibility in where the research questions could go, and we have existing data permitting immediate productivity!

General information for both positions:

Start Date: Flexible but the sooner the better! Two-year contracts with 1+ year extensions.

Funding: These are both fully funded positions. We have two, five-year federal grants that will support both the research and salary that go along with these positions.

Experience: PhD in biology, bioinformatics, or related fields. Experience with birds is not necessary. Previous experience with next-generation sequencing is ideal (especially with the data described above [epigenetic or structural variants]). Candidate should show evidence of past productivity (e.g., first-author pubs and/or grants).

Environment: We are a diverse, high-achieving and yet balanced group of researchers from all stages. We bring together expertise for a broad set of fields and are dedicated to providing high quality training for diverse career paths. The lab is part of the Biology Department (<https://bio.tamu.edu>) along with the interdisciplinary programs of Genetics (<https://genetics.tamu.edu>) and Ecology and Evolutionary Biology (<https://eeb.tamu.edu>). These programs bring together members of many departments from a variety of scientific and international backgrounds. The Biology Department is in the middle of making existing expansions into evolutionary genomics (e.g., three recent hires) making it a great place to work on this topic. Texas A&M is a Tier 1 institution with a number of research facilities. College Station is a small, friendly university town located between Austin and Houston.

To apply: Please email a cover letter and CV to kdelmore@bio.tamu.edu. The cover letter should outline your research interests, motivation, and experience. The CV should include the names and emails of at least two references.

Kira Delmore | Assistant Professor Biology, College of Science | Texas A&M University 3528 TAMU | College Station, TX 77843 1 (979) 900-2129 | kdelmore@bio.tamu.edu delmorelab.com

* My working hours may not be your working hours.

Please do not feel obligated to reply outside of your normal work schedule. *

“Delmore, Kira” <kdelmore@bio.tamu.edu>

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TreeOfLife Sanger Bioinformatics SymbiosisGenomics

I am seeking a Senior Bioinformatician to join the Blaxter group in the Tree of Life programme at the Tree of Life programme in the Wellcome Sanger Institute, Cambridge, UK.

see <https://tinyurl.com/ToL-Blaxter-Job2023-1> About the role: The position is part of the newly-funded Leverhulme Research Centre for the Holobiont [<https://www.sanger.ac.uk/collaboration/leverhulme-centre-for-the-holobiont>] and <https://www.imperial.ac.uk/holobiont/>], where a diverse team of biologists from many disciplines are examining inter-species associations from evolutionary, metabolic/physiological and ecological standpoints.

Symbiosis covers a spectrum of relationships, from temporary to lifelong, and from mutually beneficial - such as between coral and algae - to exploitative - between parasite and host. These relationships are hugely important and have evolved independently many times. Yet little is known about the underlying genetics of these complex relationships between species, how symbiotic partners adapt to one another over time, how resilient these partnerships are, how they respond to disruption and how the interactions might be supported and engineered to build better agriculture and promote conservation. What do the genomes of collaborating partners reveal of their evolving relationships? Are the dynamics of genomic change predictable, and can these dynamics be used to in turn predict the likely mode of association between species where the relationship is unclear?

Tree of Life [<https://www.sanger.ac.uk/programme/tree-of-life/>] is a growing new programme at the Sanger Institute [<https://www.sanger.ac.uk/>], with large-scale ambitions of biodiversity genomics across eukaryotes. Of particular relevance to this appointment is our involvement in the Aquatic Symbiosis Genomics project [<https://www.sanger.ac.uk/collaboration/aquatic-symbiosis-genomics-project/>], a

global initiative to generate genomics data for 500 symbiotic systems.

Within this wide topic area, the specific projects undertaken will be co-created by the Senior Bioinformatician in consultation with the group leader, other faculty and the wider programme, with an emphasis on large-scale analysis across diversity.

The Blaxter group in the Tree of Life programme works on a range of taxa, from protists to metazoa, with overarching goals of linking genomic diversity to phylogenetic diversity, and understanding the drivers of and constraints on genomic change. The group is intensely collaborative, with shared questions that we explore in different groups of species. We develop toolkits for our work that we share openly with others, and provide data platforms to support dissemination of our work. You will be embedded in our supportive and dynamic environment to produce significant work of wide impact.

Do contact Mark Blaxter mb35@sanger.ac.uk to discuss the position.

About you: You will carry out a programme of research based on reference quality genomes from the Tree of Life programme and other public data, with a particular focus on the evolution of collaboration between species in symbiotic (mutualist and parasitic) and other associations. The work will address the origins and impacts of symbiosis on genome structure, and better resolution of pattern and process in co-evolution between the varied partners found in association.

Technical Skills: - Extensive knowledge of genome assembly and analysis with a proven track record in eukaryotic species - Experience working with large genomic datasets and diverse databases - Programming in relevant, modern languages, including Python and R; experience with software development and good practice in coding - Excellent communication and organisation skills; Ability to work collaboratively and inclusively with a range of stakeholders
Competencies and Behaviours: - Demonstrates inclusivity and respect for all - Highly motivated - Dynamic and inquisitive - Ability to work collaboratively - Commitment to open science - Independent and creative

Application Process: Please apply at <https://tinyurl.com/ToL-Blaxter-Job2023-1> with your CV and a Cover Letter outlining how you meet the criteria set out above. Other information Salary range: 43,597 to 51,000 (dependant on skills and experience) Contract Type: 4 years Closing Date: 4th June 2023

Mark Blaxter

— / —

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>

TUMunich PopulationGenomics

The Professorship for Population Genetics at the Technical University of Munich, TUM School of Life Sciences, hires a Post-Doctoral researcher in the field of theoretical/empirical population genomics

The focus of our group is on understanding population genetics/genomics processes underlying plant adaptation to biotic and abiotic conditions, including dormancy, plant-parasite coevolution and adaptation to abiotic stresses. We concentrate on developing new theoretical framework and statistical inference methods making use of full genome data to uncover the causes and consequences of dormancy and of coevolutionary dynamics. Our recent projects involve population genomics of dormancy in pathogens of humans and crops, and of sweepstakes reproduction which is a common trait of many pathogens and marine invertebrates. We develop inference methods based on Approximate Bayesian Computation (ABC), Sequentially Markovian Coalescent (SMC) or Deep Learning (DL).

The post-doc position is for three years (with a possible extension of three further years) as a career step for experienced candidates to develop scientific independence. The post-doc researcher will contribute to existing projects and is encouraged to develop his/her own projects. The position includes a teaching obligation of 4 hours per week during the semester (5 SWS) which is completed within the set of BSc and MSc courses offered by the group.

The candidate should have strong background in evolutionary genetics/genomics or theoretical population genetics. Knowledge and practical experience in bioinformatics and analysis of full genome data is also required for mentoring students conducting research and internship projects. Furthermore, English skills, both written and spoken, are essential and the candidate should be willing to work in an international interdisciplinary team comprising mathematicians, bioinformaticians, and plant biologists. She/he should have a PhD in mathematical biology, population/evolutionary genomics, computational biology or closely related disciplines.

The Technical University of Munich is an equal opportunity employer and particularly welcomes applications from qualified women and individuals with disabilities. The salary is according to German/Bavarian income level TV-L E13 (100%).

Please send your comprehensive application including a letter of motivation (1 page), your CV, MSc and PhD certificates, list of publications, and names of 2 potential referees as a single pdf file by email to: silke.bauer@tum.de.

Informal enquiries to Prof. A. Tellier (aurelien.tellier@tum.de) are welcome.

Applications will be reviewed regularly from June 1st 2023 on but accepted until a suitable candidate is found. The starting date is ideally in summer/fall 2023.

Updated list of publications and projects on www.popgen.wzw.tum.de Prof. Aurelien Tellier, PhD Assoc. Prof. for Population Genetics Dept of Life Science Systems School of Life Sciences Technical University of Munich Liesel-Beckmann Strasse 2 85354 Freising - Germany www.popgen.wzw.tum.de Aurelien Tellier <aurelien.tellier@tum.de>

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UAberdeen UK EcoEvoModelling

Title: Research Fellow - Unravelling the role of genetic variation of beneficial arthropods in agroecosystems.

Duration: 3.5 years.

An enthusiastic, motivated, and creative postdoctoral Research Fellow is sought to join a collaborative team within the School of Biological Sciences to develop predictive process-based models on the effects of climate and land-use change on arthropods' genetic diversity and persistence in agro-ecosystems.

The ideal candidate should have a strong background in theoretical evolution and/or ecology, strong programming skills, strong interest/knowledge of population genetics and interest in applying those skills to improve understanding and forecasting of species' responses to anthropogenic changes. The fellow will join Dr Greta Bocedi's team (<https://gretabocedi.com/>) and a wider strong team of PIs, postdocs and postgraduate students developing and applying the RangeShifter platform (<https://rangeshifter.github.io/>; led by Dr Greta Bocedi,

Prof Justin Travis and Prof Damaris Zurell at the University of Potsdam, in collaboration with Dr Lesley Lancaster), who are embedded within a global collaborative network that will maximize both the impact of the work and the advancement opportunities to the postdoctoral researcher. Further, the fellow will be part of the Centre of Ecological Genetics (<https://bio.au.dk/forskning/-forskningcentre/centre-for-ecological-genetics/>), an international collaboration between PIs from universities in Aarhus (DK), Helsinki (FI) and Aberdeen (UK), with Aberdeen leading the modelling component. The centre's research spans several topics in ecological and evolutionary research using molecular methods and statistical and process-based modelling.

Further information and application: <https://www.abdnjobs.co.uk/vacancy/research-fellow-524959.html> Informal enquiries are welcome to Greta Bocedi, greta.bocedi@abdn.ac.uk

Closing date: 23/05/2023.

Dr Greta Bocedi Royal Society University Research Fellow School of Biological Science, University of Aberdeen Zoology Building, Tillydrone Avenue, AB24 2TZ Tel: +44 (0)1224 272392 greta.bocedi@abdn.ac.uk www.gretabocedi.com Novo Nordisk Challenge Centre for Ecological Genetics www.ecogenetics.au.dk The University of Aberdeen is a charity registered in Scotland, No SC013683. Tha Oilthigh Obar Dheathain na chathannas cl?raichte ann an Alba, ?ir. SC013683.

“Bocedi, Greta” <greta.bocedi@abdn.ac.uk>

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UArizona ComparativePopGenomics

NSF funded 2-year postdoc in comparative population genomics and transcriptomics on the diversification of biota from Baja California Peninsula

Focus on bioinformatic analyses of population genomic data via low-coverage whole genome resequencing and RNA Seq across multiple species of plants, lizards and desert rodents. University of Arizona, School of Natural Resources and the Environment

A funded 2-year postdoc is available in population genomic analyses via low coverage whole genome resequencing and RNA-Seq. The position is part of a

NSF-funded transdisciplinary GeoGenomics investigation that combines geologic, climatic, and genomic data to test multiple non-mutually exclusive hypotheses in Baja California peninsula (Mexico). The genomic data will be used to test the effects of marine seaways, volcanic activity, glacial refugia, and rainfall asynchrony on the biological diversification through signatures in the genomes of desert reptiles, mammals, and plants. The postdoc will work as part of the larger Baja GeoGenomics consortium (<https://bajageogenomics.org/>) composed of a team of geologists and biologists from University of Arizona, University of Oregon, Arizona State University, University of Arkansas, and California State University. Eagerness to work in a multidisciplinary setting and with a team is essential. The research project can focus on any, or multiple, of the following:

- * Conducting population genomic analyses to identify genetic variants from low-coverage genome sequencing
- * Parametrize models of neutral divergence for multiple species constrained by the geologic evidence
- * Perform landscape genomic analyses to test concordance with niche modeling hypotheses of expansion-contraction from glacial refugia
- * Correlate present-day ecological niches with spatial signals of natural selection both from genome sequencing and differential RNA-Seq expression
- * Develop novel bioinformatic approaches for simultaneously integrating geologic, genomic, and ecological datasets.

Interested candidates should send their CV, names of 2 references, and a brief summary of interests, including how your background would apply to these topics (and be prepared to have 2 reference letters send on request), by June 7, 2023, to both Adrian Munguia-Vega (airdrian@arizona.edu) and Melanie Culver (mculver@arizona.edu). Selected researcher(s) will work in collaboration with both Dr. Munguia-Vega and Culver, and will join Dr. Melanie Culver's Conservation Genetics Lab at University of Arizona, Tucson, AZ. Official application needs to be submitted to postdoc job posting at the University of Arizona Human Resources. <https://arizona.csod.com/ux/-ats/careersite/4/home/requisition/16199?c=arizona>

Starting date: August 2023 Payrate: \$56,484/hour with an ERE of 17.6% (includes health benefits but not retirement contributions). Recent Media coverage: <https://bit.ly/3Z7jaFH> Project Description: https://www.nsf.gov/awardsearch/showAward?AWD_ID=-1925535&HistoricalAwards=false “Culver, Melanie - (mculver)” <Culver@ag.arizona.edu>

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UBasel MicrobialEvolutionTheory- Phylogenetics

Post-doctoral position in microbial evolution or phylogenetics

A postdoctoral position is available in the research group of Richard Neher at the Biozentrum of the University of Basel. Our group works on evolution of pathogenic viruses and bacteria with a focus on seasonal influenza virus, SARS-CoV-2, enteroviruses, and drug resistance evolution in bacteria. Research in our group combines population genetics, phylogenetics, mathematical models, and next-generation sequencing to understand the complex dynamics of host-pathogen interactions. On one hand, we are interested in developing tools to analyze and visualize large datasets and maintain several popular tools such as Nextstrain (together with Trevor Bedford's group in Seattle), TreeTime, panX, and panGraph. On the other hand, we tackle fundamental questions of how microbes evolve in light of changing population immunity, drug therapy, or new environments. Adaptation via recombination, reassortment, and genome structure evolution are of particular interest to us.

Possible projects of a post-doctoral fellow include (i) novel phylogenetic and phylodynamic methods suitable for very large data sets, (ii) scalable inference from ancestral reassortment graphs of influenza, and (iii) evolution of gene content and gene order of bacterial chromosomes or plasmids. The scope of the projects is flexible, can be tailored to the applicants interest and skills, and we are open to exciting new ideas.

You would have the opportunity to pursue original research in a small, interactive, and interdisciplinary group that tackles diverse problems in computational biology. We are internationally well connected and collaborate with several other research groups in Basel and in different parts of the world. We have access to state-of-the-art computing facilities, wet lab space, and sufficient funding for conference travel and research expenses. Our team includes a professional software engineer who can turn novel methods into robust and maintainable software. Salaries are competitive.

Your profile

We are looking for a creative and collaborative person with a genuine interest in evolution and with either a

* a degree in bioinformatics, computer science, physics, applied math or similar and a strong genuine interest in biology, or * a life science degree and strong quantitative skills

If you are excited about this opportunity but unsure whether your profile matches what we are looking for, please get in touch.

Application

Please send your cover letter, statement of research interests, CV, publication list, and contact information of three references as one pdf file to Richard Neher. Please state clearly in your cover letter what your main interests are and how you think it resonates with the work of our group. Reviewing of application will start on June 1st and continue until the position is filled.

For more information, please have a look at

https://neherlab.org/202304.BZ_postdoc.html or get in touch with Richard Neher (richard.neher@unibas.ch).

Richard Neher Biozentrum University of Basel tel: +41 61-20-75834 web: <https://neherlab.org> Richard Neher <richard.neher@unibas.ch>

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UCambridge UK MetabolicDivisionOfLabor

Research Associate / Postdoc - metabolic division of labour in ant colonies University of Cambridge (UK) / University of Fribourg (Switzerland) 2-3 years fixed term

This position is part of a HFSP-funded project to unravel distributed metabolism in four ant species (led by Adria LeBoeuf - CH/UK, Bas Teusink - NL and Brian L. Fisher - US). Our team uses multi-omic metabolic modeling and long-term automated tracking of behavior and fluorescence in ant colonies to study metabolic division of labour across the superorganism.

This position requires field work, lab work (both molecular and behavioural) and computational work (bioinformatics, data analysis). We are looking for someone motivated by big questions on major evolutionary transitions / metabolic division of labour / life-history trade-offs AND ready to get your hands dirty AND lost in your code.

The position is available in the LeBoeuf Lab of Social Fluids <http://leboeuflab.com/> which will relocate from the University of Fribourg, Biology Department in Switzerland to University of Cambridge, Zoology Department in the UK in January 2024. Position is funded for 2-3 years, depending on candidate's start date and experience. Ideally, the candidate would complete a 2-4 month research stay in Switzerland in 2023 on a Swiss salary, before being hired for a 2+ year position in the UK from 2024 on a UK salary. We'll do everything we can to make the transition smooth.

Lab values: Creativity, interdisciplinarity, collaboration, open source, open access, inclusiveness, team mentality.

Who we are looking for

* Bioinformatics background * Molecular biology experience * Fondness for insects and big questions * Curious and creative * We strongly encourage women and underrepresented candidates to apply

Application

* Statement on your scientific interests, previous work, and your motivation to join this project and our research group * CV + publication list (describe your contribution) * a link to your GitHub (or coding examples) * Two reference letters (should be sent directly to the email below).

Applications and reference letters should be sent to [adrialeboeuf AT gmail DOT com](mailto:adrialeboeuf@gmail.com).

Get in touch if you have questions!

DEADLINE: JUNE 1st, 2023.

Applications will be reviewed until positions are filled.

LEBOEUF Adria <adria.leboeuf@unifr.ch>

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UCBerkeley Genomics

Postdoc:UCBerkeley.Genomics

Postdoc position in primate genome evolution; Structural Variation; genomics; long read sequencing

A fully funded postdoctoral position on the evolution of structural variation in humans and non-human primates is available in the Sudmant Lab at UC Berkeley. This work will focus on understanding how some of the most complex and rapidly evolving regions of the genome have

changed over both recent human evolution (~300KY-present) and longer timescales (~6-50MY). Current work in the Sudmant lab is generating telomere-to-telomere (T2T) genomes for several primate species as well as population-scale long read sequencing data in both primates and humans. Alongside large-scale datasets being generated by the Human Pangenome Reference Consortium (HPRC), new long-read technologies present an unparalleled opportunity to explore evolution of much of the genome that has previously been intractable. This includes highly divergent (and rapidly evolving) loci such as the MHC as well as structurally complex loci including sex chromosomes, segmental duplications, and centromeres. Pangenome graph-based approaches can further be used to explore the evolution of these loci in ancient human genomes. The candidate will work on their own independent projects and collaborate with other graduate students and postdocs in the lab.

The position is fully funded (initial 24-month appointment, extendable) with a highly competitive salary scale as was recently negotiated - (<https://www.science.org/content/article/postdoc-union-reaches-tentative-agreement-university-california>).

The ideal candidate will have strong computational and genetics experience. Our lab philosophy is firmly based on the premise that science should be fun, inclusive, collaborative, and open.

Required qualifications: Ph.D. or equivalent in genetics, genomics, biology, computer science or related fields and demonstrated record of productivity and publications. Experience with either generating or analyzing large-scale genomic data.

Please contact Peter with your CV and a brief overview of your interests. Please be prepared to provide scientific references (e.g. advisor / thesis committee members). The position is open until filled with an anticipated start date in Sept 2023.

Peter Sudmant Assistant Professor Department of Integrative Biology University of California, Berkeley <https://www.sudmantlab.org> psudmant@berkeley.edu

Peter Sudmant <psudmant@berkeley.edu>

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UChicago MacroevolutionPhylogenetics

Postdoctoral Scholar - Macroevolution/Phylogenetics,
University of Chicago

Application deadline: 30 June 2023

Seeking a postdoctoral scholar to participate in an ongoing collaborative research project (D. Jablonski-S. Edie-K. Collins-S. Huang-R. Bieler) on the origin and dynamics of taxonomic, trait, and functional diversity in time & space. Marine bivalves will be used as a model system due to their excellent fossil record, ecological diversity, highly resolved taxonomy and biogeography, and increasingly refined phylogenies. Immediate research goal is construction of a comprehensive phylogeny for bivalve genera from existing molecular phylogenies, and time-calibrating that tree using paleontological data.

Postdoctoral scholar will take the lead on construction of a genus-level phylogeny of bivalves (using supertree and/or super matrix methods) and its subsequent time calibration, and participate in research supported by the resulting phylogeny, with the opportunity to take the lead on some new research projects. Experience in tree construction/alignments required. Experience in tree inference/sequence alignments required. Familiarity with software such as RevBayes, BEAST, IQ-TREE and RaxM and experience with comparative evolutionary analysis using the R statistical computing environment is highly desirable.

One-year appointment, with potential option for a second year. Collaboration will likely extend beyond that time; we will be applying for further funding but cannot guarantee success. Starting date negotiable but prefer summer or early fall 2023. Requires either Ph.D. in hand or dissertation submitted and approved for degree. Under certain circumstances the work could be done remotely, with frequent (~weekly) Zoom sessions with Jablonski and other group members.

Please email in a single pdf a 1-2 page letter documenting research interests, experience related to research goals above, a CV, and the email addresses of at least two references to Dr. David Jablonski (djablons@uchicago.edu) at the University of Chicago. Applications required by June 30, 2023 for full consideration.

Equal Employment Opportunity Statement All University departments and institutes are charged with

building a faculty from a diversity of backgrounds and with diverse viewpoints; with cultivating an inclusive community that values freedom of expression; and with welcoming and supporting all their members.

We seek a diverse pool of applicants who wish to join an academic community that places the highest value on rigorous inquiry and encourages diverse perspectives, experiences, groups of individuals, and ideas to inform and stimulate intellectual challenge, engagement, and exchange. The University's Statements on Diversity are at <https://provost.uchicago.edu/statements-diversity>. The University of Chicago is an Affirmative Action/Equal Opportunity/Disabled/Veterans Employer and does not discriminate on the basis of race, color, religion, sex, sexual orientation, gender identity, national or ethnic origin, age, status as an individual with a disability, protected veteran status, genetic information, or other protected classes under the law. For additional information please see the University's Notice of Nondiscrimination.

Job seekers in need of a reasonable accommodation to complete the application process should call 773-834-3988 or email equalopportunity@uchicago.edu with their request.

David Jablonski <djablons@uchicago.edu>

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UCollege London GeneticsEvolution

The Department of Genetics, Evolution and Environment at University College London 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 15 June 2023.

Salary is provided by the external funding (fellowship)

secured.

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. The 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.

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. 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 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, you will need to provide the following: 1. Your CV 2. A brief document outlining your research proposal 3. A list of fellowship schemes you are planning to apply for (the main ones are listed on our website <https://www.ucl.ac.uk/biosciences/gee/fellowships>). 4. A document describing how you see yourself and your research fitting into the department.

APPLICATIONS NEED TO GO THROUGH THIS PORTAL https://www.ucl.ac.uk/work-at-ucl/search-ucl-jobs/apply?jobId=Q1KFK026203F3VBQBLO8M8M07-9877&langCode=en_GB What we offer: We provide support to ensure that fellows can successfully establish their own research group, have opportunities to gain teaching skills and play a full role in the running of the department. Our commitment starts with academic and administrative support at the application and interview stages and continues throughout the tenure of the fellowship, with regular career development and mentoring programmes.

We expect fellows to develop into strong candidates for Principal Investigator positions in the department or elsewhere. In line with this ethos, a large proportion of our past departmental fellows have progressed to permanent positions in GEE.

For further details visit our fellowship homepage: <https://www.ucl.ac.uk/biosciences/gee/fellowships> For

informal enquiries and more information, please contact the GEE Fellowship Coordinators: Dr David Murrell d.murrell@ucl.ac.uk Dr Hernán Burbano h.burbano@ucl.ac.uk

Our commitment to Equality, Diversity and Inclusion: As London's Global University, we know diversity fosters creativity and innovation, and we want our community to represent the diversity of the world's talent. We are committed to equality of opportunity, to being fair and inclusive, and to being a place where we all belong. We therefore particularly encourage applications from candidates who are likely to be underrepresented in UCL's workforce. These include people from Black, Asian and ethnic minority backgrounds; disabled people; LGBTQI+ people; and for our Grade 9 and 10 roles, women. Our department holds an Athena SWAN Bronze award, in recognition of our commitment to advancing gender equality.

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

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UDuesseldorf PlantEvolutionaryGenetics

A post-doc position (100% TV-L/13) in the research group of Prof. L. Rose at the University of Duesseldorf is available immediately.

Our lab focuses on evolutionary genetics of plant-microbe interactions. Our work on wild tomatoes centers on the evolution of disease resistance genes and their regulation. Work on Arabidopsis centers on the evolution of gene clusters and the association of Arabidopsis with cercozoans and oomycetes. Our lab is integrated in Ceplas, the Cluster of Excellence on Plant Science, and the newly established research initiative on Plant Ecological Genetics (TRR 341).

Your tasks: The post-doc is expected to become involved in on-going research projects and strongly encouraged to apply for independent third party funding in order to develop their own research profile. The post-doc has a teaching requirement of 4 SWS (contact hours per week). The courses cover basic evolutionary biology and genomics.

Our Requirements: Requirements for this position are a PhD in Evolutionary Biology, Quantitative Biology,

Bioinformatics or a closely related field. Prior experience with Population Genetics, NGS data, SNP calling, genome annotation, and standard molecular techniques is desired. Demonstrated ability to work independently, as well as interest to co-supervise students is strongly recommended. The languages spoken in the group are German and English, so a demonstrated ability to communicate effectively in at least one (and ideally both) of these languages (written and spoken) is essential.

Application procedure: Please send your application as a single pdf to Laura Rose (e-mail: laura.rose@hhu.de). Your application should include a CV, a letter of motivation and prior research experience (maximum 2 pages), relevant degree certificates and the name, contact and affiliation of 2-3 referees. The deadline for applications is June 2, 2023.

The contract will be for a maximum of three years. Further employment may be possible, but is dependent upon the German laws regulating contracts for scientific staff.

Website for more information: popgen.hhu.de/en

Laura Ellen Rose <Laura.Rose@uni-duesseldorf.de>

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UEdinburgh InsectChromosomeEvolution

Dear all,

I am looking for a postdoctoral researcher to join my lab at the Institute of Ecology and Evolution, as part of an ERC starting grant. This project investigates the evolution and molecular mechanisms of unusual chromosome behaviour in fungus gnats, a clade of flies with arguably the most complex chromosome system of any organism. Their development includes several rounds of chromosome elimination associated with soma/germline differentiation, sex determination and spermatogenesis.

The Opportunity:

Possible avenues of research, depending on the interests of the postdoc include: 1) Studying the molecular evolution of different chromosomes depending on their patterns of inheritance and elimination. 2) Using the fast turnover of sex determination within the clade as a model for studying sex chromosome evolution. 3) Studying the molecular mechanisms of chromosome elimina-

tion and meiotic drive. There will also be scope for the postdoc to develop their own research plans with an view to becoming an independent investigator. The project will involve collaboration with partners within the UK and overseas. There are substantial funds within the grant for data collection, experimental work and conference attendance. The project will be funded till the end date of the grant, June 2025.

Your skills and attributes for success:

* Interest in population genetics, chromosome biology and insect reproduction. * PhD in evolutionary or molecular genetics * Experience with analysing genome and transcriptome data * Knowledge of computational biology tools, including R and command-line interfaces. * Experience with basic molecular genetics wet lab techniques.

UE07 36,333 - 43,155 Per Annum

College of Science and Engineering / School of Biological Sciences / Institute of Ecology and Evolution

Fixed-term, expected dates: 1/08/2023-03/06/2025

Full time (35 hours per week)

For more information please email me laura.ross@ed.ac.uk and you can apply for the position here: View the external job posting < <https://elxw.fa.em3.oraclecloud.com/hcmUI/-CandidateExperience/en/job/7562> >

best wishes, laura

Dr Laura Ross Senior lecturer and Dorothy Hodgkin fellow Institute of Evolutionary Biology The University of Edinburgh Ashworth Laboratories Charlotte Auerbach Road Edinburgh EH9 3FL, UK laura.ross@ed.ac.uk +44 (0)131 650 7708 <http://lauraross.bio.ed.ac.uk> Please note that I generally do not work on Mondays

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Laura Ross <Laura.Ross@ed.ac.uk>

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UFlorida Biomechanics SexualSelection

Applications are welcome for a Postdoctoral Associate to work on the biomechanics of sexual selection and insect cuticle at the University of Florida in Gainesville.

Position description: The Miller Lab at the University of Florida welcomes applications for an NSF-funded postdoctoral researcher to take a functional and biomechanical approach to understanding the influence of nutrition on the structure and composition of sexually selected weapons in insects. This work is interdisciplinary and will involve collaborations with researchers at Imperial College London and the University of Cambridge. The postdoctoral associate will work within this international research team and have opportunities to develop complementary projects within the context of the funded research. The application deadline is July 24th. The proposed start date is March 2024 with some flexibility. This position is funded at \$50,000 USD/year plus benefits.

Project description: Tens of thousands of animal species have evolved morphological weapons that are used to compete over reproductive opportunities. In insects, these structures are built of cuticle. We have recently discovered strong effects of nutrition on insect cuticle, affecting the ability of weapons to withstand the rigors of combat. This project will follow up on those findings and test the consequences for male-male competition, selection, and evolution using the leaf-footed cactus bug, *Narnia femorata* (Hemiptera: Coreidae).

Qualifications: Well-qualified candidates will:

* Hold a PhD in evolutionary biology, functional morphology; biomechanics, behavioral ecology or a related field; * Have demonstrated skills in data collection, statistical analyses, and academic writing; * Demonstrate excellent communication and interpersonal skills.

Desirable qualities include: - Experience conducting research in functional morphology and/or biomechanics; - Involvement and/or interest in outreach and mentoring students.

Responsibilities will include: - Working as part of a team to rear insects under a variety of environmental conditions; - Using state-of-the-art equipment to conduct quantitative mechanical, morphological, and/or behavioral research; - Data analysis and writing up research

results.

Interested applicants can learn more about this position), including how to apply, at: <http://www.millerlab.net/opportunities.html> (see Postdoctoral Associate #2 description)

Diversity and inclusion are more than just words for us. These are central in guiding how we come together as a research team, cultivate excellence, and go forth into the world to share our discoveries and our love of our work.

Information about Gainesville, Florida:

Situated in the rolling countryside of north central Florida, Gainesville, is close to world-class fishing, snorkeling, canoeing, tubing, and kayaking. On land, those so inclined may enjoy birding, hiking, biking, and fishing. Home of the University of Florida, seat of Alachua County's government and the region's commercial hub, Gainesville is progressive, environmentally conscious, and culturally diverse. The presence of many students and faculty from abroad among its 99,000-plus population adds a strong cross-cultural flavor to its historic small-town Southern roots. Its natural environment, temperate climate and civic amenities make Gainesville a beautiful, pleasant, and interesting place in which to learn and to live.

Christine W. Miller (she/her) Associate Professor

Entomology & Nematology Department University of Florida www.millerlab.net

2022-2023 On Sabbatical at the University of Cambridge, UK

"Miller, Christine W." <cwmiller@ufl.edu>

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UFlorida SilkGenomicsEvolution- ButterfliesMoths

The Kawahara Lab at the McGuire Center for Lepidoptera and Biodiversity, Florida Museum of Natural History, University of Florida, Gainesville, USA, is currently seeking a postdoctoral fellow to conduct research on the silk and silk glands of Lepidoptera (butterflies and moths). The postdoc will be part of a large-scale NSF IntBio grant, "Collaborative Research: Silk protein innovation and novelty (SPIN): integrating across

disciplines to decipher silk fiber evolution” between multiple institutions (AMNH, BYU, George Washington U., U. of Utah) to study the genotype and phenotype of insect silks. The postdoc will be supervised by co-PI Akito Kawahara (UF) and will work closely with Kawahara Lab students, postdocs, and staff. They will also regularly communicate with other senior personnel and co-PIs on the SPIN project, including Ed Stanley (UF, CT-Scanning), Whitney Stoppel (UF, Engineering), Paul Frandsen (BYU, genomics), Cheryl Hayashi and Richard Baker (AMNH), Russel Stewart (Univ. of Utah), and Arnaud Martin (George Washington Univ.).

The position is for a minimum of 2 years, with a possibility of extension. Position available immediately.

Required: A Ph.D. in biology, preferably either in 1) genomics/transcriptomics, or 2) insect phenotyping. Experience with computer programming / scripting / data analysis (e.g. R, Python), and excellent communication and writing skills.

Strong interest in entomology/invertebrate biology is preferred, but not required.

The successful candidate will work closely with students and staff in the lab and lead projects on butterfly and moth silk genomics/evolution and silk gland phenotyping (CT-Scanning). Responsibilities include data analysis and interpretation, contribution to analysis strategy, code development, review of relevant literature, and preparation of project reports and manuscripts for publication in peer-reviewed journals.

The McGuire Center is committed to creating a safe and equitable work environment. Candidates from groups that have historically been underrepresented in science are strongly encouraged to apply.

Salary: \$60,000. To ensure full consideration please send a single pdf that includes: 1) 1-2 page cover letter detailing your relevant experience and fit for this position, 2) curriculum vitae, and 3) names and contact information of at least three references familiar with your work. Any questions regarding this position may be directed to Dr. Akito Kawahara, Florida Museum of Natural History, University of Florida (kawahara@fmlnh.ufl.edu). Lab website: <http://www.fmlnh.ufl.edu/mcguire/kawahara/> Formal review of applications will begin June 30, and opened until the position is filled.

Akito Y. Kawahara, Ph.D. Curator and Professor McGuire Center for Lepidoptera and Biodiversity Florida Museum of Natural History University of Florida Powell Hall, 3215 Hull Road Gainesville, FL 32611-2710 USA Tel: 352.273.2018 Email: kawahara@fmlnh.ufl.edu <http://www.fmlnh.ufl.edu/mcguire/kawahara/> “Akito Y. Kawahara” <kawahara@fmlnh.ufl.edu>

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UHelsinki UrbanDiseaseEvolution

The University of Helsinki is an international scientific community of 40,000 students, faculty and other staff. It is one of the leading multidisciplinary research universities and ranks among the top 100 universities in the world. The Organismal and Evolutionary Biology Programme is one of the three research programmes at the Faculty of Biological and Environmental Sciences. Most of its activities are centered at the Viikki campus where it comprises roughly 40 research groups which employ 40 principal investigators and 120 researchers.

Helsinki Urban Rat Project, an multidisciplinary research project, invites applications for a

POSTDOCTORAL RESEARCHER IN URBAN DISEASE ECOLOGY in the Academy of Finland funded project “Urban rats as a model species for disease ecology” for a fixed term of four years, with six month trial period, starting at 1st September 2023.

Helsinki Urban Rat Project (HURP; <https://www.helsinki.fi/en/projects/urban-rats>) is a multidisciplinary research project, started in 2018, striving to understand how rats live in urban areas and how they interact with humans. The overarching aim of the project is more peaceful coexistence between humans and rats. We use a multitude of approaches from ecology to environmental policy research and visual arts. For this project, we have received funding from Academy of Finland to delve deeper into the effects of lethal rat control in the city areas. Urban rats encounter continuous population perturbations caused by pest management professionals’ actions. Interestingly, this pest management provides a potential pseudoexperimental setting in looking at the effects of population changes on rat movement, pathogen and parasite prevalence and population structure before and after treatment. While the core of the project is in disease ecology, it can linked more towards movement ecology, population genetics, different pathogens or parasites or applied ecology in relation to the applicant’s interest. HURP has previously surveyed the pathogen and parasite diversity, tools for studying rat movement and city-level population dynamics and has established connections with stakeholders, including property-owners and pest management companies. Thus, this project presents an excellent position to per-

form highly impactful scientific work in multidisciplinary and societally relevant context.

We are looking for a candidate who is able to 1) help in recruiting field sites, 2) lead fieldwork, 3) lead pathogen analysis, 4) work with collaborators in collating other data and eventually 5) analyze and communicate these results in both scientific articles and to lay audiences such as stakeholders and local citizens. The candidate should have completed a PhD in a relevant field, such as zoology, ecology, wildlife biology, microbiology or virology. Previous experience on field work, pathogen analysis in lab, shown track record on publishing in international peer-reviewed journals and excellent communication skills (in English, Finnish and Swedish additional assets) are required. It is also possible that this position is filled with two persons with two-year contracts, where the first person concentrates on fieldwork and the second in lab work. Additional assets include driver's license and license to perform animal experiments (e.g., FELASA C). We encourage applications from recently graduated PhD holders.

We strive to be a truly interdisciplinary project, thus interaction with biologists, social scientists and artists working within HURP may form a substantial part of the project and interest to interdisciplinary work is an asset. The project sites will be quite literally in people's backyards, so ability to work with local citizens and other stakeholders is of high importance. Postdoctoral researcher will be located in University of Helsinki, Viikki campus. The position is for 48 months starting in September. Later starting date is possible, but this shortens the length of contract. The salary of the postdoctoral researcher will be based on level 5 or 6 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal performance. The starting salary of the postdoctoral researcher will be ca. 3 400-3 800 euros/month, depending on the appointees' qualifications and experience. The University of Helsinki offers comprehensive services to its employees, including occupational health care and health insurance, sports facilities, and opportunities for professional development. The International Staff Services office (<https://www.helsinki.fi/en/-university/working-at-the-university>) assists employees from abroad with their transition to work and life in Finland. A six-month trial period will be applied.

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ULausanne PlantEvolution

Postdoc position in plant evolution - Department of Ecology and Evolution, University of Lausanne, Switzerland

A postdoc in plant evolutionary biology is available in the research group of John Pannell in the Department of Ecology and Evolution, University of Lausanne. The postdoc is initially for one year, but could be extended for up to five years. The successful applicant will work on the comparative genomics of transitions in plant sexual systems and on the evolution of sex determination and sex chromosomes. Research will focus on one or both of two models that are well developed in the lab: the evolution of sexual systems and sex chromosomes in the European annual plant *Mercurialis annua* and its relatives; and the evolution of sex chromosomes and sexual dimorphism in the South African genus *Leucadendron*. The genus *Mercurialis* displays remarkable variation in the expression of combined versus separate sexes among species and natural populations of the species *M. annua*. We have also observed rapid transitions between dioecy and monoecy in *M. annua* under experimental conditions and now aim to investigate the genomic architecture of these transitions. The genus *Leucadendron* is fully dioecious, but its species vary dramatically in their levels of sexual dimorphism in terms of morphology, life history and patterns of gene expression. Recent analysis suggests that the entire genus of approximately 80 species has the same XY sex-determination system, but that the sex chromosomes have experienced different rates of gene trafficking.

For details of current research in the lab and a list of publications, see <https://www.unil.ch/dee/pannell-group>. Research scope and skills sought We are looking for a postdoc with an interest and skills in the generation and especially the analysis of genome and transcriptome data to test evolutionary and population genetic hypotheses. The postdoc will work on projects currently running in the lab, as summarised above, but his or her specific research can be tailored to personal interests and training objectives. He or she should be able to demonstrate a strong conceptual foundation in evolutionary biology and population genetics and should be equipped with skills in bioinformatics and genome sequence and gene expression analysis. An interest in plant evolution specifically is not essential but could

be an advantage. The successful candidate should also have good communication and interpersonal skills, and an ability to work in a team.

Host department and university The Department of Ecology and Evolution at the University of Lausanne hosts a broad range of research groups, and its members enjoy a lively intellectual and social life. Although the University of Lausanne is francophone, the department is highly international, and all its research activity and seminars are conducted in English. The University has seven faculties and approximately 14,300 students and 3,900 researchers from over 120 countries. It is situated on a beautiful campus on the shore of Lake Geneva, and is close to the Swiss and French Alps.

Applications Informal enquiries should be sent to John Pannell (john.pannell@unil.ch). Formal applications should be sent to John Pannell as a single pdf that should include: a cover letter detailing your research interests, experience and motivation for applying; your CV; and the names of two or three referees. In addition, you will also need to upload your application to the University of Lausanne recruitment platform following this link: <https://bit.ly/3ny1TZu>. All applications received by 22 May 2023 will receive full consideration.

University equality policy The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

John Pannell <john.pannell@unil.ch>

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U**Lausanne** Switzerland Exp**Evolution**Drosophila**Physiology**

A position of postdoctoral researcher (“premier-assistant-e”) is available in Tadeusz Kawecki’s research group at the Department of Ecology and Evolution, University of Lausanne, Switzerland (<https://www.unil.ch/-dee/kawecki-group>). We are looking for a qualified researcher interested in experimental approaches to study short-term adaptive evolution, using *Drosophila* as a model system.

Expected start date between August and November 2023. Contract length: initial contract for 1 year, renewable for 2 years; depending on project development

and funding availability, one further 2-year renewal may be possible. Starting gross salary: CHF 81,120 (approx. euro 82,000 /US\$ 89,000) per year

The researcher will join a project using experimental evolution to investigate the genetic, molecular and physiological mechanisms of evolutionary adaptation to a nutrient-poor diet in *Drosophila*. An angle on sexual selection and conflict might also be possible. The project will involve a combination of physiological and life history experiments on flies and their larvae with molecular, genetic and “omic” approaches.— The research will involve collaborations with the genomic, metabolomic and/or imaging platform of the University. In addition to this personal research (70%), the position also includes 25 % teaching activities (including master student supervision) and 5 % service for the research group and larger community (e.g., helping other group members, equipment maintenance, institutional tasks). For more background on the project see <https://doi.org/10.1098/rspb.2020.2684>, <https://doi.org/10.1093/evlett/grad018>, <https://doi.org/10.1093/molbev/msab061>, and <http://dx.doi.org/10.1098/rspb.2019.0226> . We are looking for candidates with a PhD, a strong interest in experimental evolutionary biology, solid understanding of statistics and experimental design, aptitude for laboratory research, and demonstrated scientific writing skills. Experience with molecular and/or physiological methods, and/or with experimental work with *Drosophila* or other insects would be a plus. Desired personal traits include scientific curiosity and honesty, independence and reliability in planning and carrying out experiments, good interpersonal skills and teamwork ability, good communication skills, and respect of colleagues. No-preexisting knowledge of French is required (research-related discussions, seminars etc. and a part of teaching are in English) but learning basic French would make living in Lausanne more enjoyable.

With 18 research groups and nearly 100 postdocs and PhD students 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, and there are many inter-departmental interactions and activities. 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 please contact Tadeusz Kawecki <tadeusz.kawecki@unil.ch> or Fanny Cavigliasso <fanny.cavigliasso@unil.ch>

Application must be submitted online through the University of Lausanne recruitment platform:

<https://bit.ly/3pxVaPU> (you may have to change language to English in the upper right corner of the application website).

The application should include - a cover letter detailing your research interests and motivation for applying for this position; - your CV; - a summary of your past research (1-2 pages, could focus on what you consider your most exciting contributions); - the names and email addresses of two or three referees. - your PhD diploma or a certificate of completing requirements for your PhD (if you have not yet completed your PhD please indicate the expected date).

To receive full consideration apply before 4 June 2023.

Tadeusz Kawecki <tadeusz.kawecki@unil.ch>

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ULeipzig BiodiversityAtmosphere

A post-doc position (100% TV-L/13) in the research group of Prof. B. Sánchez-Parra at the University of Leipzig is available immediately until the end of 2024.

Topic: The composition and the number of biological particles in the atmosphere depends on the biodiversity and status of terrestrial emission sources, such as soil, vegetation and water bodies.

Climate change and associated extreme events and disturbances may alter the biodiversity and emission characteristics of these sources. Forests are of great help in mitigating climate change by means of transpirational cooling and carbon sequestration. They also constitute a highly diverse source of biological particles that can be emitted into the atmosphere from the soil to the top layer of the canopy. The constituent tree species present different vertical and horizontal gradients of microclimatic conditions, which lead to the stratification of arboreal species communities. Using long-term and new bioaerosol samples from the Leipzig Canopy Crane, we will study how vertical emission patterns during climate extremes differ from normal seasonal cycles.

Your tasks: The postdoc is expected to plan and conduct bioaerosol sampling in the experimental field platforms; Prepare existing bioaerosol samples in the laboratory for sequencing analysis; Analyse sequences data using

various bioinformatics tools; Participate in internal seminars and external conferences and Publish results in international journals with peer review

Our Requirements: Requirements for this position are a PhD in a project-related field (e.g. biology, environmental sciences, bioinformatics); to have experience in laboratory and fieldwork; Good skills in R; Writing skills proven by a publication record; as a person, you are responsible and an excellent team player; Fluency in spoken and written English is mandatory (group language)

Please send your application with the usual documents (including a cover letter in English describing your motivation for the project, research interests, and relevant experience; the names and contact details of two or more scientific referees; a digital copy of your masters certificate or equivalent; and your PhD certificate [if you have not received your PhD certificate yet, please upload a short statement about the current status of your PhD and a brief summary of what your thesis is about]), quoting reference number 104/2023, to: Leipzig University, Faculty of Life Sciences, Jun-Prof. Dr. Beatriz Sanchez Parra, Talstraße 33, 04103, Leipzig by 30 June 2023

You are also welcome to email your application as a single PDF file to beatriz.sanchez_parra@uni-leipzig.de

Please note that it is not possible to guarantee confidentiality and rule out unauthorised access by third parties when communicating by unencrypted email.

Get in touch if you have questions!

Applications will be reviewed until positions are filled.

Website for more information: www.sanchezparra.com and <https://www.uni-leipzig.de/personenprofil/mitarbeiter/juniorprof-phd-beatriz-sanchez-parra> [beasanchezparra <venti66@hotmail.com>](mailto:beasanchezparra@hotmail.com)

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UMarburg 9Phd 3Postdoc Oak-microbiomeInteraction

Three PostDoc and nine PhD positions (Universität Marburg, Universität Freiburg, Helmholtz Centre for Environmental Research (UFZ), German Centre for Integrative Biodiversity Research (iDiv), Swiss Federal Institute for Forest, Snow and

Landscape Research (WSL)

The DFG Research Unit PhytOakmeter (RU 5571) “Using clonal oak phytometers to unravel acclimation and adaptation mechanisms of long-lived forest tree holobionts to ecological variations and climate change” by the Universities of Marburg, Leipzig, and Freiburg, the iDiv, UFZ, and WSL is currently inviting applications for 9 PhD Positions and 3 PostDoc positions (f, m, d). The salaries are based on the respective state and/or national tariffs for researchers. The positions are funded by the German Research Foundation (DFG) and the Swiss National Science Foundation (SNSF) for four years. This interdisciplinary Research Unit will investigate patterns and mechanisms of acclimation and adaptation (A&A) of tree holobionts to drought and above- and below ground herbivory. The model species is *Quercus robur* making use of the DF159 clone using state of the art facilities at the iDiv Ecotron and Freiburg Ecotron, the research forests of the Universities of Marburg and Basel, and the European PhytOakmeter Gradient of out planted DF159 plants.

The RU 5571 offers a vibrant academic environment, joint supervision of PhD candidates by interdisciplinary thesis committees across the partner institutions, and an accompanying program of summer schools and regular scientific online exchange with many opportunities to improve scientific and personal skills. The following research groups are offering PostDoc and PhD projects: You can find detailed information on the individual positions online at www.uni-marburg.de/en/fb17/phytoakmeter/job-opportunities. General information on the RU 5571 and the different subprojects are available at www.uni-marburg.de/en/fb17-phytoakmeter. We are seeking highly motivated candidates, who wish to conduct their PostDoc or PhD training in an interdisciplinary environment. Successful candidates

- will have completed their PhD (for PostDoc positions) or MSc or equivalent (for PhD positions) university degree in a subject area relevant for the RU 5571 program (see details for the different positions below) - are fluent in English - are keen to collaborate and share data with their PostDoc and PhD colleagues

Please be aware that the application procedure varies among the Subprojects. Details are given on the respective subproject descriptions on the mentioned homepage.

Lars Opgenoorth <opgenoor@staff.uni-marburg.de>

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UMaryland InsectEcdysisDifferences

Title: Seeking a postdoctoral associate to elucidate the insect ecdysis process across species and orders

Position description: The postdoctoral associate will take the lead on a grant-funded project that looks at the sublethal effects of insecticides on insect development. They will develop and execute research to determine the molecular mechanisms involved in causing the sublethal effects. The experiments will be undertaken with several insect orders to elucidate evolutionary differences across species. Specifically, the postdoctoral associate will undertake antibody studies to determine the role of various neuroactive peptides in insect ecdysis and RNAi studies to knockdown receptor subtypes to determine the molecular binding sites. Individuals with a strong background in molecular biology are encouraged to apply. The associate will be the senior author on one or more publications and will assist with grant writing and graduate student mentoring. The successful candidate will possess excellent organizational skills, technical writing skills, interpersonal communication skills, and the ability to meet deadlines.

Required qualifications: PhD degree in biology, molecular biology, or a relevant field (degree should be obtained prior to start date). Candidates must have significant experience in using molecular techniques like immunocytochemistry and RNAi.

Preferred qualifications: Working with live animals, particularly insects. Some experience using CRISPR Cas-9 technology.

Salary: \$52,000 plus university benefits (<http://uhr.umd.edu/benefits/>)

Closing date: For best consideration, apply by June 15, 2023. Applications will be taken until the position is filled. Tentative position start date is August 2023.

Application materials: Interested applicants should send a cover letter, CV, and a list of three references to Niranjana Krishnan (nkrish@umd.edu).

The University of Maryland, College Park, actively subscribes to a policy of equal employment opportunity, and will not discriminate against any employee or applicant because of race, age, sex, color, sexual orientation, physical or mental disability, religion, ancestry or national origin, marital status, genetic information, political af-

filiation, and gender identity or expression. Minorities and women are encouraged to apply.

Niranjana Krishnan <nkrish@umd.edu>

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UMontpellier Three SociableWeaverEvolution

Gecko/20100101 Thunderbird/102.11.0

Two-year post doc position open to work on the effects of an extreme event on physiological stress and the mediating effects of sociality

Aim:

To study the effects of an extreme event (fire) on physiological stress (measured as telomere attrition) and associated changes in fitness estimates, as well as any possible mediating effects of sociality. The study will use a long-term individual-based study of a sociable weaver population located in South Africa.

Dates: Expected to start between mid-August and mid-December

Location:

The post-doc will have a contract with the University of Montpellier (France) and be based at CEFÉ-CNRS (but will also spend ca. 3 months per year at CIBIO, University of Porto and go to Strasbourg to visit the team of collaborators based there. The post doc will be part of the sociable weaver project <https://sociableweaverproject.com/> that currently includes 4 PhD students, one postdoc and is now recruiting 3 additional postdocs. At CEFÉ, Montpellier, the postdoc will be based in a larger team including people working on another long-term study on blue tits.

Supervision : Claire Doutrelant (CEFÉ-CNRS, Montpellier, France) and Rita Covas (CIBIO, Univ of Porto, Portugal) : <https://www.cefe.cnrs.fr/fr/recherche/ee/esp/-777-c/152-claire-doutrelant> Collaboration: Matthieu Paquet (CNRS Moulis, France) for CMR analyses and François Criscuolo and Sandrine Zhan (IPHC UMR 7178, Strasbourg, France) for telomeres analyses

Salary : 2149 per month after taxes (2674 before)

Timeline: deadline is 15th June, first interviews expected beginning of July. Expected start: between mid-August and mid-December

Who? The candidate should have a relevant PhD in biological sciences, preferably behavioural or evolutionary ecology with some background on sociality, and physiology. The candidate should have a strong background in general linear mixed modelling, movement modelling, CMR analyses, managing large data sets and a proven track-record of publishing research in high-quality peer-reviewed literature. The postdoc should be able to work as part of a close collaborative team. This position will mostly entail data analyses and writing-up the results.

How to apply? For the moment, please send the following information to Claire Doutrelant and Rita Covas (emails: claire.doutrelant@cefe.cnrs.fr ; rita.covas@gmail.com): a CV, a motivation letter explaining your interest and how your experience is relevant to this project. Please also indicate the names and emails of two referees that can provide a recommendation letter. The short listed candidates will be given a link to provide all the information to the university of Montpellier.

Summary of the project

The frequency of extreme climatic events is increasing as a result of anthropogenic climate change, and there is a need to describe the physiological responses and fitness consequences of individuals to these events. In addition, social factors and individual attributes (sex, age) have the potential to affect the impact of extreme events on individuals but those have not yet been examined. The post-doc will first determine to which extent telomeres are a relevant marker of physiological stress and survival in a population of a highly social bird, the sociable weaver, which has been hit by a massive fire. This extreme event occurred in a population we have followed for 10 years, with data available for the periods pre- and post-fire. The postdoc will describe telomere dynamics in this species, how it relates to survival, and relate changes in telomeres after fire to individual and social attributes, thereby assessing the impacts of the fire and whether sociality influences resilience.

More information

This project will be using a long-term dataset managed by Rita Covas and Claire Doutrelant. A long-term longitudinal sampling of telomeres started in 2014 at 15 colonies and ca. 1600 samples are available. Blood samples were collected each year on the same individuals from age 1 up over 10-years old. Additional sampling will take place in September 2023.

A post-doc position is available for 2.5 years to study the fitness benefits and costs of social associations in Sociable Weavers using long-term data - Deadline 20 June

Theory and studies in humans suggest that co-operators are preferred as social partners, and these social preferences are expected to bring fitness benefits, but few long-term studies have investigated the fitness benefits (or costs) associated with social network dynamics in wild animals. We are opening a post-doc position to investigate the association between social network position and fitness. This position is part of an ERC funded project that is investigating the role of partner choice on the evolution of

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

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

Kind regards,

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

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UNaples UrbanPlantEvolution

UniNaples.urbanplantevol

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

We are accepting applications for a two-years post doctorate fellow position in the field of urban plants evolutionary ecology

Review of applications begins on mid-July 2023

OVERVIEW:

We are looking for an enthusiastic candidate with an interest in plant biology alongside a strong background in plant evolutionary ecology. The candidate must have completed a Ph.D. degree in the last three years, preferably in the areas of plant ecology, pollination biology, evolutionary biology, quantitative genetics, and must show a clear record of research in these areas. The work will focus on plant adaptation to biotic/abiotic drivers along the urbanization gradient. We aim to identify the effect of urbanization on the ecology and evolution of plant species with a special emphasis on plant-pollinator and plant-herbivore interactions and their interplay along the gradient.

HOW TO APPLY:

To apply, please submit in one PDF file: (i) one page cover letter including motivation and research interests, (ii) a CV, and (iii) contact information for two references electronically, to cozzolin@unina.it Review of applications will continue until the position is filled. Job can start as early as October 2023.

UNorthCarolina PopulationGenomics

The Schrider Lab (<https://www.schriderlab.org/>) in the Department of Genetics at the University of North Carolina at Chapel Hill is hiring a postdoctoral research associate. The successful candidate will perform computational research addressing problems in population and evolutionary genomics which may include but are not limited to the following:

- 1) Population genetics of mosquito species. This work may be done in collaboration with Daniel Matute in the Department of Biology at UNC (<http://dm-incompatibilities.org/index.html>).
- 2) Inferring populations' selective and demographic histories (including gene flow/introgression between closely related species)
- 3) The application of machine learning tools to these and other problems in population genetics and/or phylogenetics

This a multidisciplinary position and candidates from a variety of backgrounds will be considered and receive training to address deficits as needed. A PhD in Evolution, Genetics, Bioinformatics, Computer Science, or a related field must be completed prior to the postdoc's hire.

Those interested should email Dan Schrider (drs@unc.edu) and include their CV as an attachment.

The University of North Carolina at Chapel Hill is an equal opportunity and affirmative action employer. All qualified applicants will receive consideration for employment without regard to age, color, disability, gender,

gender expression, gender identity, genetic information, race, national origin, religion, sex, sexual orientation, or status as a protected veteran.

“Schrider, Dan” <drs@unc.edu>

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UParis Saclay ExperimentalEvolution

A post-doctoral researcher position (12 month, renewable once) is available to work in collaboration with both of our groups from Sept 2023.

The objective of this post-doctoral project is to design, run, and analyze a series of experimental evolution studies in which different environmental factors (such as temperature, food, or chemicals) are manipulated to distinguish the roles of adaptation, plasticity, and genetic constraints on the evolution of the transcriptome.

We are looking for a motivated early career evolutionary biologist, with a PhD degree obtained after 2018. Previous experience with experimental evolution would be appreciated, including lab work with micro/macro-organisms, basic molecular biology (DNA and RNA extraction), and population genetics.

The position will be part of a 3-year project funded by the French National Research Agency (ANR). The research consortium includes 2 PIs (Arnaud Le Rouzic and Anne Genissel), a PhD Student, an ANR-funded technician, and the current post-doc. This project aims at understanding and predicting the evolution of transcriptomes under stable and fluctuating selection combining both theoretical and empirical approaches. The post-doc will be co-advised by both PIs. He/she will be formally based at EGCE (Institute for Ecology and Evolution, IDEEV), and will perform the experimental work at BIOGER (Agro-Campus). Both institutes offer an exciting and active scientific life; they are located 3 km apart, on the new research campus of Paris-Saclay, 35 km south of Paris.

Application web site:

<https://emploi.cnrs.fr/Offres/CDD/UMR9191-ARNLER-003/Default.aspx?lang=EN>

Informal inquiries to:

arnaud.le-rouzic@universite-paris-saclay.fr
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UppsalaU PopulationGenomics

Postdoctoral researcher/fellow in population genomics Uppsala University, Department of Ecology and Genetics

A position as a postdoctoral researcher/fellow in population genomics 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, see www.ieg.uu.se. Project description

How and why genetic diversity varies among species is a central and long-standing question in evolutionary biology. In the 70's Richard Lewontin noted that the observed range of genetic diversity is much narrower than expected given the huge range of population sizes (“the Lewontin’s paradox”). Despite recent progress, this puzzling observation remains unresolved, likely because the various hypotheses (role of demography, selection and recombination, and life-history traits) have been studied separately. In the project, the candidate will analyze all processes together, focusing on seed plants, which offer large variations in abundance, life history traits, and genomic attributes. We will ask i) How do demography, selection and recombination shape genetic diversity among species? ii) Does it depends on life history traits? iii) Is it enough to explain the Lewontin’s paradox? We will build on a unique recombination dataset we have already gathered and on publicly available polymorphism data and life history and ecological traits for each species. The candidate will run a combination of population genomic analyses to infer past and recent demography, the intensity of selection modulated by recombination and how it depends on life history and ecological traits. Empirical results will be compared to extensive simulations.

Duties

Gathering of sequence data, population genetics analyses, computer simulations. The applicant will be responsible for gathering sequence data and analyzing them, and publishing articles.

Qualifications required

PhD degree or a foreign degree equivalent to a PhD degree in population genomics or more broadly in 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.

Qualifications desired

Good proficiency in programming (bash, Python, C++, 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, according to central collective agreement. Scope of employment 100%. Starting date 2023-08-15, or as agreed. Placement: Uppsala

For further information about the position please contact: Professor Sylvain GleÅ, Sylvain.Glemin@ebc.uu.se

Application: The application should include 1) a letter of intent describing yourself, your research interests and motivation of why you want to work as a postdoctoral researcher/fellow and why you are suitable for the position, 2) a CV 3) a short description of your education, 4) a copy of your PhD degree, your grades and a copy of your thesis, 5) name and contact information to at least two reference persons (e-mail address and phone no.), 6) relevant publications. The application should be written in English.

Applications are done at the site: <https://www.jobb.uu.se/details/?positionId=626438> You are welcome to submit your application no later than June 15 2023.

Martin Lascoux Department of Ecology and Genetics EBC, Uppsala University Norbyvägen 18D 75236 Up-

psala Sweden Tel +46 (0) 18 471 64 16 Fax +46 (0) 18 471 64 57 <https://lascouxlab.wordpress.com> Martin Lascoux <martin.lascoux@ebc.uu.se>

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USouthernCalifornia PopGen StatGen

Patrick Turley (<https://www.paturley.com/>) at the University of Southern California seeks to hire a full-time postdoctoral researcher to work on projects at the intersection of computational population genetics, statistical genetics, and behavioral genetics. The postdoc will be funded by an NIH grant targeted at applying population genetics principles to statistical models in order to develop genomics tools for studying samples with diverse ancestries. For candidates with strong interests in population genetics, joint mentorship with Doc Edge (<https://edgepopgen.github.io/edgelab/>) and physical space in the Edge lab is a possibility for this position.

Projects will require skills in population-genetic modeling, simulation, bioinformatics, statistical genetics, and data analysis, and prior training in these areas is advantageous. While computational skills will be particularly valuable, successful candidates need not be proficient with all these areas when they apply.

Patrick Turley is the director of The Behavior and Health Genomics Center, under USC's Center for Economic and Social Research, an interdisciplinary center dedicated to discovering how people around the globe live, think, interact, age, invest, and make important, life-changing decisions. USC is in Los Angeles, a diverse city with appealing weather year-round. The position has a competitive salary and benefits.

Remote work is possible for this position. We are committed to fostering a welcoming, supportive lab environment.

To apply, please send an email to pturley [at] usc [dot] edu with the subject "postdoc application materials" including a CV and cover letter that briefly describes your research experience and interests to date, your goals for your postdoctoral training, and contact information for 2-3 professional references. Please also include a writing sample, such as a published manuscript, dissertation chapter, or manuscript preprint. Informal inquiries are also welcome at the same email addresses. Review of

applications will begin immediately, and applications will be considered until the position is filled.

Patrick Turley <pturley@usc.edu>

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UTennessee InsectMicrobeInteractions

The Parker Lab in the Department of Microbiology at the University of Tennessee (www.ben-parker.org) is seeking a post-doctoral research associate. The researcher will be primarily responsible for carrying out experiments and aims of a recently funded NSF award, using an insect model system (aphids) to address mechanistic and evolutionary genetic questions about animal-microbe interactions. The researcher will use molecular, genomic, and experimental techniques in their research.

Initial appointment is for 1 year with funding available to extend up to 3 years. The lab and PI will also be supportive of efforts to obtain independent funding e.g. through NSF, NIH, or USDA. The associate will collect data, communicate with other investigators, write reports and manuscripts, and assist in advising and training of graduate and undergraduate research students.

A PhD in ecology and evolution, microbiology, entomology, or a related field must be completed by the starting date of the position and the candidate is expected to have experience with molecular biology and/or genomics. Experience publishing peer-reviewed scientific papers focused on host-microbe interactions and evolution would be seen as a strong attribute.

Please send a cover letter, CV, and the names of two references to Benjamin Parker, Assistant Professor of Microbiology (bjp@utk.edu). In addition to emailing the PI, applications should also be submitted online:

https://ut.taleo.net/careersection/ut_system/jobdetail.ftl?job=22000002C7&tz=GMT-04%3A00&tzname=America%2FNew_York

The Department of Microbiology values the quality of life of all its members, and we are committed to recruiting and retaining a diverse community and to supporting the intercultural goals of the University. Knoxville is an exciting and affordable city that has undergone a vibrant civic revitalization over the past several years and is being recognized as one of the most exciting

up-and-coming regions in the country. Nestled in the foothills of the Great Smoky Mountains, Knoxville offers a broad spectrum of educational, recreational, and cultural opportunities. All qualified applicants will receive equal consideration for employment and admissions without regard to race, color, national origin, religion, sex, pregnancy, marital status, sexual orientation, gender identity, age, physical or mental disability, or covered veteran status. Eligibility and other terms and conditions of employment benefits at The University of Tennessee are governed by laws and regulations of the State of Tennessee, and this non-discrimination statement is intended to be consistent with those laws and regulations. In accordance with the requirements of Title VI of the Civil Rights Act of 1964, Title IX of the Education Amendments of 1972, Section 504 of the Rehabilitation Act of 1973, and the Americans with Disabilities Act of 1990, The University of Tennessee affirmatively states that it does not discriminate on the basis of race, sex, or disability in its education programs and activities, and this policy extends to employment by the University. Inquiries and charges of violation of Title VI (race, color, and national origin), Title IX (sex), Section 504 (disability), ADA (disability), Age Discrimination in Employment Act (age), sexual orientation, or veteran status should be directed to the Office of Equity and Diversity (OED), 1840 Melrose Avenue, Knoxville, TN 37996-3560, telephone (865) 974-2498. Requests for accommodation of a disability should be directed to the ADA Coordinator at the Office of Equity and Diversity.

“Parker, Benjamin James” <bjp@utk.edu>

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UWashington PDF LabTech Omics

We're excited to be hiring both a laboratory technician and postdoctoral scholar through CICOES to work at NOAA PMEL's Climate Ocean 'Omics Lab group.

The University of Washington's Cooperative Institute for Climate, Ocean, and Ecosystem Studies (CICOES) is hiring two positions, a postdoctoral scholar and a laboratory technician. Both positions will contribute to research conducted in collaboration with the Climate Ocean 'Omics lab group at NOAA Pacific Marine Environmental Laboratory studying climate change impacts on zooplankton, phytoplankton, microbial, fish, and

marine mammal ecology.

Please see the job listing for more information and how to apply:

'Omics lab technician position: <https://uw hires.admin.washington.edu/eng/candidates/-default.cfm?szCategory=jobprofile&szOrderID=-222475&szCandidateID=0&szSearchWords=-CICOES&szReturnToSearch=1> Marine Molecular Biological Oceanography Postdoctoral scholar: <https://apply.interfolio.com/125122> Best,

Zack

Zachary Gold, PhD(he/him)

Group Lead

PMEL 'Omics Program

Mobile: (310) 795-0020

Office: (206) 526-6531 NOAA Pacific Marine Environmental Laboratory (PMEL) | pmel.noaa.gov

7600 Sand Point Way NE Seattle, WA 98115

Zachary Gold - NOAA Federal
<zachary.gold@noaa.gov>

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Vienna Polygenic Adaptations

Postdoc positions are available within the *Special Research Program (SFB)* < <https://www.vetmeduni.ac.at/sfb-polygenic-adaptation> >* "Polygenic adaptation: from single selected loci to the infinitesimal model" in Vienna, Austria*. Vienna is on top of the world's most liveable cities and home to one of the largest communities of evolutionary research in Europe (www.evolvienna.at).

The SFB program is funded by the Austrian Science Fund (FWF) and brings together eight research groups at four institutions in and around Vienna with the common goal of elucidating the evolutionary genetics of adaptation of complex phenotypes: *Neda Barghi* < <https://www.vetmeduni.ac.at/en/population-genetics/research/barghi-lab/group-leader> >*, **Robert Kofler* < <https://www.vetmeduni.ac.at/en/population-genetics/research/kofler-lab> >*, **Christian Schlötterer* < <https://www.vetmeduni.ac.at/en/population-genetics/research/schloetterer-lab> >*

(Vetmeduni); **Joachim Hermisson* < <https://www.mabs.at/team/> >*, **Himani Sachdeva* < <https://www.mabs.at/team/> >* (Univ. of Vienna); **Magnus Nordborg* < <https://www.oeaw.ac.at/gmi/research/research-groups/magnus-nordborg/> >*, **Kelly Swarts* < <https://www.oeaw.ac.at/gmi-research/research-groups/kelly-swarts> >* (Gregor Mendel Institute); **Nick Barton* < <https://bartongroup.pages.ist.ac.at/people/group-leader/> >* (ISTA)*. For young scientists, this cluster offers a unique environment for interaction and personal growth.

The SFB aims to develop a framework for understanding polygenic adaptation and to establish new standards for the analysis of adaptive polygenic traits in GWAS and experimental evolution studies. We will combine model-based conceptual work and data-driven approaches from GWAS and experimental evolution to achieve this goal. The models and methods that will be developed integrate population genetic and quantitative genetic approaches to detect, analyze, and interpret genomic patterns of the "architecture of polygenic adaptation".

*SFB - a collaborative environment for research and learning: *The theoretical and empirical projects of the SFB are highly synergistic and the collaborative nature of the SFB will provide an inspiring academic environment and promote curiosity-driven research. The interaction between projects of the SFB is strongly facilitated by a long-standing track record of fruitful interactions among the PIs. The PhD students and postdocs in the SFB will benefit enormously from these tight interactions.

To ensure a good integration of experiment and theory, researchers have the opportunity to spend some time in a group from the other "camp". These regular exchanges will improve the mutual understanding of concepts and problems, ensure that the theoretical work is guided by experiments (and vice versa) and will represent a true added value of the SFB. In addition to the formal supervisor, both PhD students and postdocs will have at least one co-advisor with complementary expertise.

*Courses: *The recruited early-stage researchers in the SFB will have the opportunity to acquire experience beyond their own projects and working groups.

The SFB PIs participate in joint teaching activities and representatives of all institutions are contributing to the Vienna Graduate School of Population Genetics (www.popgen-vienna.at). The PhD students will be integrated in the Vienna Graduate School of Population Genetics, which offers a 5-week introductory course that covers subjects as diverse as statistics, population

genetics, Drosophila genetics, programming, NGS data analysis (both DNA- and RNA-Seq) and quantitative genetics.

SFB postdocs will have the opportunity to participate in the teaching in introductory course in their areas of expertise. But at the same time can attend specific modules of the introductory course together with the PhD students. This joint event will have a tremendous impact on team-building and can enable scientists from different host institutions to establish strong ties which can result in research collaborations.

The IST Graduate School offers more advanced courses in evolutionary

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VirginiaStateU BioluminescentFungiOmics

Postdoctoral Position in Integrated and Comparative -Omic Study of Bioluminescent Fungi

We are seeking a creative and highly motivated postdoctoral candidate to join our team who is interested in applying cross-species multi-omics approaches, including the genomic, epigenomic, transcriptomic, and proteomic approaches, to study the evolution of bioluminescence in fungi. This is a part of the collaborative project (including multiple institutions in U.S.A. and Brazil) funded by the U.S. National Science Foundation and FAPESP to study the biodiversity in the Dry Diagonal of Brazil in comparison to the Atlantic Forest and Amazon, and the group meets regularly on a monthly basis.

The postdoctoral researcher will work at the newly founded Virginia State University Center for Biotechnology, Genomics, and Bioinformatics (VSU CeBiGeBi) under the direction of Dr. Xianfa Xie. The lab space is located in a recently renovated building and well equipped with instruments for DNA sequencing (including Illumina MiSeq, NextSeq 500, and Nanopore sequencers), other related molecular biology instruments, and a Linux server for bioinformatic analysis.

A strong background in comparative/evolutionary genomics and excellent communication, organizational,

and leadership skills are required. The applicant should have a strong work ethic, and is expected to develop creative solutions and new ideas that promote current research and her/his own future independence. The postdoc will be expected to assist with training graduate and undergraduate students in the lab, develop synergistic projects, write grant proposals, produce first authored papers, and contribute to co-authored papers. The Xie Lab has a strong commitment to maintaining an inclusive space in the lab that is welcoming to anyone who wants to experience research, thus applicants should share this commitment to diversity and inclusion.

Ideal applicants will have: * Experience with best practices for generating and analyzing NGS and Nanopore/PacBio sequencing data * Strong skills to code in at least one programming language * Productivity in high quality research (as evidenced by first-authored or coauthored publications) * Strong written and oral communication skills * Ability to work effectively and collegially with colleagues and be a productive member of a research team

Other trait not required, but preferred: * Proficiency in oral communications in Portuguese

The position is available for a minimum of one year as a full-time 12-month appointment, with possible renewal based on satisfactory performance. The compensation includes competitive salary and full benefits. Selected applicants will also benefit from funds to travel to scientific meetings annually, opportunities for mentoring students, teaching, and further career development. Additional lab funds for independent projects may also be available later. Anticipated start date is July 10, 2023, but is flexible depending on the candidate.

Applicants must have a Ph.D. in an appropriate field. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment. Women and minorities are strongly encouraged to apply.

The university is located in central Virginia, a great location with pleasant weather. It is about two hours away from the Appalachia mountains and the Shenandoah National Park, the ocean, Washington DC, and the Research Triangle in North Carolina. The “River City” Richmond is very close by and the annual Richmond Folk Festival has been attracting performers and audience from across the world. There are great opportunities for sightseeing (particularly historic sites), water activities, hiking, camping, other outdoor activities and sports, arts, etc. Plus, living in this area is much more affordable than many other places in the

U.S. and the area is generally safe as well.

If interested, please submit your application at the following site: <https://www.jobs.virginia.gov/jobs/-research-associate-chesterfield-virginia-united-states-petersburg> Review of applications will be on a rolling basis and continue until a suitable applicant is found.

Xianfa Xie, Ph.D. Associate Professor, Department of Biology Director, Center for Biotechnology, Genomics, and Bioinformatics Virginia State University xxie@vsu.edu

Xianfa Xie <xxie@vsu.edu>

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WesternU Canada VirusEvolutionBioinformatics

Postdoctoral Associate, Virus Evolution and Bioinformatics

The Poon lab (<https://github.com/PoonLab>) focuses on the development and application of computational methods to reconstruct the molecular evolution and epidemiology of human RNA viruses. We seek to fill an opening for a Postdoctoral Associate to study non-parametric clustering methods and their application to reconstruct transmission patterns from the genetic divergence of virus infections.

The lab is situated on Western University (<https://uwo.ca>) campus in London, Ontario, in a newly-renovated space adjacent to three other bioinformatics research groups (genomic epidemiology, spatial transcriptomics, machine learning).

Salary: \$70K per year, including benefits

Duration: 2 years, renewable

Start date: September 1, 2023, or earlier as needed

Required qualifications:

- a PhD in biological sciences, bioinformatics, applied mathematics, statistics, computer science, epidemiology, or a related field;
- experience working with command-line interfaces (i.e., Linux, macOS terminal);
- experience with at least one scripting language (preferably Python and/or R);

- preferably some experience with basic software development principles, e.g., version control systems (git), writing external and internal documentation, unit testing;

- ability to prepare and revise scientific manuscripts in English, as demonstrated by a record of first-author publications;

- ability to communicate and to work as part of a team

How to apply: Send a CV, contact information for at least two work-related references, and (optionally) examples of your source code to apoon42@uwo.ca

The University invites applications from all qualified individuals. Western is committed to employment equity and diversity in the workplace and welcomes applications from women, members of racialized groups, Indigenous persons, persons with disabilities, persons of any sexual orientation, and persons of any gender identity or gender expression. Accommodations are available for applicants with disabilities throughout the recruitment process.

<https://grad.uwo.ca/doc/postdoc/opportunities/-Postdoctoral%20Associate%20Position-Poon%20Lab-Virus%20Evolution%20and%20Bioinformatics.docx.pdf>
Art Poon <apoon42@uwo.ca>

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YaleU PopulationEvolutionaryGenomics

Postdoc: Yale University Population genomics

A position as a postdoctoral researcher/fellow in population and evolutionary genetics is available at the Department of Ecology and Evolutionary Biology, Yale University, in Dr. Adalgisa (Gisella) Caccone research group.

Project description: This project is looking at adaptive and non-adaptive mechanisms of phenotypic evolution in response to urbanization in the Eastern Gray Squirrel. Phenotypic divergence between cities and adjacent rural areas has been well documented but disentangling the roles of adaptive and non-adaptive drivers of divergence for heritable traits has proved challenging. Environmental differences between urban and rural areas can cause divergent natural selection, but phenotypic divergence can also result from strong genetic drift due to founder

effects and small population size in cities. Gene flow between urban and rural areas should reduce phenotypic divergence, but the strength of this homogenizing force likely varies among cities due to differences in landscape structure. Studies of phenotypic variation and population genetic structure across multiple cities are needed to advance our understanding of how urbanization causes trait evolution via adaptive and non-adaptive pathways. This project seeks to fill this knowledge gap.

This project is funded by a NSF grant. The Yale PI is Adalgisa Caccone (<https://caccone.yale.edu/>). The project is in collaboration with the research groups of Bradley Cosentino (<https://landscapemosaic.org/-index.html>) and James Gibbs (<https://www.esf.edu/-EFB/gibbs>).

Duties: The postdoctoral hire will be responsible of collecting and analyzing population genomic data, based on whole genome data.

Qualifications required: For this position, the candidate must hold a PhD degree within evolutionary biology or another relevant field, with experience in population genomics. Since this is an ongoing project in its third year, the ideal candidate needs to have experience on how to look at selection signals in whole genome data, which for the most part have been already collected.

They need to be able to express themselves fluently in spoken and written English, work independently, thrive in a multicultural and collaborative environment, and willing to support the training of undergraduate and graduate students.

The position is for two years. The postdoc will also be engaged to support research and training of faculty, graduate and undergraduate students at the Yale Center for Genetic Analysis of Biodiversity (<https://cgab.yale.edu/>), providing experience on one-on-one training and supervising different types of genomic related projects.

You are welcome to submit your application by June 15, 2023. Applications will be reviewed as they come in. The tentative start of the position is August 1st, 2023. To apply please send your CV, a one page description of your interest and qualifications and how they fit with the job description, and list names and emails of two persons that can provide support letters.

For inquiries please contact: Adalgisa (Gisella) Caccone (Adalgisa. Caccone@yale.edu)

“adalgisa.caccone@yale.edu”
<adalgisa.caccone@yale.edu>

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WorkshopsCourses

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FreieU Berlin
PlantMorphologyAndSystematics
Aug7-18

Berlin Summer Course in Plant Morphology and Systematics

7-18 August 2023

This two-week short course (7th-18th August, 2023) will be 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: 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 10 and a maximum of 20 participants.

REGISTRATION FEE:

early bird - before 1 July: 800 euro

after 1 July: 950 euro

(Registration includes coffee breaks, daily lunches with snacks, and an excursion, but does not include travel and lodging).

HOW TO APPLY AND SECURE A PLACE: Please contact Louis Ronse De Craene (l.ronsedecraene@gmail.com) to request an application form.

To secure a place on the course you will be asked to pay a deposit of euro 100.

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 flowering plants, with a focus on floral diversity and the significance of flowers for systematics and evolution as a whole. 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 7 August: Student presentations - introduction to morphology of vegetative structures and flowers, inflorescence and flower structure (floral diagrams and formulas); overview of major groups of flowering plants.

Tuesday 8 August: Major characteristics of Flowers and special attributes (phyllotaxis, aestivation, merism, symmetry, floral tubes and hypanthia).

Wednesday 9 August: Floral evolution from the ANITA grade to Mesangiosperms

Thursday 10 August: Monocot evolution: variations on a theme

Friday 11 August: Basal eudicots and rise of the core eudicots

Saturday 12 August: excursion to Sans Souci (Potsdam)

Sunday 13 August: day off

Monday 14 August: Rosid diversification I

Tuesday 15 August: Rosid diversification II

Wednesday 16 August: Rosid-Asterid transition

Thursday 17 August: Asterid diversification I

Friday 18 August: Asterid diversification II - Conclusions and wrap-up followed by BBQ

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 De Craene 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:

If you have any special request due to any condition that may interfere with your access to the course, please let us know.

WHO WE ARE:

We are both experts in floral morphology and evolution. Louis has a strong expertise in the evolution of flowers within the framework of the most

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Indianapolis Adaptive Evolution Aug14-16

LIFE: Leveraging Innovations From Evolution Scoping Workshops

NSF is partnering with Knowinnovation to host two LIFE Scoping Workshops (one in-person and one virtual) that will bring together diverse scientists to think on specific research challenges and opportunities, including technological and educational training needs, that leverage convergent evolution to investigate the evolution of innovation and adaptive traits.

If you are eager to engage with diverse researchers to spark creative paths forward to advance our understanding of LIFE, join us! We encourage researchers with interest and expertise in a variety of fields.

More information and registration: <https://apply.knowinnovation.com/life/> A virtual Town Hall will be held May 15, 2023 1:00 pm - 2:30 pm ET to help answer any questions.

Link to register for the Town Hall: <https://app.smartsheet.com/b/form/-ad7bbe00e7334c39afb542f517465d10> Registration Deadline for the Town Hall - May 14, 2023 by 5 PM ET

Application Deadline for the Scoping Workshops - June 5, 2023 by End of Day

“Wisecaver, Jennifer H” <jwisecav@purdue.edu>

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

Online Adaptation Genomics Jun26-30

Dear all,

We are excited to announce our upcoming course on Adaptation Genomics, taking place from 26th to 30th June 2023. To foster international participation, this course will be conducted online, allowing you to join us from anywhere in the world.

Course website: (<https://www.physalia-courses.org/courses-workshops/courseadaptationgenomics/>)

Course Overview: Explore the fascinating realm of the genomic basis of adaptation through population genomics approaches. Our instructors will guide you from raw genomic data handling and exploration to advanced methods, including genotype-environment associations based on both sequence and structural variants. Through hands-on exercises, you will gain bioinformatics skills, learn to manipulate, visualize, and interpret genomic data and patterns.

Target Audience and Assumed Background: This course is designed for graduate students and researchers interested in utilizing genomic tools to investigate adaptation. Participants should have a basic background in evolution and population genetics. Prior experience in UNIX-based command line and R is advantageous, but don't worry if you lack it - a short tutorial can be provided. The course will run in a Linux environment on remote servers, and data analysis and visualization will be performed using R and RStudio.

Learning Outcomes: Master the handling of genomic data from raw reads to genetic variants. Calculate fundamental population genetic statistics. Visualize genetic population structure. Identify signatures of selection in the genome. Account for putative structural variants. Understand the potential and limitations of different methods in studying the genomic basis of adaptation. Don't miss this invaluable opportunity to expand your expertise in adaptation genomics and gain confidence in applying these methods to your own research. Join us for an engaging and informative course that will equip you with the necessary skills to unlock the secrets of adaptation.

For more details and registration, visit our website: (<https://www.physalia-courses.org/courses-workshops/courseadaptationgenomics/>)

Full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops>)

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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Online BEAST2 PhylogeneticInference Jul10-21

Dear colleagues,

We are happy to announce a new course: "Bayesian

phylogenetic inference with BEAST2", organized by Transmitting Science.

Online live sessions on the 10th, 12th, 17th, 20th, and 21st of July, 13:00-16:00 and 17:00-20:00 (Madrid time zone). Total course hours: 35.

Instructors: Dr. Jöelle Barido-Sottani [1] (Ecole Normale Supérieure de Paris, France) and Dr. Bethany Allen [2] (ETH Zurich, Switzerland).

Course Overview:

Bayesian phylogenetic inference is a powerful tool for reconstructing phylogenies while accounting for complex evolutionary dynamics. It allows prior knowledge to be integrated into the inference and also provides a detailed picture of the uncertainty present in the dataset. However, the number and complexity of the available models and options can be daunting for users and can make it difficult to apply inference tools effectively in practice. In this workshop, participants will learn the theoretical concepts underlying the different models involved in Bayesian phylogenetic inference, and get hands-on experience using these models in BEAST2. Particular attention will be given to more complex tree models, such as the fossilized birth-death model used to integrate past information into phylogenies, as well as rate-heterogeneous models which allow for variations in evolutionary dynamics across clades. Finally, the course will give practical information on setting up and troubleshooting analyses in BEAST2.

Registration and more information: <https://www.transmittingscience.com/courses/evolution/bayesian-phylogenetic-inference-with-beast2/> Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com Twitter @SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and op-

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Links:

[1] <https://www.transmittingscience.com/-instructors/joelle-barido-sottani/> [2] <https://www.transmittingscience.com/instructors/-bethany-allen/> Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

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Online EvoBioCrashCourse Jun12-27

Dear EvoBio community,

This summer (June 12th - 27th), the second edition of the EvoBio Crash Course will take place. This is a project aimed at students interested in evolutionary biology world-wide but especially in the Global South: we recognize that for many students in the Global South, systemic knowledge gaps and other barriers persist. In a two-week free, online crash course we hope to provide knowledge on evolutionary biology through a series of lectures, discussion sessions, and practicals. Overall, we seek to increase our participant's chances of obtaining access to high-level graduate programmes, and an opportunity at a career as future evolutionary biologists. Last year's course had over 700 registered students from

62 countries. The course will cover the following topics:

Introduction to Evolutionary Biology, Genetics, Speciation & tree-thinking, Behavioural ecology, Paleobiology & long-term evolution, Evolvability & Plasticity, Evolutionary Theory, Evolutionary Conflicts, and Application Procedures.

If this is of interest to you, then we warmly invite you to sign up for this course! Whilst the course is broadly aimed at BSc students, participants of all levels are welcome. No previous knowledge of evolutionary biology is required for the course. Furthermore, we would greatly appreciate it if you could share the registration form and spread the word. The form can be found here, registration is open until May 30th: https://docs.google.com/forms/d/e/1FAIpQLScBdW0tkR3LP94KJYcViHy00EaKn8fa9U7I3cFpri_fYjyz7Q/viewform?usp=sf_link For more information, you can see our website or our Twitter account (don't hesitate to retweet!) - and feel free of course to email us, under evobio.crash.course@gmail.com.

Website: <https://evobiocrashcourse.github.io/> Twitter: <https://twitter.com/EvoBioCC> Best regards,

Jana Riederer

On behalf of the EvoBio Crash Course team

"Riederer, J.M." <j.m.riederer@rug.nl>

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Online GradStdProfDevel May18-19

FREE professional development workshop for graduate students working on any aspect of animal behavior and related fields (e.g., ecology, evolution, physiology, toxicology, and more!)

Please join us for a motivating and inspiring two-day virtual workshop focused on peer coaching; community building; and justice, equity, diversity, and inclusion.

REGISTER HERE BY MAY 5: tinyurl.com/3fmm3pn7

The workshop will take place over two half-days May 18th and May 19th, 2023 from 1:00 - 4:30 EST.

The workshop topics will include discussions of mentorship, community building, and JEDI (justice, equity, diversity, and inclusion) as well as a career panel and the formation of long-term peer to peer coaching networks.

Peer-coaching circles: A major goal of the workshop is to build peer-coaching circles, which create supportive environments and provide networking opportunities, and also allow scientists, especially those from minoritized groups, to learn how to navigate the culture common to the sciences and to academia. These circles provide support for you as a grad student and your next career steps.

Our keynote speaker will address strategies for thriving in STEM with an interactive and empowering session on Responsive Mentoring.

Dr. Charissa Owens (<https://cofc.academia.edu/CharissaOwens/CurriculumVitae>)

Career panel: We will also have a career panel to provide insights into a wide variety of different careers, including industry, government, non-profits, and academia.

Graduate students who identify as members of minoritized groups across a variety of axes (e.g., racial or ethnic group, gender identity, sexual orientation, first-generation college student, disability, neurodivergence, veteran status, and other disadvantaged backgrounds) are strongly encouraged to apply.

In the registration link, we are collecting data on participants in the workshop and peer coaching program so that we can understand how to best support graduate students. All questions are optional, and data will only be shared or published in anonymized and aggregated forms.

If you have any questions, please contact the organizers: Drs. Delia Shelton (shelton.delia@gmail.com), Alex Trillo (prrillo@gettysburg.edu), Beth Reinke (eareinke@neiu.edu), Elizabeth Hobson (hobsoneh@ucmail.uc.edu), Caitlin Wells (cpwells@rams.colostate.edu), Alycia Lackey (alycia.lackey@louisville.edu), and Ginny Greenway (egreenway@ufl.edu).

Alycia CR Lackey Assistant Professor Department of Biology University of Louisville alyciarlackey.weebly.com

“Lackey, Alycia” <alycia.lackey@louisville.edu>

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Online GWAS Jun5-9

Dear all, there are the last seats available for our upcoming Genome-Wide Association Studies (GWAS) course,

designed to equip participants with the essential knowledge and skills needed to conduct a comprehensive and rigorous GWAS analysis. Join us for an immersive learning experience that will empower you to conduct robust and reproducible GWAS studies.

Dates: online, June 5th-9th

Course website: [<https://www.physalia-courses.org/courses-workshops/course49/>]

In this course, we will guide you through the step-by-step process of constructing a reliable analysis pipeline for GWAS. You will gain a comprehensive understanding of the necessary components involved in a typical GWAS study, enabling you to develop a reusable and reproducible bioinformatics pipeline. The course is structured into modules spanning five enlightening days. Each day will commence with introductory lectures, followed by interactive class discussions to solidify your grasp of key concepts. The remaining duration of each day will be dedicated to practical hands-on sessions, ensuring that you gain practical experience in applying the learned techniques. Our practical sessions are designed to be engaging and immersive. You will have the opportunity to observe and mirror exercises demonstrated by our experienced instructors, allowing you to understand essential skills effectively. Moreover, you will work individually to complete exercises, applying the acquired skills under the guidance of our instructors. Following each exercise, results will be analyzed and discussed as a group, facilitating a deeper comprehension of the implications. Course Topics: - Introduction to Genome-Wide Association Studies (GWAS) - Study design and data collection - Quality control and data preprocessing - Statistical analysis methods - Interpretation and visualization of results - Building a reusable and reproducible bioinformatics pipeline This course is ideal for students, researchers, and professionals seeking to enhance their expertise in GWAS. Whether you have limited prior knowledge or are already familiar with the fundamentals, our course will provide valuable insights and practical skills to advance your research.

Full list of our courses and Workshops: [<https://www.physalia-courses.org/courses-workshops>]

We look forward to welcoming you to our GWAS course and sharing this exciting learning experience with you.

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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Online IntroductionToCRISPR Oct9-12

Dear all,

We are thrilled to announce our upcoming workshop on Introduction to CRISPR for Ecology and Evolution Studies. This comprehensive program will provide you with both theoretical knowledge and hands-on experience in genomic data analysis, using practical examples carefully selected from the latest scientific literature.

Dates: Online, October 9th-12th.

Course website: (<https://www.physalia-courses.org/courses-workshops/course53/>)

This workshop is designed to equip participants with the essential skills and understanding required to implement the CRISPR-Cas9 tool in their own projects, specifically within the fields of ecology and evolution. Throughout the workshop, we will focus on experiment design, method selection, and data analysis, ensuring you gain the expertise needed to confidently incorporate CRISPR techniques into your research.

The workshop features a combination of fundamental theoretical lessons and engaging hands-on sessions. The theoretical lessons will provide you with a strong foundation in the principles and applications of the CRISPR-Cas9 genome-editing tool. In the hands-on sessions, you will work with practical examples, utilizing web-based tools, license-free software, and UNIX-based command line programs. All data used in the workshop is drawn from up-to-date scientific literature, ensuring its relevance and applicability to real-world scenarios.

Each day will include dedicated “Discussion and Q&A” sessions, allowing you to interact with the instructors and fine-tune your own projects. This personalized guidance will help you navigate specific challenges and optimize your experimental designs.

This workshop is ideal for undergraduate and graduate students, researchers, and technicians in the biological sciences who are eager to incorporate the CRISPR-Cas9 tool into their projects within the fields of ecology and

evolution. A basic background in biology, particularly in genetics and molecular biology, is required. Participants are expected to have a solid understanding of the central role of nucleic acids (DNA/RNA) in evolution. Additionally, familiarity with bioinformatics tools such as BLAST homology-based search and multiple sequence alignment is beneficial, as most hands-on sessions involve sequencing data analysis. However, prior experience with command-line based programs is not mandatory, as an introduction to UNIX commands will be provided.

By the end of this workshop, you will have achieved the following learning outcomes:

- Understanding the fundamentals of the CRISPR-Cas9 genome-editing tool
- Designing reliable CRISPR-based gene knockout experiments
- Annotating genes of interest in non-model species
- Designing and evaluating species-specific single guide RNAs (sgRNAs)
- Efficiently synthesizing sgRNA and assembling optimized Cas9/sgRNA mixes
- Screening for G0 CRISPR mutants using a fast genotyping method
- Designing genotyping strategies tailored to project needs
- Analyzing Cas9-induced genomic variants using Sanger and Illumina deep sequencing

Full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops>)

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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Online IntroductionToNextflow Sep25-26

Dear all, I hope this email finds you well. I am thrilled to announce our upcoming course on Introduction to Nextflow, a widely adopted workflow system for running high-throughput, data-intensive applications across

various infrastructure environments. The course is scheduled to take place on 25th and 26th September 2023 and will be conducted online, allowing participants from around the world to join us conveniently. Course website: (<https://www.physalia-courses.org/courses-workshops/-course60/>) OVERVIEW: Nextflow has rapidly emerged as one of the primary technology platforms for computational workloads in life sciences. This framework enables scientists to write code in any scripting language, define software dependencies with containers, connect tasks using an event-driven dataflow programming DSL, and seamlessly deploy workflows across local machines, grid computing systems, or public cloud infrastructure. TARGET AUDIENCE AND ASSUMED BACKGROUND: The Introduction to Nextflow workshop is designed for users who aim to quickly gain proficiency in Nextflow technology, starting from basic to advanced concepts. The majority of the practical sessions will utilize command-line tools; therefore, familiarity with a *nix environment (e.g., Linux or MacOS) and the shell (e.g., Bash) is highly desirable. PROGRAM: The course will be conducted over two days, with classes held from 2 pm to 8 pm CET. Monday: Introduction to Nextflow Basic Scripting in Nextflow Channels Processes Operators Executors RNA-Seq pipeline Tuesday: Configuration Pipeline Parameters Workflows Modules Sharing Pipelines RNA-Seq pipeline 2 We will provide you with a repository containing all the necessary materials and software required for the course. Additionally, an AWS cloud environment will be made available to facilitate the practical sessions effectively. Full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops>)

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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Online LongitudinalDataInR Jun26-29

Dear all, We are excited to announce our upcoming course on Introduction to the Analysis of Longitudinal Data with R! This course is designed to provide you with comprehensive knowledge and practical skills to effectively analyze and interpret longitudinal data using the R programming language.

Dates: June, 26th-29th

Course website: (<https://www.physalia-courses.org/-courses-workshops/longitudinal-data-in-r/>) COURSE OVERVIEW: Longitudinal data, which involve repeated measurements over time or space, pose unique challenges in analysis and interpretation. In this course, we will explore the main challenges associated with longitudinal data from both classical statistical and machine learning perspectives. Specific topics covered will include forecasting, epidemiology, and gene-expression experiments. You will gain insights into visualization, exploratory data analysis, modeling, and validation techniques for longitudinal data analysis. FORMAT: The course is structured into modules spanning four days of intensive learning. Each day will feature engaging lectures accompanied by class discussions on key concepts. Practical hands-on sessions will be conducted, enabling you to apply the acquired skills through collaborative exercises. These exercises will encourage interaction with instructors and fellow students, fostering a dynamic learning environment. Results will be interpreted and discussed throughout the exercises. Towards the end of the course, we will conduct a Kahoot quiz to recap and highlight the essential concepts covered. Additionally, ample time will be provided for discussing specific research problems and participant questions. TARGET AUDIENCE AND ASSUMED BACKGROUND: This course is designed for advanced students, researchers, and professionals interested in analyzing longitudinal data in real-life applications within the field of biology. Whether you are an absolute beginner or an experienced user seeking to enhance your understanding of longitudinal models and scripting code, this course is suitable for you. We will start with an introduction to general concepts and approaches for dealing with longitudinal data. Subsequently, we will explore applications in forecasting, epidemiology, and gene expression. While a background in biology and familiarity with inferential and predictive

experiments is beneficial, attendees from various disciplines are welcome. The course will primarily utilize R, Markdown/Jupyter Notebooks, and the Linux command line. Although a basic understanding of R programming and the Linux environment is advantageous, it is not mandatory. **LEARNING OUTCOMES:** By the end of the course, you will have gained: The ability to recognize and address spatial and temporal dependencies in your data. Proficiency in the most common methods for analyzing data with repeated records. Knowledge and principles of data forecasting. Insight into specific applications of longitudinal data analysis in domains such as epidemiology and gene expression experiments. The skills to design, analyze, and interpret scientific experiments with a time component. Don't miss this opportunity to enhance your expertise in the analysis of longitudinal data with R! Join us for an enriching learning experience that combines theoretical foundations with hands-on practical exercises.

Full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops>)

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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Online LowCoverageWholeNGS Oct2-5

Dear all,

registration is now open for the 4th edition of the course “Population genomic inference from low-coverage whole-genome sequencing data”

Dates: online, 2-5 October 2023

Instructors: Dr. Nina Overgaard Therkildsen (Cornell University, USA) Dr. Tyler Linderoth (University of California Berkeley, USA), Dr. Arne Jacobs (University of Glasgow, UK) and Dr. Nicolas Lou (University of

California, Berkeley, USA)

Course website: (<https://www.physalia-courses.org/courses-workshops/course64/>)

In this course, we will explore workflows and the underlying rationale behind producing, processing and analyzing low-coverage sequencing data for population genomic inference. Given that most species have insufficient reference data to allow reliable genotype imputation, we will focus on a genotype likelihood-based methodology that can be applied to any system. We will primarily cover methods and algorithms implemented in the ANGSD software package and associated programs, providing best-practice guidelines and a discussion of how participants can make maximal use of low-coverage whole genome re-sequencing data for their studies.

The course is aimed at researchers who might have previous experience with next-generation sequencing (NGS) data (e.g. exome/RAD/pooled sequencing) and wish to explore the potential for using low-coverage whole-genome sequencing for their studies.

All hands-on exercises will be run in a Linux environment on remote servers. Statistical analyses and data visualization will be run in R.

Full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops>)

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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Online MappingTraitEvolution Jun5-9

Dear colleagues,

Transmitting Science is offering a new edition of the course Mapping Trait Evolution - 6th edition. This course will be held live online (synchronous). Max 18

participants.

Dates: June 5th-9th, 2023, from 14:00 to 18:00 (Madrid time zone).

Instructor: Jeroen B. Smaers (Stony Brook University, USA).

COURSE OVERVIEW The course provides a comprehensive overview of the state-of-the-art methods in mapping phenotypic trait evolution and will provide participants with a springboard to using these methods to answer their own research questions. We focus on analyses that use a phylogenetic tree and observed trait information from tip taxa (extant and/or extinct) to describe how traits have changed along the branches of a phylogeny. The course covers methods that estimate and test patterns related to changes in mean, covariation, and rate. Applications for continuous and categorical, and univariate and multivariate research designs are discussed. At the end of this course, participants will have developed an understanding of: (1) Brownian motion and Ornstein-Uhlenbeck models of evolution. (2) How these models can be applied to estimate and test patterns of trait evolution. (3) What the advantages and disadvantages are of different models/methods. (4) How to recognize which model/method is most appropriate given a particular dataset and research question. We provide several data sets that will be used to exemplify the application of these methods. We do, however, encourage participants to work with their own data so as to get direct experience with analysing precisely what they expect to analyse. Methods from the following R packages will be discussed: ape, geiger, phytools, evomap, Iiou, bayou, surface, OUwie, mvMORPH, geomorph (this list may change as new packages become available). Important note: Please bear in mind that this course is not about reconstructing (building) phylogenetic trees, the methods we cover in this course assume that a phylogeny is known.

You can find more information here: <https://www.transmittingscience.com/courses/-evolution/mapping-trait-evolution/> or writing courses@transmittingscience.com

Best regards

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com Twitter @SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE

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Online ModernStats Aug31-Dec14

Dear all,

I am very excited to announce a brand new course for the autumn semester (31 Aug to 14 Dec), entitled “Modern Statistical Thinking for Biologists”. This course will help you build basic statistical thinking skills, and to apply them to real data using R. The course is aimed at beginners, with no pre-requisites in terms of maths or stats skills.

The goal is to approach statistics not as it appears in text books but in the way that it is actually practiced in the 21st century. This means a strong focus on data visualisation and exploration. It also means that we will put the emphasis less on P-values and statistical tests (although we will talk about that too!) and more on parameter estimation. If you don’t know what that means, don’t worry - just trust me that it is less annoying than P-values. Another innovative aspect of the course is that we will rely heavily on Bayesian concepts - a powerful way of doing statistics that is becoming extremely common in biology and biomedicine, and is often considered more intuitive for beginners than the approach that introductory courses usually start with.

In terms of the format, the usual Mondego Science formula applies: we will have one 2.5-hour Zoom session per week, as well as weekly assignments with individual written feedback each time. The course also includes a journal club and two group projects.

For more information and registration, please see here: <https://www.mondegoscience.com/courses/statistical-thinking> Best, Rosina.

Rosina Savisaar <rosinasavisaar@gmail.com>

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Online NCBItools Two Jul13 Aug3

Dear EvoBio Community,

The National Center for Biotechnology Information is offering free, virtual, summer workshops highlighting the use of NCBI tools for comparative and evolutionary genomics. Here is the first:

Title: Exploring the Relationship Between Two Eukaryotic Genomes Using the Comparative Genome Viewer Event Date: July 13th, 2023 1-3pm Eastern Time Application Due Date: June 28 Link to workshop page: <https://ncbiinsights.ncbi.nlm.nih.gov/event/comparative-genome-viewer-07-2023/> Direct Link to Application form: https://nlmenterprise.co1.qualtrics.com/jfe/form/SV_0Nyp63wA8hgFn1Y Description:

The Comparative Genome Viewer (CGV) is a visualization tool that helps you quickly compare two genomes based on assembly-assembly alignments provided by NCBI. CGV includes $\frac{1}{2}$ eukaryotic (animal, plant and fungal) $\frac{1}{2}$ assemblies, $\frac{1}{2}$ and $\frac{1}{2}$ many cross-species comparisons. You can view chromosome-scale rearrangements, search for genes, and display aligned regions at the sequence level. In this workshop, you will have the opportunity to:

Compare the human T2T CHM3 assembly to the current reference assembly, GRCh38.14 Explore the extent of $\frac{1}{2}$ gene order conservation (synteny) $\frac{1}{2}$ between two organisms Transfer a viewed region to the Genome Data Viewer where you can expand your analysis View pairwise alignment at the sequence level Download a FASTA alignment file for a region, or download complete whole genome alignment data Generate a scalable vector graphics image (SVG) of your current view

This online, interactive workshop is designed for any life scientist, including research students and educators, who want to visually compare genomes to gain biological insight and share these insights with others. $\frac{1}{2}$ Some familiarity with genomics vocabulary and concepts is recommended for attendees.

Due to curricular and technical limits, we’ve capped the number of spots to provide the best workshop experience. If you register to apply, you will be notified of your application status approximately 2 weeks before the scheduled event. If you have questions about the NCBI Outreach Events program or this specific

workshop, email us at workshops@ncbi.nlm.nih.gov.

Thanks! E. Sally Chang, PhD [C] Genomics Education Specialist, NCBI/NLM/NIH

Dear EvoBio Community, The National Center for Biotechnology Information is offering free, virtual, summer workshops highlighting the use of NCBI tools for comparative and evolutionary genomics applications. Here is one:

Title: Exploring Evolutionary Relationships Using BLAST
 Event Date: August 3rd, 2023 1-3pm Eastern Time
 Application Due Date: July 24th
 Link to workshop page: <https://ncbiinsights.ncbi.nlm.nih.gov/event/blast-evolution-08-2023/>
 Direct Link to Application form: https://nlmenterprise.co1.qualtrics.com/jfe/form/SV_2rZVmGp2nPm9Lg
 Description:

Identification of evolutionarily related DNA or protein sequences (homologs) is a crucial step in many biology workflows. For example, homologous sequences are used to infer relationships between organisms, understand how sequence changes affect observable traits, and identify potential animal models for genetic disorders. NCBI's BLAST program is a standard tool for identifying homologs, and this virtual workshop will teach you best practices for using it for your analysis goals. You will learn when and how to use important but often misunderstood aspects of the BLAST programs and databases, such as when it's helpful to change the BLAST program by using filters and adjusting parameters such as word size, e-value cutoff, and maximum target sequences.

In this workshop, you will use web-based NCBI resources to: Select the correct NCBI alignment tool and BLAST database for your search goal. Use other NCBI sequence analysis services including COBALT, a multiple protein sequence alignment tool. Make use of the new organism-based nucleotide and ClusteredNR protein databases to easily assess the taxonomic diversity of your BLAST results. Visually examine results using auxiliary tools such as TreeViewer, Multiple Sequence Alignment, Graphical Sequence, and the Genome Data viewers.

This online, interactive workshop is designed for any life scientist, including research students and educators, who wants to use BLAST in their

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Online Phylogenetic Macroevolutionary Analysis May 29-Jun 2

Dear colleagues,

There are a couple of slots still available for the course "Introduction to Macroevolutionary Analyses Using Phylogenies".

Format: Live Online (synchronous). Places are limited to 16 participants.

Dates and schedule: May 29th - June 2nd, 2023 from 15:00 to 19:00 (Madrid time zone). 20 hours of online live lessons, plus 20 hours of pre-recorded classes and assignments.

Instructor: Dr. Juan L. Cantalapiedra (Universidad de Alcalá, Spain)

More information and registration: <https://www.transmittingscience.com/courses/evolution/introduction-macroevolutionary-analyses-using-phylogenies/> Check here Ambassadors Institutions to see if you can apply for a 20 % discount (<https://www.transmittingscience.com/funding/ambassador-institutions/>)

Course Overview

Phylogenetic trees have changed the way we study and understand life on Earth. Taking phylogenetic information into account in our analyses is critical to account for the non-independence of biological data. Also, phylogenies allow us to get a deep-time perspective of the processes that have shaped the evolutionary history of groups, including diversification and trait evolution.

This course will introduce participants to the use, modification and representation of phylogenetic trees. Also, we will focus on the use of phylogenetic information to reconstruct ancestral characters and biogeographic histories, using different phylogenetic comparative methods.

This course will also tackle trait evolution modelling and the assessment of phylogenetic signal. Finally, we will learn about the shape of phylogenetic trees and their evolutionary causes, and how to estimate the rates of diversification throughout the history of groups. Participants are encouraged to bring their data sets to use in the practical classes.

The course includes an optional first introductory day to basic R.

Important note: Please bear in mind that this course is not about reconstructing (building) phylogenetic trees.

Software: Mesquite, FigTree, R (ape, TreeSim, TreePar, Geiger, OUwie, BioGeoBEARS).

Best wishes

Sole

– Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com Twitter @SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or <http://transmittingscience.com/additional-terms>. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www.aepd.es. Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

Links:

<https://www.transmittingscience.com/instructors/juan-l-cantalapiedra/> Soledad De Esteban-Trivigno

[<soledad.esteban@transmittingscience.com>](mailto:soledad.esteban@transmittingscience.com)

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

Online RNaseq Jun12-16

RNA-seq Data Analysis Workshop

The DAC aims to facilitate advanced bioinformatic, computational, and statistical analysis of complex genomics data for the Dartmouth research community.

Hosted by Data Analytics Core, DataAnalyticsCore@groups.dartmouth.edu

Location Zoom link to be provided

Monday, June 12, 2023, 12-5pm

Tuesday, June 13, 2023, 12-5pm

Thursday, June 15, 2023, 12-5pm

Friday, June 16, 2023, 12-5pm

This workshop series introduces bulk RNA-seq data analysis, with a particular emphasis on differential expression analysis. REGISTER HERE <https://sites.dartmouth.edu/cqb/current-workshops/> Part I of this workshop, days 1 and 2, will discuss data generation, QC, and data reduction:

- * Develop a working understanding of the analytical workflow for a modern RNA-seq experiment
- * Build a working knowledge of sample preparation considerations for RNA-seq experiments
- * Learn how to process raw NGS data in FASTQ format to generate a gene expression matrix
- * Learn how to perform a detailed quality control analysis of RNA-seq data

Part II of this workshop, days 3 and 4, will cover differential expression (DE) analysis.

- * Develop a working understanding of fundamental bioinformatics and statistical concepts for a typical bulk RNA-seq DE analysis
- * Learn how to leverage the R/Bioconductor framework to perform DE analysis
- * Learn how to use unsupervised data analysis methods (e.g. principal components analysis) to explore RNA-seq datasets
- * Perform a complete DE analysis on a real RNA-seq dataset

Registration Fees are as follows: Dartmouth College, CQB Labs : \$0 Dartmouth College, CQB Mentor Labs : \$120 NH-INBRE affiliates : \$120 Dartmouth College, not CQB affiliated : \$240 External Academic Attendees:

\$360 Non-Academic Attendees : \$600

Shannon Soucy, PhD Co-director, Data Analytics Core
Dartmouth College

Shannon Margaret Soucy
<Shannon.Margaret.Soucy@dartmouth.edu>

(to subscribe/unsubscribe the EvolDir send mail to gold-
ing@mcmaster.ca)

[workshops/course45/](#))

Best regards, Vale

Valentina Sardina Course coordinator info@physalia-courses.org (<http://www.physalia-courses.org/>) mo-
bile: +49 17645230846 Follow us on ([@PhysaliaCourses](https://mas.to/-@PhysaliaCourses))

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

(to subscribe/unsubscribe the EvolDir send mail to gold-
ing@mcmaster.ca)

Online SpeciesDistributionModels Sep18-22

Dear all,

looking to expand your skills in species distribution and ecological niche modeling? Look no further than this online course offered by Physalia Courses! The Species Distribution and Ecological Niche Modelling in R course, taking place from September 18th to 22nd, 2023, will provide participants with a comprehensive understanding of correlative species distribution models and ecological niche models, and how to apply them to their research.

This course will cover everything from the theory behind these models to the practicalities of building and validating them. Participants will have the opportunity to work with species occurrence data of their choice and learn how to use these models for a variety of purposes.

Ideal for students, researchers, and practitioners at any stage of their career, this course requires no prior experience with R, although it is recommended. All R scripts will be provided and explained in detail, ensuring that participants leave the course with the skills necessary to apply these models in a reproducible and automated way.

Don't miss out on this opportunity to expand your knowledge and skills in species distribution and ecological niche modeling.

Visit the course website for more information and to register: (<https://www.physalia-courses.org/courses->

Virtual GenomeAnnotation Jun12-15

The Computational Biology Core at the University of Connecticut is offering a virtual Genome Annotation workshop June 12-15, 2023.

The workshop will cover an introduction to linux and high performance computing before going through multiple genome annotation methods.

The goal is to familiarize attendees with the basic concepts and approaches for annotating a genome with a variety of input evidence. All code will be provided in a public github repository, and session recordings will be available to all participants after the workshop.

WHERE: Virtual (zoom)

WHEN: 9:00 AM - 12:00 PM June 12-15, 2023

COST: \$350 (UConn affiliates) \$483 (External participants)

Registration is first come first serve, more information here: <https://bioinformatics.uconn.edu/cbc-workshops/> Registration form: <https://forms.gle/-vfo6Hogou3mYrFXBA> Questions? E-mail cbcsupport@uconn.edu

“Nahom, Mia” <mia.nahom@uconn.edu>

(to subscribe/unsubscribe the EvolDir send mail to gold-
ing@mcmaster.ca)

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly 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 send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most 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.