
E v o l D i r

February 1, 2025

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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Beijing SMBE2025 Jul20-24 HumanAncientDNA

Dear colleagues,

We are organizing an SMBE symposium titled:

“Human history and past social organisation in the light of palaeogenomes: new methods, new findings”

to be held during the Society for Molecular Biology and Evolution annual meeting in Beijing, China, between July 20-24, 2025.

Deadline for abstract submission is January 30, 2025.

For more information about the symposium, please see below and visit the SMBE website at <https://-smbe2025.scimeeting.cn/> . We are looking forward to seeing you in Beijing!

Hannah Moots and Mehmet Somel

Title:

Human history and past social organisation in the light of palaeogenomes: new methods, new findings

Invited speaker:

María C. Ávila Arcos, National Autonomous University of Mexico

Abstract:

At the crossroads of genetics and archaeology, archaeogenetics brings together these disciplines in new and unique ways. The last decade has seen the emergence of a remarkable body of work using paleogenomes data to examine past social dynamics, describing various modes of human mobility and their cultural consequences, pre-historic “postmarital” residence and consanguinity patterns, the role of genetic relatedness in kinship structures, patterns pathogen transmission, or the exchange of domestic animals in past societies. This has been possible through contextualization of genetic results using material culture, bioarchaeological data and social theory, providing a glimpse into various facets of daily life in the past. In this symposium we invite talks a) that cover exciting new findings from diverse periods and regions of the world on social dynamics inferred using archaeogenomic data, b) that present novel methodological approaches tailored for inference of relevant patterns from ancient genomes (e.g. identifying genetic relatedness and mobility), and c) that showcase creative approaches synthesizing genetic data with archaeological data and models. This session aims to examine how ancient DNA, by its interdisciplinary nature, bridges questions about cultural and biological change and how this nascent field is positioned to contribute to theory-building in relation to social structure and evolutionary biology.

Organizers:

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

Mehmet Somel (Middle East Technical University, somel.mehmet@googlegmail.com), ing@mcmaster.ca)

Dates:

Abstract submission deadline: Jan 30, 2025

Early bird registration deadline: Apr 20, 2025

Abstract submission details: https://smbe2025.scimeeting.cn/en/web/index/25070_2367426

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

Mehmet Somel <somel.mehmet@googlemail.com>

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Beijing SMBE IDEA ProposalCall Jul20-24

It is our greatest pleasure to share with the evoldir community that we are organizing our annual IDEA symposium (Number 25) at the SMBE 2025 (July 20-24) Meeting in Beijing, China. This symposium celebrates SMBE's commitment to fostering an inclusive, equitable, and diverse scientific community by addressing systemic inequities and empowering underrepresented groups in molecular biology and evolution. Please join us if you'd like to share your efforts that:

Highlight community-driven efforts to increase participation and dismantle barriers. Share strategies for creating inclusive scientific environments. Advance diversity, equity, and accessibility in molecular biology and related fields. Explore education-focused initiatives.

The symposium will close with an interactive discussion to share practices, celebrate achievements, and inspire change.

Submission Deadline: The deadline is soon, January 30, 2025, 23:59 (GMT +8)

Submission Link: https://smbe2025.scimeeting.cn/en/web/index/25070_2367426 We look forward to your contributions!

Best regards,

Tugce Bilgin

On behalf of the IDEA Taskforce

SMBE IDEA taskforce <smbe.idea@gmail.com>

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Berlin EvoDevoSexPlant Mar25-28

Berlin.EvoDevoSexPlant.March25-28

“Dear colleagues,

We are pleased to announce that the international PLANT EVO-DEVO symposium entitled “Evolution of Plant Reproduction” will be held at the Department of Plant Physiology (conference room: E. Schieffmann) of the Free University in Berlin (Germany) from March 25 to 28, 2025.

This symposium offers young researchers (master's students, PhDs, post-docs) the opportunity to present their work (oral presentation or poster) to a broad audience, fostering exchanges and connections within the international scientific community. This symposium is organized by the research unit ICIPS (for Innovation and Co-Evolution in Plant Sexual reproduction) and funded by the German Research Foundation (DFG).

This symposium will be divided into eight consecutive sessions with each session being introduced and closed by renowned invited speakers:

- * Innovation of Pollen (invited speakers: V. Franklin-Tong & M.-X. Sun),
- * Evolution of Embryos and Endosperm (invited speakers: G. Ingram & C. Kessler),
- * Evolution of Ovules and Seeds (invited speakers: L. Colombo & A. Plackett),
- * Evolution of Carpels and Fruits (invited speakers: M. Bartlett & C. Scott),
- * Evolution of Fertilization mechanisms in plants (invited speakers: W. Friedman & T. Higashiyama),
- * Evolution of Redox-dependent Mechanisms (invited speakers: I. Monte & H. Renault),
- * Co-Evolution of Signalling System and Gene Regulatory Networks (invited speakers: K. Kaufmann & S. Schornack),
- * Bioinformatics solutions to harness the EvoDevo Data Universe Chaos (invited speakers: U. Scholz & J. Clark).

Registration and abstract submissions for 15-minute oral presentations or posters are open until January 31st via the website: <https://dfg-icips.org/berlin2025/>. Stay updated by: * Following us on Twitter: @DFG_ICIPS * Subscribing to our mailing list (at the bottom of the webpage): <https://dfg-icips.org/berlin2025/>

For questions or more information, please contact Dr. Romain Scalone by email: romain.scalone@bot1.bio.uni-giessen.de

Feel free to share this announcement with your network!
We look forward to welcoming you in Berlin, The ICIPS Organizing Team”

Dr. Romain Scalone

Scientific Coordinator (Research Unit ICIPS & Project RanOmics) Depart.: Plant Developmental Biology Justus-Liebig-University Giessen, Institute of Botany Carl-Vogt-Haus (CVH) - EG - Room 8 (<https://www.uni-giessen.de/JLUmaps/>)

Heinrich-Buff-Ring 38

35392 Giessen - Germany - Tel.: +49 (0) 641 99 35 171 (Mo., Di. & Mi.) Privat.: +49 (0) 1523 7000 383 Email: romain.scalone@bot1.bio.uni-giessen.de

“Scalone, Romain” <romain.scalone@bot1.bio.uni-giessen.de>

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CallForAbstracts
EvolSexChromosomes SMBE2025
Jul20-24

Call for abstracts: symposium on the Evolution and Regulation of Sex Chromosomes and Sex Determination at SMBE2025

Annual meeting of the society for molecular biology and evolution (SMBE) will be held in July 20-24, 2025, in Beijing, China

Qi Zhou from Zhejiang University and Wen-Juan Ma from Vrije Universiteit Brussel are pleased to announce the upcoming symposium on the Evolution and Regulation of Sex Chromosomes and Sex Determination at SMBE2025.

Sex chromosomes are prevalent in eukaryotes and have evolved independently. However, it remains a mystery how sex chromosomes stopped recombination, and why sex chromosomes remain highly stable in some lineages like mammals and birds but undergo frequent turnovers in many others. Additionally, the upstream sex-determining genes are largely unknown in majorities of species. And among the few species with the sex-determining genes identified, it is unclear how their downstream pathway is structured and evolved. Excitingly with the advent of genomics, an increasing number of non-model species begin to offer insights into

these fundamental questions. Recent studies identified sex-determining regions and characterized regulatory mechanisms underlying sex determination and sexual differentiation across a wide range of species.

We are pleased to confirm Prof. Tatiana Giraud (Université Paris-Saclay, CNRS) as an invited speaker. She is a pioneer in studying sex chromosomes of various ecological and agriculturally important fungal species. Her work will be setting the stage for contributed speakers and together offer a comprehensive perspective on the evolution and regulation of sex chromosomes and sex determination.

Deadline for abstract submission: Thursday, January 30, 2025, 23:59 (GMT +8).

For more information and to submit your abstract, please visit: <https://smbe2025.scimeeting.cn/en/web/index/25070> Don't miss the opportunity to share your research, engage in stimulating discussions, and network with peers in this exciting area of evolutionary biology!

We look forward to seeing you in Beijing this summer!

Best regards,

Wen-Juan Ma

Prof. Dr. Wen-Juan Ma Assistant Professor Evolutionary Genomics of Sex Lab Research Group of Ecology, Evolution and Genetics (bDIV) Biology Department Vrije Universiteit Brussel Pleinlaan 2 - 1050 Brussels, Belgium Office F5.60 T +32 (0)2 629 3416 <http://www.wmalab.com> <https://bdiv.research.vub.be/en/home-0> <https://academic.oup.com/jeb/pages/why-publish> wen-juan.ma@vub.be

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Ede Netherlands
EvolutionaryBiology Apr8

Dear colleagues,

We are excited to welcome you to the 2025 NLSEB meeting that will be held on Tuesday April 8th at the Reehorst hotel in Ede, the Netherlands.

We have two very exciting plenary talks by Inge Loes (Utrecht University) and by Hassan Salem (Max Plank institute) and by the winner of the 2024 Netherlands Evolutionary Biology Prize (will be announced during the meeting). The program, as always, includes two

parallel presentation sessions, a cultural intermezzo, and plenty of time for poster presentations and socializing with your fellow evolutionary biologists, to strengthen your networking connections and to establish new collaborations.

Registration is now open. To join us on April 8th visit our website (<https://www.nlseb.nl/nlseb2025-meeting>) and follow the registration link. Via the same registration link you can also submit an abstract (to be considered for a talk or poster presentation). The deadline for registration and abstract submission is February 10.

“Kupczok, Anne” <anne.kupczok@wur.nl>

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Germany EvolutionImmunity Sep15-19

Ecological immunology workshop, 15-19 September 2025
- Call for abstract submissions -

Dear colleagues,

Abstract submission is now open for the above meeting to be held at Werbellinsee, close to Berlin, Germany. Please submit your abstract by the 7th of March.

We are delighted to announce our confirmed invited speakers: Alex Best (University of Sheffield, UK) Ewa Chrostek (Jagiellonian University, Krakow, Poland) Katja Dierking (Christian-Albrechts-Universität zu Kiel, Germany) Marc Dionne (Imperial College London, UK) Dieter Ebert (Universität Basel, Switzerland) Carolyn Elya (Harvard University, USA) Andrea Graham (Princeton University, USA) Mark Hanson (University of Exeter, UK) Ben Longdon (University of Exeter, UK) Nagaraj Prasad (Indian Institute of Science Education and Research, Mohali, India) Sarah M. Short (The Ohio State University, USA) Angela Smilanich (University of Nevada, Reno, USA) Robert Unckless (University of Kansas, USA) Crystal Vincent (Queen Mary University of London, UK)

For abstract submission, please see the workshop homepage: https://ssl2.cms.fu-berlin.de/-bcp/en/biologie/arbeitsgruppen/zoologie/ag_rolff/-Workshops/Ecological-Immunology-Workshop-2025/-PM-Registration/index.html The meeting is the next installment in a loose series of workshops on ecological

& evolutionary immunology / insect immunity, that started in 2001 in Sheffield, the most recent one being in Blossin (close to Berlin) in 2022. These meetings bring together researchers with different backgrounds but with a shared interest in immunity and host-microbe interactions with a focus on insects, and where we encourage the presentation of unpublished results.

The hallmarks of these workshops are the open atmosphere fostering free exchange, as well as the fact that they are small (~90 participants), and affordable. The format consists of invited speakers, contributed talks and a dedicated poster session. Long breaks provide plenty of opportunity for informal exchange. Past workshops have initiated new collaborations and ideas focusing on frontier research.

The premises are basic but in a beautiful location conducive to the success of the meeting. We will be located at a lakeside, offering great swimming.

Important dates: 7th March Abstract submission deadline 31st March Decisions on abstracts 14th April Registration deadline and payment of fees due 15th Sept Start of conference

Please do forward this advert to anyone who you think may be interested!

We hope that you will be able to join us!

Best wishes from the organisers,

Sophie Armitage & Jens Rolff

If you have any queries, please email us: ecol.immunol.workshop@biologie.fu-berlin.de

Sophie Armitage PhD (she/her)

Freie Universität Berlin Institute of Biology
Königin-Luise-Str. 1-3 14195 Berlin Germany
<https://armitagelab.com/> Sophie Armitage
<saoarmitage@zedat.fu-berlin.de>

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Milovy Czechia EMPSEB30 Jun2-6

Dear colleagues,

The 30th iteration of the European Meeting for PhD Students in Evolutionary Biology (EMPSEB30) will take place June 2-6 2025 in the Czech Republic. EMPSEB aims to provide a platform for students to learn from

each other and, equally, to foster a sense of community. We invite all PhD students working on questions of an evolutionary flavour to submit abstracts via our website <https://empseb30.mpipz.mpg.de/registration>. The deadline (recently extended) is now January 30 2025.

Please note that the European Society for Evolutionary Biology supports EMPSEB attendance via two grants (see <https://eseb.org/prizes-funding/>). These grants also have application deadlines at the end of January. Additional travel support might become available (based on sponsorship outcomes), but do not count on it.

We will have plenaries spanning diverse themes in evolutionary biology, as well as professional-development workshops. The list of invited speakers and further information can be found on the EMPSEB30 website: <https://empseb30.mpipz.mpg.de>. Please spread the word and feel free to forward this message to your colleagues.

We look forward to having you!

The EMPSEB30 organising committee (Jannika Elfert, Lukas Koch, Jana KruÅlicova, Sanghamitra Kumar, Prachitha Nagendra, Pavla Novotna, Alina Schüller, Nikita Tikhomirov, Gaurav Athreya)

“Athreya, Gaurav” <gathreya@uni-mainz.de>

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Montpellier EvolBehaviour Aug11-15

Dear all,

We are pleased to announce the 17th edition of the international conference Ecology & Behaviour (E&B), to be held at the Centre d’Ecologie Fonctionnelle et Evolution (CEFE) in Montpellier from August 11 to 15, 2025 .

This conference offers young researchers (master’s students, PhDs, post-docs) the opportunity to present their work (oral presentation or poster) to a broad audience, fostering exchanges and connections within the international scientific community.

Why join us? The conference is entirely free of charge (no registration fees) only your travel expenses and your dinners are required.

Themes for this year:

* Movement Ecology * Evolutionary Ecology * Functional Ecology * Behavioral Ecology * Conservation Ecology * Ecology and society

Each session will be introduced by renowned invited speakers.

Abstract submissions for 10-minute oral presentations or posters will open from January 15th to March 28th via our website: [<https://ecobhvr2025.sciencesconf.org/>] .

Stay updated:

* Follow us on Bluesky : @ecobhvr2025 * Subscribe to our mailing list : [<https://listes.services.cnrs.fr/www/-subscribe/eco.bhvr>]

For questions or more information: eco.bhvr.org@services.cnrs.fr Feel free to share this announcement with your network!

We look forward to welcoming you, The E&B Organizing Team

Laurine Mathieu

Laurine MATHIEU <laurine.mathieu@cefe.cnrs.fr>

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Nashville EvolAndMedSociety Jul8-10 AbstDeadlineFeb3

February 3 abstract deadline

Please forward this message to all possibly interested people and groups.

The Tenth Annual Meeting of the International Society for Evolution, Medicine, and Public Health will be July 8-10 at Vanderbilt University in Nashville, Tennessee, USA.

Full information is at <https://isemph.org/ISEMPH-2025/> Students, researchers, clinicians, and teachers are all invited to present their research, hear the latest advances from renowned scientists, renew old friendships and make new ones at workshops, discussions and social events. You can also enjoy all that Nashville and Tennessee have to offer. Music!

The ISEMPH 2025 website offers full information about dates and deadlines, Registration, Abstract submission for talks and posters, abstract submission for symposia, the Program, Accommodation, Travel, and more.

Register early to get substantial discounts; fees are refundable until two weeks before the meeting if your plans change. Fees are lower for members so you may want to join the society or renew your registration before registering for the meeting.

The Vanderbilt Evolutionary Studies Initiative is also hosting a two-day symposium to mark the 100th anniversary of the Scopes “Monkey” Trial on the weekend following the conference. More than twenty speakers will talk about evolution, education, religion, and the law - the event will also include lunches and book signings by several authors. Learn more here. You can register for both events with your ISEMPH 2025 registration.

Send questions about travel and logistics to hosting-committee@evmed.org, questions about abstracts to programcommittee@evmed.org, and all other questions to manager@evmed.org.

Randolph Nesse <nesse@umich.edu>

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New Delhi
PAGPopConservationGenomics
Mar 18-20

Call for Abstracts Population and Conservation Genomics Workshop PAG Asia 2025/India, Plant and Animal Genome International Conference <https://intlpagasia.org/2025/> March 18-20, 2025, Westin Hotel, Gurgaon, New Delhi Region, India

The Population and Conservation Genomics (PCG) workshop will be held at the Plant and Animal Genome International conference PAG Asia 2025/India. It is on the same lines as the annual workshop that I have organized for over the past 18 years at the main PAG conference in San Diego, California, USA. You are invited to attend this Workshop and submit abstracts for oral presentations on any population and conservation genomics aspect of both plants and animals. The topics may include (but not limited to): population genomic diversity and structure; molecular evolution; pangenomes; phylogeography; landscape genomics; seascape genomics; natural selection and local adaptation; ecological and evolutionary genomics; population epigenomics; paleogenomics; eDNA; bioinformatics in population and conservation genomics; population genomics of speciation; metapopulation genomics; application of genomics

in breeding, forensics, biogeography, demography inferences, and conservation and management of genetic resources; genomic effects of domestication, management practices, fragmentation, bottlenecks, climate and environment change, and transgenic deployment; and gene conservation; etc.

The Workshop is scheduled on March 20, 2025, and has a provision for 6 invited speakers. Most of the invited presentations will be selected from the submitted abstracts. Please send your abstract of no more than 250 words by e-mail to Om Rajora (Om.Rajora@unb.ca) as an attached Word file no later than February 12, 2025. Please make sure to include complete affiliations of all authors and email address of the corresponding author. You will be notified by February 14, 2025, whether your abstract has been selected for an oral presentation. Thereafter, the selected presenters will need to submit their abstract to the PAG website. Authors whose abstracts are not selected for oral presentations are highly encouraged to present a poster at the conference.

Inquiries and Abstract Submission

For information and questions regarding the Population and Conservation Genomics workshop, please contact Om Rajora at the following coordinates.

Dr. Om P. Rajora University of New Brunswick Fredericton, NB E3B 5A3, Canada. E-mail: Om.Rajora@unb.ca
Tel: (506) 458-7477

Om Rajora <om.rajora@unb.ca>

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

Online AmerSocOfNaturalists
May 29-30

The American Society of Naturalists will be participating in a joint meeting with the Society of the Study of Evolution and the Society of Systematic Biologists in May and June 2025! This includes hosting a special symposium during a virtual conference of the three societies on May 29-30.

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

The ASN Symposium Committee invites you to submit proposals for a special symposium. Proposed symposium topics should support the Society’s goal to advance the conceptual unification of the biological sciences and

to further knowledge in evolution, ecology, behavior, and organismal biology. Topics could center around important emerging issues in evolution, ecology, or behavior or focus on a pivotal historical paper, tracing its impact and exploring current cutting-edge research inspired by this work.

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

Please submit proposals by email (cas383@miami.edu) no later than midnight Eastern Time on January 31, 2025. Send your proposal as a single pdf attachment, under subject heading "ASN 2025 Virtual Symposium Proposal".

In line with the ASN's commitment to diversity, we encourage including speakers from groups who have been historically excluded from STEM. Therefore, proposals that include a diverse list of speakers from a range of backgrounds, institutions, career stages, geography, gender, race, etc. are especially encouraged. Further, we especially encourage early career researchers to propose sessions as organizing symposia can advance their careers through building broader scientific networks and a record of scientific leadership.

Additionally, the Society's selection committee will evaluate proposals based on their potential to attract a substantial audience and stimulate discussion, the significance and timeliness of the topic, and on the topic differing substantively from recent symposia hosted by the Society. Applicants will be notified of the decision within one week of the proposal deadline.

Christopher Searcy

ASN Symposium Committee Chair

Department of Biology

University of Miami

cas383@miami.edu

"Searcy, Christopher A" <cas383@miami.edu>

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Online Celebrating Roger Butlin Jan9

Dear colleagues,

On ****Thu**** (9 January) we will celebrate Roger Butlin's retirement and his huge contribution to our field. It is possible to join online!

The celebration will be a session at the upcoming Population Genetics Group meeting (7-9 January, Sheffield, UK). PopGroup itself is an in-person meeting, but Roger's session will be streamed as a webinar as well.

Date: Thu 9 January Time: 2pm GMT $\pm \frac{1}{2}$ (note the potential time difference!) Format: A 2-hour session with talks presenting interesting research as well as stories from Roger's life in science
Link: <https://us06web.zoom.us/j/83972880389?pwd=-fJMFBFqOrcH3RuuCyrwVQnPej2a30X.1> Best wishes,
Rui Faria Kerstin Johannesson Jonna Kulmuni Sean Stankowski Anja Westram

Anja Marie Westram <anja.m.westram@nord.no>

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

Online ESEB Internal Conflicts STN Jan16

Dear colleagues,

We would like to invite you to the next online seminar for the "Internal Conflicts and Organismal Adaptation" Special Topic Network (STN) funded by the European Society for Evolutionary Biology, which will take place on January 16th, 14:00 UTC. Our speakers for this seminar are:

John Werren (University of Rochester): Cooperating on conflict: Selfish genetic elements, heritable microbes, and genetic conflicts.

Bengt O. Bengtsson (Lund University): Decades of conflicts: A personal history.

In this seminar, we will look back on the early study of internal conflicts when biologists started identifying selfish genetic elements and grew aware of their importance

to organismal (mal-)adaptation. We hope this will serve as both a 'history lesson' that can help understand how we got to where we are now, as well as an opportunity to reflect on how we can move the field forward. We expect the meeting to take approximately 1.5 hours.

Meeting details:

Link: <https://georgetown.zoom.us/j/98076313746>

Date: January 16th, 2025.

Time: 14:00 UTC.

If you would like to get on our mailing list and take part in our upcoming events, please visit our website (<https://internalconflictsstn.wordpress.com/>) for more information.

Sincerely,

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

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

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Online Meiosis May7-28

Dear Colleagues,

Happy New Year! We are excited to host the 2025 MAYosis webinar series, which will be held on four consecutive Wednesdays from May 7 through May 28, 2025. The MAYosis is a virtual seminar series dedicated to all aspects of meiosis (including evolutionary ones). It aims to expand and strengthen our community and provide a forum to spotlight junior researchers.

Each of the four sessions (2-hour presentation sessions plus 1-hour discussion) will feature six speakers: one invited keynote and five talks selected from submitted abstracts. Only trainees or junior faculty (within 12 years from the completion of the PhD) will be considered for a talk. Invited talks will be 15 minutes plus 10 minutes for questions, and selected talks will be 12 minutes plus 5 minutes for questions. A one-hour general open-mic discussion will be held at the end of each session.

Talks will begin promptly at 4 pm CET (7 am PST; 12 am JST).

The MAYosis 2025 website is open.

<http://meiosis.cornell.edu/mayosis2025/> Please advertise this series as widely as possible amongst your friends and colleagues.

All attendees must register (registration is free).

<https://ucdavis.zoom.us/meeting/register/-tJEsde2vrT8oG9ACZvNGTb-0VyGBpbXDVPCS#/-registration> Abstract submission is open on the website, and the abstract deadline is March 8, 2025.

<http://meiosis.cornell.edu/mayosis2025/abstracts.html> The full program will be available from late March 2025.

The Organizing Committee:

Bernard de Massy, IGH, Montpellier

Friedrich Baudat, IGH, Montpellier

Chloé Girard, I2BC, France

Mathilde Grelon, IJPB, Versailles

Valerie Borde, Institut Curie, Paris

Bertrand Llorente, CRCM, Marseille

Thomas Robert, CBS, Montpellier

Marie-Emilie Terret, Collège de France, Paris

Jean-René Huynh, Collège de France, Paris

Rajeev Kumar, IJPB, Versailles

Mathieu Rousseau-Gueutin, IGEPP, Rennes

Heidi Serra, iGReD, Clermont Ferrand

Laurent Duret, LBBE, Lyon

Satoshi Namekawa, UC Davis

For any question please email to:

contact.mayosis2025@igh.cnrs.fr

Laurent Duret <Laurent.Duret@univ-lyon1.fr>

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Roscoff JacquesMonodConf Sep15-19

Dear colleagues,

We are pleased to announce the organization of a CNRS funded Jacques Monod Conference on “*/Evolutionary and ecological genomics of polyploidy in plants:temporal dynamics across scales of biological organization from molecules to ecosystems/*” to be held in Roscoff (France), September 15-19, 2025.

Deadline for registration is 5 may 2025, and details on the Conference can be found at

< <https://www.insb.cnrs.fr/fr/evolutionary-and-ecological-genomics-polyploidy-plants-temporal-dynamics-across-scales-biological> > (English version)

< <https://www.insb.cnrs.fr/fr/genomique-et-ecologie-evolutive-des-plantes-polyplodes-dynamique-temporelle-differentes-echelles> > (French version)

Invited speakers.:

BARKER Michael —(Department of Ecology & Evolutionary Biology, University of Arizona, USA)
 BONNEMA Guusje —(Department of Plant Sciences, University of Wageningen, Netherlands) *CASACUBERTA Josep* *(Center for Research in Agricultural Genomics, Barcelona, Spain) *CHOULET Frédéric* —(INRAE Site de Crouelle, Clermont-Ferrand, France)
 CONOVER Justin —(Molecular and Cellular Biology Department, University of Arizona, Tucson, USA)
 D’HONT Angélique —(CIRAD, Montpellier, France)
 GLEMIN Sylvain —(CNRS UMR Ecobio, Université de Rennes, France) *HU Guanqing* —(Agricultural Genomics Institute at Shenzhen, China) *KOLAR Filip* —(Department of Botany, Faculty of Science Charles University, Praha, Czech Republic) *KOVARIČEK Ales* —(Institute of Biophysics, Academy of Sciences of the Czech Republic, Brno, Czech Republic)
 LASCOUX *Martin* —(Uppsala University, Sweden) *LEITCH Andrew* —(Queen Mary University of London, England) *LEITCH Ilia* —(Royal Botanic Gardens Kew, England) *MANDAKOVA Terezie* —(Mazaryk University, Brno, Czech Republic) *MASON Annaliese* —(INRES, Pflanzengarten der Universität Bonn, Germany) *NOVIKOVA Polina* *(Max Planck Institute for Plant Breeding Research, Koln, Germany)
 PARISOD Christian —(Département de Biologie, Université de Fribourg, Switzerland) *ROUSSEAU-GUEUTIN Mathieu* —(IGEPP, INRAE, Le Rheu, France) *SALMON Armel* —(UMR CNRS Ecobio, Université de Rennes, France) *SERRA Heide* *(Institut de Génétique, Reproduction et Développement, CNRS/INSERM/Université Clermont Auvergne, Clermont-Ferrand, France) *SOLTIS Pamela* *(Florida Museum of Natural History, USA) *VAN DE PEER Yves* —(VIB UGent Center for Plant Systems Biology, Belgium) *VEKEMANS Xavier* *(Université de Lille, Villeneuve d’Ascq, France) *WINCKER Patrick* *(Geno-

scope, Evry, France)

Best regards,

Malika AINOUCHE (U. Rennes, France) & Jonathan WENDEL (Iowa State University, USA)

Malika Ainouche Professeur Emérite, Université de Rennes UMR CNRS 6553 Ecobio Bât 14 A Campus de Beaulieu 35 042 Rennes Cedex (France) <https://ecobio.univ-rennes.fr/evolution-des-genomes-traits-dhistoire-de-vie-et-adaptation> Malika Ainouche <malika.ainouche@univ-rennes1.fr>

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Seoul RECOMB-CG Apr14-25

The 22nd RECOMB-CG conference is co-located with RECOMB 2025 in Seoul, South Korea.

<https://recomb-cg.org> The RECOMB satellite conference on Comparative Genomics, founded in 2003, brings together leading researchers in the mathematical, computational, and life sciences to discuss cutting-edge research in comparative genomics, with an emphasis on computational approaches and novel experimental results. The program includes invited speakers, contributed talks, and poster sessions.

Contributions on any theoretical and/or empirical approach to genome-wide comparison are welcome. Topics of interest include, but are not limited to: Genome evolution Genome rearrangements Genomic variation, diversity, and dynamics Gene identification and annotation Methods for genome assembly Cancer evolutionary genomics Comparative epigenomics Population genomics Pangenomics Phylogenomics and phylodynamics Paleogenomics Epidemiology and related areas Metagenomics Machine learning in genomics

We encourage submissions that offer new biological findings or otherwise highlight their relevance to biology. Accepted contributions will be presented at the RECOMB-CG 2025 meeting. Selected contributions will be invited to participate in a special issue of the Journal of Computational Biology (with publication fees).

<https://recomb-cg.org/submit/> Key Dates All deadlines are “anywhere on earth.”

Event

Date

Paper submission deadline
February 7, 2025 (Friday)
Author notification for papers
February 24, 2025 (Monday)
Final camera-ready version due
March 3, 2025 (Monday)
Poster submission deadline
April 4, 2025 (Friday)
Registration open
TBA
Conference starts
April 24, 2025 (Thursday)
Conference ends
April 25, 2025 (Friday)
David Sankoff <david.sankoff@uottawa.ca>
(to subscribe/unsubscribe the EvoDir send mail to gold-
ing@mcmaster.ca)

**SMBE Beijing CallAbstracts
PhylGeneFlow Jul20-24**

Dear Colleagues,

The annual meeting of the Society for Molecular Biology and Evolution (SMBE), will be held in Beijing China, July 20-24, 2025.

We are inviting abstract submissions for our symposium, “Phylogenomics in the presence of gene flow: opportunities and challenges” (Symposium #11). All the scientists who have been developing models and methods or doing empirical studies inferring gene flow are highly encouraged to submit abstracts to this symposium.

****The deadline for abstract submissions is January 30, 2025****

Details are as follows:

SMBE 2025 Annual Meeting of the Society for Molecular Biology and Evolution <https://smbe2025.scimeeting.cn/en/web/index/25070.2131033> Symposium 11: Phylogenomics in the presence of gene flow: opportunities and challenges

Organizers: Xiyun Jiao, Southern University of Sci-

ence and Technology, China Thomas Flouris, University College London, UK

Invited Speaker: Anne Yoder, Duke University, USA

Comparative analyses of genome-scale data have revealed the prevalence of cross-species gene flow in organisms. This phenomenon causes discordance of genealogical relationships in different genomic regions, creating difficulties in phylogenomic inference. There are other biological processes which can lead to gene tree incongruence, such as incomplete lineage sorting, recombination, etc. It is important to take them together with gene flow into account when inferring species histories. Treating different types of genomic data differently is also necessary, such as coding vs. noncoding data, which may contain different amounts of signal. The multispecies coalescent model with gene flow provides a natural framework to incorporate all these factors, and analyses using genomic sequence data under this model have already unveiled intriguing speciation patterns. However, the model is complex and the processes of coalescent, introgression/migration, and sequence evolution are highly stochastic, which makes it difficult to analyze genome-scale data efficiently. Thus so far, the field faces not only statistical challenges of developing suitable models and methods, but also computational challenges of analyzing genome-scale data. This symposium will highlight advances and challenges in developing models and methods for phylogenomic inference with gene flow and also exciting patterns of species divergence and cross-species gene flow revealed by analyses of genomic data.

Dates:

Abstract submission deadline: Jan 30, 2025

Early bird registration deadline: Apr 20, 2025

Abstract submission details: https://urldefense.com/v3/_https://smbe2025.scimeeting.cn/en/web/index/-25070_2367426_!!Mak6IKo!MdiJ9HX13kwd5zLE4INfQKkgzbcMz1dr

Look forward to seeing you in Beijing!

Xiyun Jiao <jiaoxy@sustech.edu.cn>

Xiyun Jiao <xiyunjiao@gmail.com>

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ing@mcmaster.ca)

SMBE Beijing GenomeArchitecture AbstExtension

Dear Colleagues,

We are inviting abstract submissions for our symposium, “Novel Insights on Genome Architecture Evolution” (Symposium #8)

2025 Conference for the Society for Molecular Biology & Evolution, July 20-24 in Beijing China.

Note that the abstract submission deadline has been extended to Saturday, February 15, 2025, 23:59 (GMT +8)

Details are below:

SMBE 2025 Annual Meeting of the Society for Molecular Biology & Evolution: [https://urldefense.com/v3/_https://smbe2025.scimeeting.cn/en/web/index/-25070_2131033_...!!Mak6IKo!M8S2HoOwA14tpkvXQLXb9oGKNiVdYxg:CVx8uiAR0C3jFt_3aZ3uDAQ1PCneh8n5Pnb2kiiO5z50E5fXhUqhG3biFcu00zyarNz5jg\\$](https://urldefense.com/v3/_https://smbe2025.scimeeting.cn/en/web/index/-25070_2131033_...!!Mak6IKo!M8S2HoOwA14tpkvXQLXb9oGKNiVdYxg:CVx8uiAR0C3jFt_3aZ3uDAQ1PCneh8n5Pnb2kiiO5z50E5fXhUqhG3biFcu00zyarNz5jg$)

“Novel Insights on Genome Architecture Evolution”

Organizers: Carol Eunmi LEE, University of Wisconsin-Madison, USA Sean Chun-Chang CHEN, Taipei Medical University, TAIWAN

Invited Speaker: Chris Jiggins, University of Cambridge, UK

The rapid expansion of genomic data is revolutionizing our ability to make unprecedented discoveries regarding patterns, mechanisms, and consequences of genome architecture evolution. With comprehensive genome sequencing across diverse taxa, we can now address fundamental questions on how large-scale structural variation in genomes arise and how they might impact adaptive potential and speciation. For instance, we are only beginning to uncover how chromosomal rearrangements, such as fusions, fissions, and inversions, contribute to adaptation and speciation. In addition, we are gaining new insights into how allopolyploid hybridization in plants results in novel genome architectures and potentially leads to highly invasive species. Moreover, we can now explore how genome architecture evolution leads to morphological and functional innovations, such as the evolution of animal body plans. Thus, this symposium will assemble researchers who investigate the dynamics of genome architecture evolution in multicellular organisms. We especially welcome talks that focus on large scale genomic comparisons that delve into mechanisms

underlying genome structural variation and evolution and impacts of that variation on responses to selection or the evolution of novelty. Conceptual and theoretical talks that provide novel perspectives are also welcome. As such, this symposium aims to highlight the importance of genome architecture in shaping evolutionary trajectories and adaptive potential.

Dates:

Abstract submission deadline: February 15, 2025

Early bird registration deadline: April 20, 2025

Abstract submission details: https://urldefense.com/v3/_https://smbe2025.scimeeting.cn/en/web/index/-25070_2367426_...!!Mak6IKo!MdiJ9HX13kwd5zLE4INfQKkgzbecbMZ1dr
Carol Eunmi LEE <carollee@wisc.edu>

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SMBE Beijing GenomeArchitectureEvolution Jul202-24

Dear Colleagues,

We are inviting abstract submissions for our symposium, “Novel Insights on Genome Architecture Evolution” (Symposium #8)

2025 Conference for the Society for Molecular Biology & Evolution, July 20-24 in Beijing China.

The deadline for abstract submissions is January 30, 2025

Details are below:

SMBE 2025 Annual Meeting of the Society for Molecular Biology & Evolution https://smbe2025.scimeeting.cn/en/web/index/25070_2131033 Novel Insights on Genome Architecture Evolution

Organizers: Carol Eunmi LEE, University of Wisconsin-Madison, USA Sean Chun-Chang CHEN, Taipei Medical University, TAIWAN

Invited Speaker: Chris Jiggins, University of Cambridge, UK

The rapid expansion of genomic data is revolutionizing our ability to make unprecedented discoveries regarding patterns, mechanisms, and consequences of genome architecture evolution. With comprehensive genome sequencing across diverse taxa, we can now address funda-

mental questions on how large-scale structural variation in genomes arise and how they might impact adaptive potential and speciation. For instance, we are only beginning to uncover how chromosomal rearrangements, such as fusions, fissions, and inversions, contribute to adaptation and speciation. In addition, we are gaining new insights into how allopolyploid hybridization in plants results in novel genome architectures and potentially leads to highly invasive species. Moreover, we can now explore how genome architecture evolution leads to morphological and functional innovations, such as the evolution of animal body plans. Thus, this symposium will assemble researchers who investigate the dynamics of genome architecture evolution in multicellular organisms. We especially welcome talks that focus on large scale genomic comparisons that delve into mechanisms underlying genome structural variation and evolution and impacts of that variation on responses to selection or the evolution of novelty. Conceptual and theoretical talks that provide novel perspectives are also welcome. As such, this symposium aims to highlight the importance of genome architecture in shaping evolutionary trajectories and adaptive potential.

Dates:

Abstract submission deadline: Jan 30, 2025

Early bird registration deadline: Apr 20, 2025

Abstract submission details: https://urldefense.com/v3/_https://smbe2025.scimeeting.cn/en/web/index/-25070_2367426_!!Mak6IKo!MdiJ9HX13kwd5zLE4INfQKkgzbeALDnVPOtadcrSve2nMqz1dAw232N234

Carol Eunmi LEE <carollee@wisc.edu>

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2025) is the end of this week (February 2). This is the premier speciation-focused conference, which happens approximately every two years. There are still spots available for new attendees. Some submitted poster abstracts will be selected to give talks as well.

Please consider attending, or bring this to the attention of colleagues studying speciation or adjacent topics. The meeting welcomes graduate students, postdocs, researchers, and faculty. You can register here: <https://www.grc.org/speciation-conference/2025/> Registration for, and information about, the student- and postdoc-only Speciation Gordon Research Seminar (March 1-2 2025) can be found here: <https://www.grc.org/speciation-grs-conference/2025/> February 1 is the deadline to apply for the GRS.

We hope to see many of you there!

Dr. Daniel I. Bolnick Professor, Ecology and Evolutionary Biology & Institute for Systems Genomics President, The American Society of Naturalists
daniel.bolnick@uconn.edu

MAIL TO: Department of Ecology and Evolutionary Biology Affiliate Professor, Molecular & Cellular Biology; Institute for Systems Genomics 75 N. Eagleville Road, Unit 3043 University of Connecticut Storrs, CT 06269-3043, USA

Office Phone: 860-486-3156 Lab Phone: 860-486-3937
Cell Phone: 512-809-6217

Office: PBB 305C Lab: PBB 317&319, ATW 232, 234, 236

“Bolnick, Daniel” <daniel.bolnick@uconn.edu>

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Ventura California Speciation CallForRegistration

The deadline to apply to attend the Speciation Gordon Research Conference (Ventura California March 2-7,

AuburnU InsectDiversityInvasionBiol	14	TelAvivU EvolutionaryGenetics	21
CaliforniaStateU MontereyBay ComparativeGenomics	14	TrentU DeerEpigenetics	21
Hannover PlacozoaGenomics	15	Trondheim Norway ModelingGenomicData	22
MasseyU NewZealand EvolutionaryToxicology	16	UBristol UK SocialEvolution	22
NTNU Norway EvolutionaryEcol	16	UGroningen ErasmusMundus EvolBiol	23
QueensU Belfast EvolutionOfParentalCare	17	UPadua Italy EvolutionaryBiology	24
Reneco AbuDhabi AvianConservation	17	UppsalaU FungalGenomics	24
SGN Frankfurt Paleobiology	18	USouthBohemia EvolutionaryEcol	25
SRUC Edinburgh PlantEvolution	19	USunshineCoast Australia KoalasChlamydia	27
Stockholm Two IslandEvolutionaryGenomics	20	UVienna Austria DemographicResponseAlpineBiota	27

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AuburnU InsectDiversityInvasionBiol

The Hardy Lab at Auburn University (<http://hardylab.skullisland.info>) is recruiting graduate students (MS or PhD) interested in exploring the diversity of herbivorous insects, and using comparative analyses to better understand invasion biology. The work addresses general questions about the evolution of where species occur, and aims to promote more sustainable agriculture and the conservation of natural resources. It will also shed light on the history of the species diversification in aphids.

Some prior experience with entomology and data science would help, but is not required. The most important things are being curious about the research themes, and being eager to learn how to do comparative biodiversity science.

The Hardy Lab values diversity and social equity. Members of groups that have been historically excluded from scientific research are especially urged to apply.

Anticipated state date of August of 2025.

The position will stay open until it is filled. I will start reviewing materials on February 7.

The position comes with a renewable 12-month stipend, starting at \$30K, a tuition remission, and benefits.

To Apply: Start by sending your CV and a short (< 1 page) description of your research interests to Nate B Hardy (n8@auburn.edu). If it looks like you could be a good fit, I'll reach out to further discuss the position, and pass along more details about applying to the AU Graduate School.

nbh0006@auburn.edu

CaliforniaStateU MontereyBay ComparativeGenomics

California State University, Monterey Bay / Moss Landing Marine Lab

Position: Funded position for M.S. Student - Bacterial Bioremediation of Pesticides or Marine Comparative Genomics

Application Deadline: February 1, 2025

Are you passionate about environmental science, microbiology, molecular methods, evolutionary biology, vertebrate comparative genomics, or bioinformatics? The Jue Lab < <https://csumb.edu/juelab/> > research team at California State University, Monterey Bay (CSUMB) is seeking an enthusiastic, highly-motivated individual to fill a funded Master's Graduate Student Research Assistant position who would contribute either to projects focused on the bioremediation of pesticides using bacteria and ongoing work on the implementation and development of pesticide-remediating bioreactors for local agricultural lands or projects related to vertebrate comparative genomics with a particular interest in evolution of marine fishes. Depending on the applicant's interests, the successful candidate would apply to and join the Environmental Science Masters of Science program < <https://csumb.edu/environmentalscience/> > at CSUMB or the Marine Science Masters of Science program < <https://mlml.sjsu.edu/gradprog/about/> > at Moss Landing Marine Laboratory (MLML) under the supervision of Dr. Nathaniel Jue. The student would begin graduate studies and work on research projects in the Fall of 2025.

About Us: The Jue lab is committed to addressing environmental challenges and key questions in ecology and evolution through innovative research using a combination of field, lab and computational approaches that implement genomic and bioinformatic tool sets. Our current projects aim to develop sustainable solutions for the remediation of pesticide-contaminated soil and water using low-cost, high-impact natural processes and to develop new projects in comparative genomics, with a particular interest in the evolution of reproductive styles in fishes. We're looking for a dedicated Master's student to join us on these exciting projects.

Position Description: As a Master's Student Graduate Research Assistant, you will have responsibilities in the following areas:

- Facilitating and providing administrative support to NIH NHGRI Undergraduate Training program in Genomics that is part of collaboration between CSUMB and University of California Santa Cruz's Genomics Institute.
- Research and Experimentation: Collaborate with our team to design and conduct field and lab experiments related to pesticide bioremediation using bacteria or comparative genomics.
- Data Collection and Analysis: Gather and analyze data, contributing to the development of research projects.
- Literature Review: Stay up-to-date with the latest research related to our projects, your thesis topic, and related fields.
- Lab Assistance: Assist in maintaining the lab, preparing reagents, mentoring undergraduate researchers, and ensuring a safe research environment.
- Communication: Collaborate with fellow researchers, present findings within the lab, and potentially at conferences.
- Publication: Contribute to research papers and publications in peer-reviewed journals.
- Full-time graduate assistant duties on summer training program and lab research projects and half-time research assistant duties during the school year.

Required Qualifications:

- Bachelor's degree in a relevant field (e.g., biology, marine science, environmental science, microbiology).
- A strong interest in environmental microbiology and bioremediation or genomics and bioinformatics.
- Excellent analytical and research skills.
- Strong written and verbal communication abilities.
- Enthusiasm, dedication, and the ability to work both independently and as part of a team.

Preferred Qualifications:

- Experience with genetic/genomic, metabolomic, and/or water quality data
- Molecular biology and microbiology lab experience
- Programming skills in R, Python, or UNIX/LINUX command line
- Experience and in-

- Interest in field experimentation
- Valid driver's license
- Ability to lift 50 lbs easily
- Experience in mentoring undergraduates from diverse backgrounds

What We Offer:

- An exciting research opportunity at the intersection of environmental science and applied microbiology.
- Hands-on experience with cutting-edge molecular laboratory techniques and bioinformatic methods.
- Opportunities for co-authorship on research papers and present work at local, regional and national meetings/conferences.
- A supportive and collaborative research environment.
- Two years of annual stipend (~\$24,000), tuition waiver (~\$7,800),

— / —

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

Hannover PlacozoaGenomics

PhD position available immediately (three years) in the Schierwater lab for a motivated young investigator to undertake molecular genetic analyses in or more of the following areas: Polarity/cancer research on the placozoon *Trichoplax*, evolutionary systematics of Placozoa, conservation genetics of dragonflies and/or environmental genomics of marine ecosystems. Interest in fundamental questions of evolutionary adaptation and speciation is essential. Experience with functional genomics and/or transcriptome analysis and/or eDNA and bioinformatics is desirable. The successful candidate will have ample opportunity to pursue additional projects and define his own project within the broad molecular ecology/evolutionary genetics scope of the lab. We provide excellent working conditions.

The student will receive a monthly stipend of 1200 Euros and be paid extra for teaching assistance.

Please email CV, brief statement of research interests and experience and the name of at least one reference to Bernd Schierwater (bernd.schierwater@ecolevol.de).

Bernd Schierwater

Professor & Director Institute of Ecology & Evolution
TiHo Hannover, Foundation Buenteweg 17d D-30559
Hannover Germany

Bernd Schierwater <bernd.schierwater@ecolevol.de>

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MasseyU NewZealand EvolutionaryToxicology

MasseyU_NewZealand. Evolutionary_toxicology

A PhD project investigating the evolution of resistance in a mammal to plant chemical defences.

Plants and herbivorous animals have a coevolutionary relationship that drives selection to protect leaves in plants and selection to circumvent plant defences in animals. Our system involves the brushtail possum (*Trichosurus vulpecula*) that is native to Australia and invasive in New Zealand. Some populations of brushtails in Australia have naturally evolved resistance to fluoroacetate poison produced in plants they eat. A synthetic version of the same poison is widely applied in New Zealand to kill toxin-naïve possums.

Our recent work with transcriptomes has identified a set of genes implicated in fluoroacetate resistance. For some background information see: <https://link.springer.com/article/10.1007/s00360-024-01591-z> and <https://onlinelibrary.wiley.com/doi/full/10.1002/ece3.9633> You will investigate variation at these genetic loci and assess their relative expression levels in possums exposed to fluoroacetate. You will generate DNA and RNA data and use quantitative PCR with a view to establishing the genes most influential in toxin resistance and their mode of action. A goal will be to develop PCR markers that enable rapid screening of significant loci in possums and other mammal species exposed to fluoroacetate. from sympatric insect taxa to compare ice+ activity of hosts and their microbiomes.

Start date: 2025 Location: The successful applicant will be based on the Manawatū campus of Massey University, Palmerston North, NEW ZEALAND. Massey University is a smoke-free work environment.

Lead researcher in New Zealand is Steve Trewick of the Te Taha Tawhiti research group: <https://evolves.massey.ac.nz> is within the Wildlife & Ecology Group. This will be part of a collaborative programme supported by funding from the Australian Research Council.

Admission criteria & candidate requirements: You will need a good first degree from an internation-

ally recognised university; minimum upper second class Hons or a Master's degree in an appropriate subject. You should have a background in Evolution/Biochemistry/Genomics, good statistics skills (preferably experience with R) and a strong interest in evolutionary ecology.

How to Apply: In the first instance we encourage you to contact us by email to discuss your interest with Steve: s.trewick@massey.ac.nz

Steve Trewick <S.Trewick@massey.ac.nz>

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NTNU Norway EvolutionaryEcol

Fully funded PhD position in Evolutionary Ecology available at Norwegian University of Science and Technology (NTNU), Trondheim, Norway. Deadline for applications: January 27th 2025

<https://www.jobbnorge.no/en/available-jobs/job/-271754/phd-candidate-in-evolutionary-ecology> The PhD position is associated with a major research project funded by the European Research Council and NTNU, with an overall aim of providing new understanding of spatial and seasonal population and evolutionary dynamics in nature.

Specifically, the primary focus of the PhD will be to quantify links between different types of animal movements, including dispersal (and resulting immigration to new populations) and reversible seasonal migration. Understanding how these different types of movement co-occur and interact will provide new capability to predict how spatial population dynamics will respond to dramatic changes in seasonal climates and environments.

The empirical objectives will be achieved by applying advanced statistical models to multi-year field data collected in a partially-migratory meta-population of European shags in Scotland. There will also be opportunities to contribute to fieldwork, quantitative genetic analyses and/or theoretical modelling, depending on the interests of the successful applicant. Full training in quantitative, analytical and modelling skills will be provided.

The PhD position provides an exciting opportunity to gain broad experience and expertise working at the interface of evolutionary ecology, population ecology, and movement ecology. It will provide broad training in

research skills, and will suit a candidate who is motivated to undertake high-level research in evolutionary ecology. The goal is a completed doctoral education to obtain a doctoral degree. The four-year position includes research time, course components, and one year of embedded teaching and other professional duties.

The position will be hosted within a dynamic international research group based at NTNU, with strong collaborative links to University of Aberdeen and UK Centre for Ecology & Hydrology in Scotland, UK. There will be opportunities for international mobility among the collaborating groups, and for conference and workshop participation.

Informal enquiries are welcome to Professor Jane Reid (jane.m.reid@ntnu.no)

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

“Reid, Dr Jane M.” <jane.reid@abdn.ac.uk>

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QueensU Belfast EvolutionOfParentalCare

Fully funded 3 years PhD studentship for UK and international students

Social and ecological drivers of parental care Institution: Queen’s University Belfast, School of Biological Sciences Supervisors: Dr Isabella Capellini (QUB); Dr Domhnall Jennings (QUB); Dr Catherine Sheard (University of Aberdeen)

There are astonishing differences in whether, how, and for how long, animals care for their offspring. Despite the considerable research on parental care, our understanding of how and why care diversity originates in species lacking care and of what promotes its persistence over evolutionary time is very limited.

Aim. By combining state of the art phylogenetic comparative approaches and large scale datasets of parental care forms across hundreds of species in highly diverse taxonomic groups, this project will test hypotheses on whether species’ reproductive ecology, social behaviour and offspring characteristics, promote the evolutionary origin and/or maintenance of male and female parental

care behaviours in vertebrates (amphibians, mammals, fish, dinosaurs, birds) and/or invertebrates (e.g. crustaceans).

The student will have the opportunity to shape the project to better fit their own research interests by selecting which questions to address and in which taxonomic group. The project benefits by access to already assembled datasets of parental care diversity in thousands of amphibians, mammals and fish (e.g. Furness and Capellini 2019, 2022; Vanadzina et al. 2021; West and Capellini 2016).

Deadline: 7th of February 2025

Full project description and link to application here.

Isabella Capellini <isab972@yahoo.co.uk>

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

Reneco Abu Dhabi Avian Conservation

Background Studying animal movements is of paramount importance for understanding the complex interactions between wildlife and their environment. Movement ecology studies provide invaluable insights into species’ and individuals’ behavioural patterns, resource utilisation, and adaptive strategies, which are essential for effective conservation and management efforts.

The study of post-release movement patterns in captive-bred animals released into the wild is especially important for the success of conservation and reintroduction programmes. Because the transition from captivity to the wild is fraught with challenges, understanding how released individuals navigate and use space within their new environment is crucial for elucidating factors affecting individual survival and long-term population viability. By examining the movement ecology of released animals, and comparing it to their wild-born counterparts, it is therefore possible to gain insights into the ability of captive-bred individuals to locate resources, avoid predators, and establish territories key behaviours that may be compromised by a captive upbringing. This knowledge may eventually allow to refine rearing and release strategies, optimise selection of sites for release, and identify potential impediments to successful translocations.

Aims This project will evaluate within- and among-individual variation in movements and space-use of North African Houbara Bustards (*Chlamydotis undulata undulata*) in Eastern Morocco, including captive-bred and wild-born individuals. More specifically, it will address the following questions:

* To what extent do individuals differ in their movement parameters (i.e. individual repeatabilities) * How do movement parameters covary among individuals (movement syndromes) * What is the relationship between individual movement syndromes and individual parameters such as sex, age, origin (captive-bred, wild-born), vs. local ecological conditions?

Data & Methods The student will analyse a large multi-year GPS dataset, consisting of relocations collected at 5-min intervals (24h), from more than 600 captive-bred and 50 wild-born houbaras released in Eastern Morocco. A range of movement parameters will then be extracted from GPS data, and analysed using linear mixed models (GLMMs), allowing estimation of fixed effects (individual parameters: e.g. age, sex, origin; extrinsic predictors: e.g. habitat type) and partitioning of movement variance (e.g. individual repeatability). Multivariate mixed models will further allow modelling the co-variation between different movement parameters.

Working environment The Master will be part of a long-term research project, established and developed by Reneco International Wildlife Consultants LLC and the International Fund for Houbara Conservation.

The successful candidate will be based at his/her chosen university and will be expected to spend time at Reneco HQ in Abu Dhabi, UAE, to conduct analyses under the supervision of Reneco PI, Dr. Enrico Sorato. Additionally, the project will include a visit to the field research site in Eastern Morocco to gain hands-on experience with the study system.

For enquires and applications, please contact Enrico Sorato: esorato@reneco.org

Dr Enrico SORATO Senior Researcher in Animal Behaviour and Ecology RENECO INTERNATIONAL WILDLIFE CONSULTANTS LLC 3902, Sky Tower Al Reem Island, Abu Dhabi, UAE P.O. Box 61741 Mobile UAE: +971 (0) 502586746 Email: esorato@reneco.org

SORATO Enrico <esorato@reneco.org>

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SGN Frankfurt Paleobiology

Doctoral student (m/f/d) in paleobiology and geoinformatics (75%)

The Senckenberg Gesellschaft für Naturforschung (SGN) was founded in 1817 and is one of the most important research institutions in the field of biodiversity. At its 13 locations throughout Germany, scientists from almost 40 nations conduct cutting-edge research on an international scale. The Society's headquarter is in the Main metropolis of Frankfurt in the heart of Germany. This is also where one of the best-known Senckenberg facilities, the Senckenberg Natural History Museum, is located. The Senckenberg Society for Nature Research (SGN) at the location in Frankfurt am Main is seeking to fill the following position as soon as possible

Doctoral student (m/f/d) in paleobiology and geoinformatics (75%)(Part time) As part of the recently established Emmy Noether Research Group "Spatial signal and bias in the fossil record of seed plants in the late Mesozoic", we are hiring a doctoral student (m/f/d) in paleobiology and geoinformatics for a 3-year fixed term contract. The project aims to identify the geological and biological causes of the patterns observed in Jurassic and Cretaceous floras by combining spatially explicit data from the rock record with trait-based data from the plant fossil record, in order to fully disentangle the different causes of the apparent quasi-synchronous radiation of seed plants. This position will focus on understanding the distribution of the rock record and the sampling effort of fossil plant sites across the globe during the Jurassic and Cretaceous. Your tasks:

Build a database of rock formations across the Jurassic and Cretaceous based on available information from geological maps and other literature. Obtain data from the Paleobiology Database and similar paleobiological databases on the sampling of the plant fossil record during the Jurassic and Cretaceous. Analyze the variation of rock availability through time using state-of-the-art statistical methods. Identify the causes of sampling variation in the plant fossil record across time and space, and predict areas of high potential for future sampling. Disseminate results in scientific journals and international conferences. Your profile: Essential

-Diploma or Masters degree in Geology, Paleontology, Paleobiology or a related discipline.-Good knowledge of the statistical programming language R.-Strong in-

terest in large-scale data analysis applied to geology and macroevolution.-Good communication skills, in order to work in a highly collaborative and international environment.-Very good command of written and spoken English. Desirable

-Good knowledge of GIS software.-Experience with geo database or other forms of spatially explicit data.-Experience with the Paleobiology Database.-Knowledge of stratigraphy and the plant fossil record. We offer

- An attractive and challenging job in a motivated, dynamic team in a research institution of worldwide standing. - The possibility to conduct a PhD thesis. - Flexible working hours - possibility of mobile working - support with childcare or caring for family members (certified by the "audit berufundfamilie") - service ID card with free entry to all municipal museums - annual bonus - company pension plan

Location: Frankfurt Scope of employment: Part Time, 75% Type of contract: 3 year fixed term contract Salary: According to the German collective agreement of the State of Hesse (pay grade E 13, TV-H)

Senckenberg is committed to diversity. We benefit from the different expertise, perspectives and personalities of our staff and welcome every application from qualified candidates, irrespective of age, gender, ethnic or cultural origin, religion and ideology, sexual orientation and identity or disability. Women are particularly encouraged to apply, as they are underrepresented in the field of this position; in the case of equal qualifications and suitability they will be given preference. Applicants with disabilities ("Schwerbehinderung") will be given preferential consideration in case of equal suitability. Senckenberg actively supports the compatibility of work and family and places great emphasis on an equal and inclusive work culture.

How to apply: Please send us your complete and meaningful application documents (letter of motivation, CV, training and employment references) as single pdf-file quoting Ref. #01-25002 by 16th of February 2025 to recruiting@senckenberg.de or apply directly on our homepage using the online application form.

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt a.M. E-Mail: Recruiting@Senckenberg.de For more information, please contact Prof. Dr. Dieter Uhl via email: Dieter.Uhl@Senckenberg.de Further information about the Senckenberg Gesellschaft für Naturforschung can be found at www.senckenberg.de. Mario Coiro <mar.coiro@gmail.com>

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SRUC Edinburgh PlantEvolution

PhD position available at the Department of Plant and Soil Sciences, SRUC, Edinburgh, UK

What are the consequences of sexual dimorphism for habitat choice? Lessons from an actinorhizal dioecious plant (*Hippophae rhamnoides* L.)

Supervisors: Roberta Bergero, Luis Novo, Stephanie Jones

About the project: The aim of the project is to examine the consequence of habitat choice on the evolution of sexual dimorphism. This is an area of research very poorly investigated that can generate fundamental knowledge on the evolution of dioecy and solve long-standing enigma on sexual antagonism and the evolution of sex chromosomes. You will use the model species *Hippophae rhamnoides* L., a dioecious shrub commonly found along the Scottish coast. Studies on the ecological distribution of male and female plants from this species show sexual dimorphism. You will test whether sexual dimorphism for habitat choice could have triggered (or being the consequence of) sexual differences on other aspects of the plant biology, including metal uptake physiology, plant nutrition and differential recruitment of nitrogen-fixing bacteria.

Objectives:

Generate sex-linked markers from pools of male and female genomic DNAs from native and introduced Scottish populations. Carry out greenhouse growth assays in metal-contaminated and non-contaminated soils on juveniles sexed with developed molecular markers Test for sexual differences in above-ground and below-ground bioaccumulation of heavy metals, Test whether the recruitment of soil nitrogen-fixing bacteria differ between male and female plants

Interdisciplinary Training and Techniques: You will work within a cross-disciplinary team with expertise spanning plant genetics, plant phytoremediation and soil sciences. This PhD position provides an exciting opportunity to gain broad expertise working at the

interface of evolutionary ecology, plant symbiosis and phytoremediation.

How to apply:

<https://www.findaphd.com/phds/?Keywords=3Dbergero> For questions contact Dr Roberta Bergero, email: roberta.bergero@sruc.ac.uk

Please don't print this e-mail unless you really need to. This e-mail message is confidential to the intended recipient at the email address to which it has been addressed. If the message has been received by you in error, it may not be disclosed to or used by anyone other than the intended addressee, nor may it be copied in any way. If it is not intended for you please inform us, immediately, then delete it from your system. If the content is not about the business of the organisation then the message is not from us nor is it sanctioned by us. Anything in this e-mail or its attachments which does not relate to SRUC's or SRUC Innovation Limited's official business is neither given nor endorsed by SRUC or SRUC Innovation Limited.

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Roberta.Bergero@sruc.ac.uk

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Stockholm Two Island Evolutionary Genomics

There are two PhD positions advertised in this e-mail. One on Cabo Verde Brassicaceae (above) and one on Indo-Pacific birds (below).

PhD student in evolution of Diplotaxis in Cabo Verde

*<https://recruit.visma.com/spa/public/-apply?guidAssignment=ea9a5a9a-dd7a-4722-89eb-faa90b8c94a7&description=True> * <what>* On remote oceanic islands, colonizing lineages often undergo founder effects. Moreover, each time a species

disperses to a new island, an additional bottleneck is introduced. Despite these constraints, islands are hotspots for diversification, including remarkable examples of adaptive radiations. This presents a paradox: how can lineages depleted of genetic variation evolve such extensive phenotypic and ecological diversity, ultimately forming adaptive radiations?

In this project, we aim to sequence the Diplotaxis radiation in Cabo Verde (Brassicaceae). Our objective is to explore the biogeographical distribution of the species, examine patterns of genetic diversity across their range, and link phylogenetic and ecological traits to underlying genetic diversity, and explore the role of structural variants in evolution.

* <how>* This project study will integrate a variety of molecular and bioinformatic approaches, benefiting from a large herbarium collection. We will utilize: 1) population genomic tools 2) conduct simulations of genomic data using software like SLiM and msprime; 3) examine the role of structural variants in adaptation 4) Use genome assembly and comparative genomics to obtain and compare genomes

* <benefits>* Possibilities to attend a conference each year Strong supervisory support and mentoring to pursue an academic career; Attractive welfare benefits Career development programmes Stockholm's family-friendly surroundings with their rich opportunities for culture and outdoor activities Possibility to visit collaborators in Czechia, Norway and other places.

PhD student in Evolution of Indo-Pacific birds

*<https://recruit.visma.com/spa/public/-apply?guidAssignment=96837826-746d-4e8c-844d-22f2d2ef7bf4&description=True> <what> On remote oceanic islands, colonizing lineages often undergo founder effects. Moreover, each time a species disperses to a new island, an additional bottleneck is introduced. Despite these constraints, islands are hotspots for diversification, including remarkable examples of adaptive radiations. In this project, we aim to focus on different lineages of birds in the Indo-Pacific to understand the impact of sexual selection and hybridization in genetic variation of different lineages.

<how> This project study will integrate a variety of molecular and bioinformatic approaches. We will use mostly population genomic tools and simulations of genomic data (SLiM and msprime);

<benefits> Possibilities to attend a conference each year; Strong supervisory support and mentoring to pursue an academic career; Attractive welfare benefits; Career development programmes; Stockholm's family-friendly surroundings with their rich opportunities for culture

and outdoor activities Possibility to visit collaborators in Germany and other places.

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islandevolution.github.io [group website]

jcerca.github.io [personal website]

Google Scholar < <https://scholar.google.pt/-citations?user=Z11vWPEAAAAJ&hl=en> >

Evolutionary Biologist

Swedish Museum of Natural History

(20% @ the University of Oslo)

Recently published (May 2024) :: Why Do Some Lineages Radiate While Others Do Not? Perspectives for Future Research on Adaptive Radiations < <https://pubmed.ncbi.nlm.nih.gov/38692838/> >

Recently published (May 2024) :: Consistent accumulation of transposable elements in species of the Hawaiian Tetragnatha spiny-leg adaptive radiation across the archipelago chronosequence <

<https://academic.oup.com/evolinnean/article/3/1/kzae005/7681133?loginelse> >

Tel Aviv U Evolutionary Genetics

How do Stress-related Genes Evolve to Cope with Extreme Climate?

PhD in Evolutionary Genetics

A PhD position is available in the research group of Prof. Frida Ben-Ami, from Tel Aviv University, Israel (www.ben-ami.com).

Joint project of Frida's lab and Prof. Yampolsky's lab in East Tennessee State University. The project investigates the evolution of stress-related genes and their expression. In particular, we will focus on the expression of paralogous trehalose synthesis genes and their local adaptation in a model crustacean, *Daphnia magna*.

The successful candidate will combine experimental work with *Daphnia*, molecular biology methods, and bioinformatics to compare expression of the target genes in *D. magna* genotypes exposed to diverse environmental stressors.

Requirements:

- MSc degree in Biology or equivalent

- Interest in Evolutionary Biology

- Skills in Python and/or R - an advantage

- Background in Experimental Biology or Aquatic Ecology - an advantage

- Excellent communication and writing skills in English

- Good work ethics

Please send your application by email (all material in one PDF) to Frida Ben-Ami (frida@tauex.tau.ac.il). Applications should include a CV, a list of publications and a statement about your research interests (motivation letter). Please provide names and email addresses of two persons who are willing to write a letter of recommendation. Application deadline is February 28, 2025.

Prof. Frida Ben-Ami | Tel Aviv University, Life Sciences | www.ben-ami.com Frida Ben-Ami <frida@tauex.tau.ac.il>

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Trent U Deer Epigenetics

Graduate Student Position - Mule Deer Epigenetics

We are recruiting a fully-funded MSc or PhD student to study the epigenomics of mule deer in Wyoming. The student will take advantage of hundreds of mule deer samples to build epigenetic clocks and study variation in mule deer aging. Depending on interest and expertise, project flexibility exists where the student can explore variation in age estimates from longitudinal sampling or how stressors impact rates of aging. Students will have the flexibility to adapt the project to their interests and the opportunity to collaborate and work with our partners in Wyoming.

Location: The student will join the lab group of Aaron Shafer at Trent University in Peterborough, ON, and will be enrolled in the Environmental and Life Sciences Graduate Program (ENLS). The student will have access to networking and training opportunities through the project leads with the Wyoming Fish and Game Department, with the potential to undertake research that aims to have a broader impact.

Qualifications and Eligibility: The successful candidate must have a BSc or MSc (for the PhD position) in Biology, Bioinformatics, or a related discipline. The ideal candidate will have an interest in mammal biol-

ogy/epigenetics/bioinformatics, experience conducting independent research, have strong written and oral communication skills, and experience using R to analyse data. Prior experience using high performance computing would be considered an asset but is not required. The candidate must meet the requirements for admission to graduate studies at Trent University.

Salary: Students will receive a stipend, which may include teaching assistantships. The stipend can be increased if the candidate is successful at securing external scholarships.

To Apply: Please send the following to Prof. Aaron Shafer (aaronshafer [at] trentu.ca): A statement outlining research interests, career goals, and how your previous experience and training relates to this project and has prepared you for a PhD or MSc. 1. Your c.v. 2. Unofficial transcripts from your undergraduate and MSc (for the PhD position) 3. Contact information for two references

Deadline: 15 Feb 2024 or until position filled

Aaron Shafer <aaronshafer@trentu.ca>

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Trondheim Norway Modeling Genomic Data

PhD position in statistical modeling for genomic data

The Norwegian University of Science and Technology, Trondheim, Norway Application deadline: March 4th—2025

The position is part of the research project “Prediction of genetic values and adaptive potential in the wild” funded through a Consolidator Grant by the European Research Council (ERC). A major goal of the project is to develop cutting-edge statistical methodology to analyze large-scale genomic data, which is currently generated for many wild animal populations. To this end, the project combines modern statistical methodology and builds on the current state-of-the art in animal breeding, human genomics, ecology and evolutionary biology. The student will thus work with a cross-disciplinary team of researchers and can contribute towards the development of methods that will make an impact to better understand evolution and the robustness of wild animal populations, with the ultimate goal to help preserving

biodiversity.

The PhD candidate will work at NTNU in Trondheim, and the fellowship will be hosted by the Department of Mathematical Sciences (<https://www.ntnu.edu/imf>). The successful applicant will be offered a three-year position, with the possibility for extension up to 12 months if teaching duties are attained. The project is a close collaboration with evolutionary ecologists from the Department of Biology (<https://www.ntnu.edu/biology>) and the Gjørevoll Centre (<https://www.ntnu.edu/gjaerevoll>) at NTNU, as well as with international researchers in the field.

The project leader and your main supervisor will be Associate Professor Stefanie Muff.

Read more about the position and how to apply here: <https://www.jobbnorge.no/en/available-jobs/-job/272247/phd-candidate-in-statistical-modeling-for-genomic-data> Dr. Henrik Jensen Professor, Deputy of Research Department of Biology and the Gjørevoll Centre NTNU NO-7491 Trondheim NORWAY — Web: <https://www.ntnu.edu/employees/henrik.jensen> —

Henrik Jensen <henrik.jensen@ntnu.no>

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UBristol UK Social Evolution

PhD IN SOCIAL EVOLUTION AT THE UNIVERSITY OF BRISTOL (UK)

Keen to do a PhD in animal social evolution? Intrigued by the evolution of cooperation and conflict? Unfazed by challenging fieldwork? You have until Monday 13th January to apply for our PhD exploring the behavioural ecology of the social wasps of Africa, including a 3-month internship in wildlife filmmaking at the BBC Natural History Unit.

For how to apply, see: www.tinyurl.com/-AfricanWaspsPhD For information about the Social Strategy Lab at the University of Bristol, see www.patrickckennedy.com About the Project:

In this PhD, you will explore what makes the powerful powerful. Why do some animals dominate others, and how do they stay in power? You will turn to one of the most fascinating social organisms on the planet: the beautiful and long-neglected wasps of Africa (*Belonogaster*). To reveal the drama of social life in the wild,

you will use field-cameras to track dominance displays, submission, social networks, and struggles for control of social groups. You will be supported to devise creative behavioural experiments with wild wasps (e.g., manipulating food resources to test key hypotheses about where power comes from) and novel evolutionary game theory to illuminate the strategies individuals pursue. Finally, you will zoom out to survey the vast diversity of power struggles across vertebrates and invertebrates, with the potential to develop cutting-edge meta-analyses. During your PhD, you will conduct an internship with wildlife-filmmakers at the BBC Natural History Unit in Bristol, learning how insect behaviour is filmed and how science is translated into documentaries. This PhD will provide you with highly diverse set of skills, including designing and running ambitious field-experiments, macro-videography for studying behaviour, mathematical and computational modelling, and the ability to innovate in evolutionary biology and ecology.

Location:

You will be part of the lab group of Dr Patrick Kennedy at the University of Bristol, and will be part of the NERC GW4+ Doctoral Training Partnership. You will also benefit from working with co-supervisors focused on different dimensions of this project: social evolution experiments (Prof Andy Radford, Bristol), game theory modelling (Dr Andy Higginson, Exeter), and filmmaking (Paul Williams, BBC Natural History Unit). You will be based in the state-of-the-art Life Sciences Building at the University of Bristol.

Qualifications and Eligibility:

The successful candidate must have a high grade in a BSc or MSc in biology (or a related discipline), and will be able to demonstrate (1) an excellent academic track-record, (2) a clear and demonstrable passion for the study of animal behaviour and evolutionary biology, and (3) enthusiasm and practical capacity for conducting intensive fieldwork.

Internship at the BBC:

The BBC Natural History Unit are the CASE partner. You will complete an internship placement at the BBC Natural History Unit, planned to take place during production of the major upcoming BBC series on insects, 'Hidden Planet', which will provide the student with an understanding of wildlife filmmaking (with a direct focus on insect behaviour) and how academic research is translated into natural history documentaries. Whilst working at the BBC, in-kind contributions include support with desk space at BBC offices in Bridgewater House, Bristol, as well as access to the BBC's dedicated studio filming space. The team can provide informal,

and potentially some formal, BBC training during the placement.

How to apply to the University of Bristol:

For details on how to apply (including links to the application website), see: www.tinyurl.com/-AfricanWaspsPhD This PhD is part of the competition-funded NERC GW4+ Doctoral Landscape Award. This means that the application process has two stages:

1. First, the supervisors will identify the top applicant to this project.
2. The top applicant will then be nominated to interview for PhD funding in a competitive process alongside other projects.

Funding Notes:

Studentships pay full fees and a stipend at the UKRI rate for three and half years, beginning in September 2025. Information for international students: There are a limited number of full studentships for international students. International applicants need to be aware that you will have to cover the cost of your student visa, healthcare surcharge & other costs of moving to the UK to undertake a PhD.

Dr Patrick Kennedy Lecturer in Biological Sciences | Social Strategy Lab < <http://www.patrickckennedy.com/> >, University of Bristol

Office 2B18, School of Biological Sciences, Life Sciences Building University of Bristol, 24 Tyndall Avenue, BS8 1TQ, UK

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UGroningen ErasmusMundus EvolBiol

Dear all,

We are pleased to announce that the application portal for the Erasmus Mundus Master Programme in Evolutionary Biology (MEME, <https://www.evobio.eu/>) is now open until the 2nd of March 2025 (<https://www.evobio.eu/application>). The program will be run - as before - between the University of Groningen (Netherlands), Uppsala University (Sweden), the University of

Montpellier (France), and the Ludwig-Maximilian University of Munich (Germany), with Harvard University (USA) and University of Lausanne (Switzerland) as associated partners.

Contact: MEME@rug.nl.

Please spread the word !

Best regards

Pascal, on behalf of MEME coordinators

Pascal Milesi Associate Professor, SciLifeLab Group Leader Docent in Evolutionary Functional Genomics

Plant Ecology and Evolution program Department of Ecology and Genetics, Uppsala University Norbyvägen 18D 752 36 UPPSALA Sweden

+46 (0) 7 69 31 25 89

När du har kontakt med oss på Uppsala universitet med e-post innebär det att vi behandlar dina personuppgifter. För att få mer information om hur vi behandlar dina personuppgifter, läs här: <http://www.uu.se/om-uu/-dataskydd-personuppgifter/> E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: <http://www.uu.se/en/about-uu/data-protection-policy> Pascal Milesi <pascal.milesi@scilifelab.uu.se>

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structure on the official Master in Evolutionary Biology page (<https://biologia.biologia.unipd.it/en/laurea-magistrale/master-degree-in-evolutionary-biology/>)

Admission Information: Find out about admission requirements and procedures for international students on the University of Padua's admission page (<https://www.unipd.it/en/studying-padova-admission>).

Application Portal: Submit your application through the Apply@Unipd portal (<https://apply.unipd.it/>).

Scholarships and Financial Aid: Learn about available scholarships and financial support for international students on the scholarships page (<https://www.unipd.it/en/studying-padua/funding-and-fees-scholarships-international-students>).

International Student Services: Access resources and support services for international students on the International Student Council page (<https://www.unipd.it/en/international-student-council-elections>).

Discover more about this unique opportunity to study evolutionary biology at one of Europe's oldest and most prestigious universities. Visit our website to learn more and apply!

Carlotta Mazzoldi <carlotta.mazzoldi@unipd.it>

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UppsalaU FungalGenomics

UPadua Italy EvolutionaryBiology

Join the Master in Evolutionary Biology at the University of Padua (Italy) The University of Padua offers an international Master's Degree in Evolutionary Biology, entirely taught in English and open to students worldwide. The program focuses on understanding the processes and mechanisms of evolution, and on studying biodiversity and conservation, providing a strong foundation for research and applied careers in biology.

With access to modern facilities, experienced professors, and opportunities for hands-on fieldwork, this program combines academic learning with practical skills. Students will study in a dynamic and inclusive environment, gaining the tools needed to address key challenges in biology today.

Useful Links:

Program Details: Explore the curriculum and course

PhD student in Systemic Biology Uppsala University, Department of Organismal Biology PhD student in Systematic biology Are you interested in working with fungal genomics, with the support of competent and friendly colleagues in an international environment? Are you looking for an employer that invests in sustainable employeeship and offers safe, favourable working conditions? We welcome you to apply for a PhD position at Uppsala University.

Research in the Fungal Accessory Genome Evolution (FungAGE) lab focuses on understanding the evolution of genomes and the genetic basis of adaptation in fungi. We recently discovered that many fungi harbour massive transposable elements, named Starships, that mobilize a vast diversity of fungal genes. We have now deciphered how the Starships move within genomes, but a growing amount of evidence suggests that they are also capable of moving between genomes. The main goal of this PhD position is to explore the evolutionary dynamics of the

Starship elements and the fungal host genome through comparative genomic techniques. Ideally, this will reveal trade-offs between harbouring a given Starship and growth under specific environmental conditions. Additional objectives will seek to quantify such trade-offs by growing fungal strains under laboratory conditions.

Duties This project will primarily make use of existing comparative genomic pipelines that we have developed in the group. The development of new pipelines will also be a core part of this project. As such, familiarity with coding languages is an asset. Fungal culturing using a variety of media and conditions may also be a part of the project, therefore interest in both computational and laboratory research is desired. Analysis of results with statistical methods, such as those implemented in R will also be important. Results will be written for publication in scientific journals and presented at international conferences.

Requirements To meet the entry requirements for doctoral studies, you must hold a Master's (second-cycle) degree in Evolution Biology, Bioinformatics or a closely related area, or have completed at least 240 credits in higher education, with at least 60 credits at Master's level including an independent project worth at least 15 credits, or have acquired substantially equivalent knowledge in some other way. Experience with running bioinformatic tools is a necessity, which may include: working in UNIX environments, scripting in python/perl/, or working with whole genome alignments.

Strengths in organization, problem solving, communication, and collaboration are required. The applicant should have documented experience and proficiency in oral and written presentation in English.

Additional qualifications Additional assets include experience with analyzing genomic data and microbial culturing, particularly of fungi. Experience with communication of scientific concepts within an academic setting, including forming hypotheses and conducting statistical analyses is also a plus.

Rules governing PhD students are set out in the Higher Education Ordinance chapter 5, §§ 1-7 and in Uppsala University's rules and guidelines.

About the employment The employment is a temporary position according to the Higher Education Ordinance chapter 5 § 7. Scope of employment 100 %. Starting date 250301 or as agreed. Placement: Uppsala

For further information about the position, please contact: Aaron Vogan, aaron.vogan@ebc.uu.se

Please submit your application by 31 January 2025, UFV-PA 2024/4334.

Are you considering moving to Sweden to work at Uppsala University? Find out more about what it's like to work and live in Sweden.

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

Read more about our benefits and what it is like to work at Uppsala University <https://uu.se/om-uu/jobba-hoss/> The position may be subject to security vetting. If security vetting is conducted, the applicant must pass the vetting process to be eligible for employment.

Please do not send offers of recruitment or advertising services.

Submit your application through Uppsala University's recruitment system.

Type of employment Temporary position Contract type Full time First day of employment 2025-03-01 Salary Fixed salary Number of positions 1 Full-time equivalent 100% City Uppsala County Uppsala län Country Sweden Reference number UFV-PA 2024/4334 Contact Aaron Vogan, 073-8745597 Union representative ST/TCO, tco@fackorg.uu.se Seko Universitetsklubben, seko@uadm.uu.se

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USouthBohemia EvolutionaryEcol

Title: PhD: USouthBohemia.EvolutionaryEcology

Text:

Faculty of Science, University of South Bohemia in Āeské BudĀjovice, Czech Republic is seeking qualified applicants for the position of

PhD in Evolutionary Ecology-Bird Migration

The recently established research group Global Life-history, Ornithology & Behavioural Ecology (GLOBE) -

<https://GLOBEresearchgroup.com> new webpages will be launched soon - focuses on ecology, behaviour, life-history strategies and population dynamics of wild animals, particularly birds, including impacts and consequences of recent environmental changes. The GLOBE research group is led by Vojtěch Kubelka from the Department of Zoology and Centre for Polar Ecology at the Faculty of Sciences, University of South Bohemia in the Czech Republic and has been recently awarded a prestigious ERC CZ grant: Animal migrations in a changing world - still advantageous strategy or maladaptive behaviour? for years 2024-2029.

Animal migrations represent one of the greatest spectacles in nature, providing crucial ecosystem services as well as resources for human communities. Why do animals migrate? It has been thought that animals migrate to reproduce at higher latitudes, taking advantage of lower predation pressure, fewer parasites and seasonally high pulses in food supply. However, it has been highlighted that recent climate change and human pressure impacts can erode such benefits and migratory animals are declining globally with poorly understood underlying mechanisms.

We strive to tackle pressing issues: Are there still latitudinal gradients in predation, parasitism and seasonal food availability, supporting the benefits of migratory behaviour? How are migratory animals able to cope with environmental changes? What are the most important drivers and life stages limiting populations of migratory animals? To achieve this, we are executing comprehensive research of migration profitability, combining experimental, observational and comparative approaches - investigating latitudinal gradients in predation, parasites, food supply and whole life-cycles of tracked shorebirds, a suitable model taxon with intraspecific variability in migratory strategies and exposed ground nests - at 16 study sites from the Arctic to Patagonia.

We seek to appoint a PhD student to contribute to this new project. The particular targeting of the PhD project will be developed together with the successful applicant within the framework of the ERC CZ project.

What would be your main responsibilities:

Study PhD at the Faculty of Sciences, University of South Bohemia in Āeské BudĀjovice, Czech Republic in the Zoology programme

Execute ornithological fieldwork at selected study sites across Western Palearctic and South America in association with international collaborators Combine experimental and observational fieldwork with a comparative approach based on extracting relevant information from

published literature Prepare and write manuscripts for publication in peer-reviewed journals Optional activities include engaging in the supervision of undergraduate students and participation in funding applications for research in collaboration with other team members Participate in conservation activities Present and promote the results at conferences and seminars and disseminate the project outputs

What we offer:

A four-year position combining employment on the ERC CZ project and governmental financial support during the course of the PhD study English-speaking, stimulating and friendly international research environment in the multicultural GLOBE research group Extensive international networking and mentoring opportunities with 100+ collaborators of the GLOBE research group worldwide Fieldwork at the ERC CZ project study sites and access to the datasets obtained along latitudinal gradients from Morocco to the Arctic and from tropical South America to Patagonia

Excellent instruments, equipment and multiple research platforms within the GLOBE research group and Faculty of Sciences, University of South Bohemia in Āeské BudĀjovice, Czech Republic

Full logistical support for own follow-up research funding applications Flexible working time, full health insurance, student benefits Professional administration support and assistance with all personal, economic or logistical needs including the relocation and settlement in CZ Meals allowance, special mobile services, university kindergarten Work-life balance in a historical middle-sized university city, budejce.cz/en/, offering multiple opportunities for outdoor, sport & cultural activities

Competitive candidates are expected to have:

Master's degree or equivalent in ecology, or relevant field of life sciences

A foundation of knowledge in two or more fields: evolutionary ecology, climate change biology, demography and population dynamics, predator-prey

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USunshineCoast Australia KoalasChlamydia

We are looking for a PhD Candidate! PhD Title: Understanding the impact of chlamydial threat management in koalas

The team at Detection Dogs for Conservation (University of the Sunshine Coast, Australia) see: https://lnkd.in/d5uuQh_M <https://lnkd.in/dKSX5URA> <https://lnkd.in/dDmpE3R9> is looking for a wildlife passionate, conservation minded, kind and dedicated PhD candidate to join us for a new project.

Please share around!

The research side is funded, but the candidate will need to secure their scholarship - with the application deadline on the 21st of March (this round is for domestic students only, international will be later in the year). The team will support the candidate to deliver the application.

Candidates need to contact us at: <DDC@usc.edu.au> attention: Katrin, Carme and Romane, before the 31 of January with their CV, including 2 referees and a short email with their motivation.

What will the PhD entail? – Keywords: landscape ecology, disease (chlamydia), koalas – Activities: - Working within the Detection Dogs for Conservation team at the University of the Sunshine Coast (Sippy Downs Campus), a team of ~ 15 with other students and staff - Going in the field assisting the detection dogs, drones, scat collection and/or koala tracking - Doing molecular analyses of non-invasive scat samples - Statistical analyses and public engagement as required

What we are looking for is a candidate that... 1/ is self motivated, 2/ has a background in fields of / similar to ecology, zoology, biology, veterinary science, 3/ has a scientific mindset, 4/ adheres to our values of inclusivity, kindness, compassion and equity, and 5/ is competitive to secure a UniSC domestic scholarship (e.g., Honours first class, publication(s), etc).

See scholarship info: <https://lnkd.in/dgmAZ4hS> Research Training Program (RTP) Scholarship

What the candidate can expect from us: we will treat you with kindness and compassion, we will support you to achieve your goals for your PhD and beyond, and

welcome you to a small team which intends on creating a positive culture in academia.

Dr. Katrin Hohwieler (she/her) Conservation Scientist
90 Sippy Downs Drive, Sippy Downs 4556 m: 0435 350132 | e: khohwie1@usc.edu.au Postdoctoral Research Fellow, University of the Sunshine Coast

Please note: I only work Mondays, Tuesdays, and Wednesdays. Please be patient if I don't respond immediately.

khohwie1@usc.edu.au

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UVienna Austria DemographicResponseAlpineBiota

In a project fully funded by the Austrian Science Fund (FWF), the successful candidate will explore demographic responses of alpine biota (flowering plants and arthropods) to past climatic oscillations.

Specifically, the following question will be addressed:
- Did high-elevation species of the European Alps respond to Pleistocene climate oscillations by postglacial expansion or by postglacial contraction? - Were these range shifts affected by the ecological characteristics of these species? - Are past population size and range changes predictive of changes expected under current global climate change?

By comparatively studying species from different plant and animal lineages, it will be possible to distinguish both (i) general patterns (i.e., applicable to many species) from idiosyncratic ones (i.e., applicable to single or a few species only) and (ii) patterns specific to certain major groups (e.g., animals vs. plants) from patterns specific to certain ecological groups (e.g., species from swards vs. screes). By identifying characteristics affecting the response of high-mountain species to global warming in a predictable manner, this research can significantly contribute towards generating hypotheses with respect to the fate of high-elevation species under current global climate change.

To this end, the demographic histories of 20 plant and 10 animal species from the European Alps and jointly occurring in all major alpine habitat types will be inferred based on RADseq-data employing coalescent-based modelling, and their fit to the postglacial contraction and

the postglacial expansion hypothesis, respectively, will be assessed using standard model testing approaches. To assess whether population size changes were accompanied by range size changes, past and current potential distribution ranges, assessed via species distribution modelling, will be compared.

The position is open from March 2025, but the start date is more flexible and can be adjusted depending on the successful candidate's availability.

Requirements: - MSc degree or equivalent in Biology or a related field - Very good written and oral English skills
- Experience in molecular and bioinformatic applications
- Ideally field experience in high mountain ecosystems

We offer: - A three-year PhD (pre-doc) contract with flexible starting time, ideally not later than spring 2025, with an annual gross salary (as of 2025) of 47,520,00 €(social and health insurance included) - Work in a friendly, collaborative, and highly international research environment at the Department of Botany and Biodiversity (<https://botanik.univie.ac.at/>), providing outstand-

ing research facilities and infrastructure and support from scientific and technical staff of the Department - Great network opportunities with our project collaborators at University of Innsbruck (Research Group Molecular Ecology and Research Group Biodiversity) and with other groups at UVie and elsewhere (e.g., Gregor Mendel Institute of the Austrian Academy of Sciences, Institute of Science and Technology Austria) - Possibility for completion of a PhD study in Biology within the Vienna Doctoral School of Ecology and Evolution (VDSEE; <https://vds-ecology-evolution.univie.ac.at/>)

Ideally, apply via the website <https://jobs.univie.ac.at/-job/University-assistant-predoc/1164774501/> If not possible and/or for any further inquiries, please contact the PI directly via email: gerald.schneeweiss@univie.ac.at

“Gerald M. Schneeweiss”
<gerald.schneeweiss@univie.ac.at>

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CornellU AquaticConservation

Assistant / Associate Professor in Aquatic Ecology and Fisheries Science in the Department of Natural Resources and the Environment, Cornell University, Ithaca, NY, USA

The Department of Natural Resources and the Environment welcomes applications for a 9-month, full-time, tenure-track position in aquatic ecology and fisheries science at the level of Assistant or Associate Professor. The position will entail 50% research and 50% teaching. Responsibilities will center around research complemented by teaching and mentoring within the Department of Natural Resources and the Environment (DNRE). DNRE is a leader of sustainability science within the College of Agriculture and Life Sciences

(CALS); our collective expertise in the natural and social sciences is paired with vigorous traditions of non-academic partnerships and stakeholder engagement. We seek to build upon existing strengths in aquatic ecology and ecosystem management within DNRE and other Cornell units by hiring a researcher interested in leveraging both field expertise and regionally collected long-term data resources.

The successful candidate will be expected to establish an internationally recognized research program that attracts external funding to advance freshwater science and improve the management of lake ecosystems. Research will be based primarily in regional freshwater systems including work at the Cornell Biological Field Station (CBFS). The Station sits on the shore of Oneida Lake, and its research facilities enable field sampling, controlled experiments at multiple scales, and analysis of a wide variety of sample types. CBFS continues to build upon its globally notable data assets, including 65+ years of limnological and fish community data from Oneida Lake, and annual lower trophic data from Lake Ontario (since 1995) and the other four Laurentian Great Lakes (since 2012). These long-term data are well suited for connecting the physical, chemical, and biological dynamics of lake ecosystems with climate drivers, land cover change, and societal outcomes (fisheries, harmful algal blooms, recreational opportunities). For decades, CBFS has been a focal point for collaboration between Cornell and the New York State Department of Environmental Conservation (NYSDEC), creating opportunities for innovative management experiments, professional development of agency staff, and translation of knowledge to inform fisheries management decisions. There are also ample opportunities to synergize with Cornell researchers associated with the Adirondack Fishery Research Program, the USGS Cooperative Fish and Wildlife Research Unit, and the Center for Conservation Social Sciences.

Outstanding research scholarship is expected, as is excellence in and commitment to teaching, translation of knowledge, advising, and inclusive mentoring of undergraduate and graduate students. We seek colleagues with a record demonstrating success and/or promise across all these areas, and who will be supported by and contribute to a vibrant culture of inclusive excellence at Cornell. As such, candidates are expected to engage in service and leadership activities within the department, the college and university, and relevant professional societies. We welcome candidates who understand the barriers facing marginalized identities who are underrepresented in academia, the classroom, and higher education careers (as evidenced by life experiences and educational background). We encourage

applications from candidates who have experience in building an equitable and diverse scholarly environment through teaching, mentoring, research, outreach, life experiences, and/or service.

Applications received by January 20, 2025 will be given full consideration. Applications will be accepted until the position is filled.

Full posting available here: https://apps.hr.cornell.edu/-recruiting/facultyview.cfm?posting_id=-_JOB_POSTING-3-90230 nt246@cornell.edu

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FloridaIntLU MarineMicrobialEvolution

The Department of Biological Sciences, in conjunction with the Institute of Environment at Florida International University invites applications for an Open Rank, (Assistant, Associate, or Full Professor) position in Marine Microbial Ecology to add to FIU's growing expertise in understanding the Biscayne Bay ecosystem. This position is one of multiple positions funded through the Institute of Environment across multiple academic Departments by the new Biscayne Bay initiative, including a complex systems modeler (Department of Mathematics and Statistics), a biogeochemist (Department of Chemistry and Biochemistry) and a coastal physical oceanographer (Department of Earth and Environment). Scientists who study nutrient cycling, microbial metabolism, oxygen depletion, benthic-pelagic coupling, and/or water quality regulation are encouraged to apply. Candidates using modern molecular tools, including big data/omics approaches, that can integrate their research with the new, state-of-the-art Water-Omics Facility to investigate natural and anthropogenic stressors within Biscayne Bay and surrounding waters are especially encouraged. The successful candidate will be expected to have a strong publication record, maintain an active, externally-funded research program, supervise graduate students in our graduate program, and teach undergraduate and graduate courses in their area of expertise and in the general marine sciences curriculum. This search is open-rank, but hires at the Associate or full Professor level will require transferrable research funds. The successful candidate will be expected to work across disciplines with their colleagues in the Institute of Environment (<https://environment.fiu.edu/>). The minimum

requirements are a Doctoral degree in a related field from an accredited institution, a demonstrated record of achievement in teaching and service, and active academic research.

Qualified candidates are encouraged to apply to Job Opening ID 533915 at careers.fiu.edu and attach a cover letter, curriculum vitae, and statements of mentoring, teaching, and research philosophy. Candidates will be requested to provide names and contact information for at least 3 references who will be contacted as determined by the search committee. Review of applications will begin on December 6, 2024. Applications will be accepted until the position is filled. Please direct any questions to Dr. James Fourqurean at Jim.Fourqurean@fiu.edu.

Heather Bracken-Grissom, PhD Assistant Director of the Coastlines and Oceans Division, Institute of Environment Professor, Dept. of Biological Sciences Research Associate, Invertebrate Zoology, National Museum of Natural History (NMNH) Hope Spot Champion, Florida Keys and Ten Thousand Islands Past North American Governor, The Crustacean Society

Florida International University-Biscayne Bay Campus 3000 NE 151 Street, MSB-361 North Miami, Florida 33181, USA 305 919-4190 (Phone) 305 919-5838 (lab) CRUSTOMICS: Crustacean Genomics and Systematics Lab <http://www.brackengrissomlab.com/> heather.brackengrissom@fiu.edu

Heather Bracken-Grissom <hbracken@fiu.edu>

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IndianaU Evo Genomics

Research Associate in Chromosome Evolution in Beetles and Flies (Bracewell Lab)

A full-time Research Associate (RA) position is available in the laboratory of Dr. Ryan Bracewell in the EEB program at Indiana University Bloomington to help study functional genomics and chromosome evolution in beetles and flies (*Drosophila*). The RA will oversee insect colony maintenance, will perform DNA/RNA extraction, Illumina sequencing and long-read sequencing library preparation (RNA-seq, Hi-C, Nanopore, PacBio), chromosome squash and fluorescent in situ hybridization (FISH), and general data collection/management. The RA will also be responsible for ordering lab supplies, maintaining lab equipment, and helping to mentor un-

dergraduate students. Some fieldwork is also possible for those interested but will not be required. Information about the Bracewell lab is available at <https://ryanbracewell.com>. B.S. in Biology or a related field with previous research experience in genetics, genomics, molecular biology, and/or evolution is required. M.S. or Ph.D. applicants will also be considered. Good communication skills and the ability to work independently as well as part of a team are expected. Salary will be commensurate with education and experience, benefits included. Best consideration date is March 1st, 2025. The expected start date is late spring/negotiable. 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/27713>. For questions about the position and more details on the research, please contact Dr. Ryan Bracewell (rbracewe@iu.edu).

The department of Biology is a large, unified department with strong undergraduate degrees, nationally-ranked graduate programs, and world-class research spanning the breadth of biological questions and experimental systems - from ecosystems to microbiology and developmental biology, from evolution to cell biology, from molecular biology to systems biology, bioinformatics, and genomics. It is always an exciting time for Biology - enormous advances in global genome analysis coupled with unprecedented developments in interdisciplinary research have made the 21st century the Century of Biology. For more information about the department, you can find it here: About: Department of Biology: Indiana University Bloomington.

The Department of Biology is part of The College of Arts+ Sciences, the oldest and largest academic division of Indiana University. The College values diversity, equity, and inclusion as a core strength and essential element in the success of its educational mission. For the full statement, click here. 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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SangerInst UK SymbiontMicro- biomeGenomicsEvolution

Two postdoctoral positions in the Wellcome Sanger Institute, UK, on the analysis of the genomes of eukaryotic and prokaryotic cobionts - symbionts, pathogens and microbiomes - of a wide range of eukaryotic hosts.

Closing Date: 26th January 2025

We have an exciting opportunity for two Postdoctoral Fellows to work in the general area of symbiosis genomics. 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 in biology and evolution and have arisen 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 or antagonistic 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?

One position will focus on analysing eukaryotic cobionts serendipitously identified in Darwin Tree of Life genomic data, as well as symbiotic systems explicitly sequenced, for example as part of the Aquatic Symbiosis Genomics project. 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. The scope of the work will include the evolution of collaboration between species in symbiotic (mutualist and parasitic) and other associations.

The second position is a collaboration between the Tree of Life (ToL) and the Parasites and Microbes (PaM) programmes at Sanger to collate, annotate and explore the biology of the bacterial and archaeal cobionts discovered during eukaryotic host genome sequencing. You will identify cobionts in genome sequence datasets as they are generated and build a catalogue of host-microbe associations. You will explore the evolutionary and systems biology of host-microbiome interactions, including

identification of phylogenetic associations between hosts and microbes, exploration of virulence and other phenotypes in pathogens, exploration of phage metagenomes, definition and functional analysis of horizontal DNA transfers into host genomes, and other topics. Where required, additional data will be commissioned to better evidence particular aspects of host and microbe.

The specific projects undertaken will be co-created by the bioinformaticians in consultation with the principal investigators, with an emphasis on large-scale analysis across diversity. The positions are associated with the Leverhulme Research Centre for the Holobiont, where a diverse team of biologists from many disciplines are examining inter-species associations from evolutionary, metabolic/physiological and ecological standpoints.

Do contact Mark Blaxter mb35@sanger.ac.uk to discuss the positions and the wider environment at the Sanger Institute.

3 years fixed term contracts, salary range 38,000 - 49,156
Closing Date: 26th January 2025 Recruitment Process:
Zoom interviews w/c 3rd Feb, Face to face Interviews
w/c 10th Feb

Direct links to job specifications and application forms: Eukaryotic symbionts https://sanger.wd103.myworkdayjobs.com/en-US/-/WellcomeSangerInstitute/details/Postdoctoral-Fellow_JR102432 Microbiome analysis across Tree of Life https://sanger.wd103.myworkdayjobs.com/en-US/WellcomeSangerInstitute/details/Postdoctoral-Fellow-Microbiomes-of-Tree-of-Life-_JR102528 Hybrid Working at Sanger: We recognise that there are many benefits to Hybrid Working; including an improved work-life balance, with more focused time, as well as the ability to organise working time so that collaborative opportunities and team discussions are facilitated on campus. The hybrid working arrangement will vary for different roles and teams. The nature of your role and the type of work you do will determine if a hybrid working arrangement is possible.

Equality, Diversity and Inclusion: We aim to attract, recruit, retain and develop talent from the widest possible talent pool, thereby gaining insight and access to different markets to generate a greater impact on the world. We have a supportive culture with the following staff networks, LGBTQ+, Parents and Carers, Disability and Race Equity to bring people together to share

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SunYatSenU Shenzhen Evolution

Tenure-track faculty positions at the School of Ecology Sun Yat-sen University, Shenzhen, China

About SYSU EEB (<http://eco.sysu.edu.cn>) Celebrating its centennial anniversary, the Ecology & Evolution discipline of Sun Yat-sen University (SYSU) has a long heritage, tracing its roots back to the Department of Biology at the foundation of SYSU in 1924 by Dr. Sun Yat-sen. The Ecology discipline (where evolution is treated as a subdiscipline) of SYSU is ranked first in the discipline quadrennial evaluation among all universities in China in 2012 and 2017. Its undergraduate program was awarded an “A+ top Discipline” by the Ministry of Education of China. SYSU is ranked among the top 1Å in the disciplines of Molecular biology & Genetics and Environmental sciences & Ecology worldwide based on the essential scientific indicators (ESI). Nature Index 2024 ranks SYSU at 14th in biological sciences and 7th in earth & environmental science worldwide.

Our recent research focuses on the mechanisms of biodiversity and evolution, sustainable development and humans-nature interactions, addressing both basic and applied research frontiers. SYSU faculty’s research in evolution currently covers phylogenomics, population genomics, hybridization & speciation, non-coding element evolution, mutation rate evolution, cancer evolution, behavioral ecology, genetic load, evo-devo, somatic cell lineage-tracing, spatial-omics and more, covering a broad range of taxa.

Established in 2018, the School of Ecology (<http://eco.sysu.edu.cn>) is located on the Shenzhen Campus of SYSU, at the heart of the Guangdong- Hong Kong- Macao Greater Bay Area. The school, first of its kind in China, represents an innovative initiative for SYSU to further develop the EEB discipline. Given our strong foundation in key ecology and evolutionary sub-disciplines, we stay committed to building a set of core research directions with distinguished and leading scientists in the fields of 1) mechanisms of biodiversity formation and evolution, 2) maintenance and conservation of biodiversity,

Applicants with expertise in all evolutionary subdisciplines are welcome, including but not limited to * Evolutionary & population genomics * Experimental evolution * Computational method development & machine learn-

ing * Evolutionary theory * Epigenetic evolution (incl. cultural/meme evolution) * Behavioral ecology (incl. human & plants) * Evolution of aging and life history * Pathogen & disease evolution * Evolution of crops and domesticated animals

We are particularly interested in candidates connecting theory with empirical data, applying evolution to medical & human-related research, linking micro- and macroevolution, unifying evolution and ecology.

The School of Ecology offers a diverse, productive, collaborative and well-equipped research environment that is highly supportive of both junior and senior faculty. SYSU provides an internationally competitive start-up package for incoming new faculty members.

2. Job Openings and Description * 1-2 faculty at the level of Assistant Professors (tenure-track), Associate Professors (tenure-track) or in exceptional cases, tenured Associate Professors.

3. Requirements * Nationality: unlimited * A background in related fields of evolutionary biology with a PhD or equivalent degree * A strong academic record evidenced by publications, grants and awards * Openness to collaborative research * The applicant is expected to develop a vibrant extra-murually funded research program, as well as teach undergraduate and graduate courses in their areas of expertise. * Excellent written and oral communication skills.

4. Contact For more information and inquiries about the positions, please contact Dr. Rongfeng Cui at cuirf@mail.sysu.edu.cn. Review of applications will continue until the positions are filled.

cuirf@mail.sysu.edu.cn

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UAlabama ComputationalBiology

The Department of Biological Sciences at The University of Alabama invites applications for one tenure-track position at the Associate/Full Professor level in Computational Biology, as part of a machine-learning focused cluster hire. The appointment will begin on August 16, 2025. <https://careers.ua.edu/jobs/associate-professor-full-professor-computational-biology-artificial-intelligence-machine-learning-in-biological-sciences-tenure-tenure-track>

525397-tuscaloosa-alabama-united-states Detailed Position Information The successful candidates for the position “Machine Learning/AI in Biological Sciences” will be expected develop and apply machine learning and/or artificial intelligence (broadly defined) to answer biological questions. The search is open with respect to biological subfield, with areas of interest including but not limited to: prediction and design of nucleic acid or protein structures and functions; drug discovery and disease characterization; genomics and genotype-to-phenotype mapping; image analysis and 3D reconstructions; systems biology and data integration; and biological predictions at any scale. Individuals focusing on solely computational approaches as well as those with combined theoretical and experimental-based inquiry will be considered. More information about the department can be found on the department’s website <https://bsc.ua.edu/>. The successful candidate will be expected to take advantage of a new \$96 million-dollar High Performance Computing and Data Center that will come online in 2026.

The minimum qualifications for this position are Ph.D. or equivalent in biological sciences or a closely related field, postdoctoral experience, scholarly publications, and experience in ML/AI. Candidates are expected to have an outstanding research record commensurate with their career stage and develop a high quality, externally funded research program, as well as teach and mentor at the undergraduate and graduate levels effectively.

The successful candidate is expected to possess a national/international reputation with an active research program, a record of securing multiple external research grants, and an outstanding record of teaching at the undergraduate and graduate level. Extraordinary candidates will be nominated for the Endowed Shelby Distinguished Faculty position:

<https://provost.ua.edu/the-shelby-endowment-for-distinguished-faculty/> Minimum Qualifications The minimum qualifications for this position are Ph.D. or equivalent in biological sciences or a closely related field, postdoctoral experience, scholarly publications, and experience in ML/AI. Candidates are expected to have an outstanding research record commensurate with their career stage and develop a high quality, externally funded research program, as well as teach and mentor at the undergraduate and graduate levels effectively.

Preferred Qualifications The successful candidate is expected to possess a national/international reputation with an active research program, a record of securing multiple external research grants, and an outstanding record of teaching at the undergraduate and graduate level.

Instructions and Required Materials for Application Applications should include a cover letter, current curriculum vitae, research statement, teaching statement, and provide contact information for 3 letters of reference to be sent upon request. The review of applications will begin February 15, 2025, and the review will continue until the position is filled.

About the Division/College/School The College of Arts and Sciences at The University of Alabama offers an exciting and dynamic environment for faculty seeking to make an impact in their field and in the lives of the innovators and changemakers of tomorrow.

As the largest college at The University, we house over 8000 students and 1000 faculty and staff across our 25 departments.

With nationally recognized programs and award-winning faculty, our College has positioned itself as a leader in higher education. Our facilities and resources include state-of-the-art laboratories, research centers, and performance venues, providing students with hands-on learning experiences and opportunities for research and creative expression.

The College is committed to the liberal arts philosophy that fosters creative and critical thinking and a lifetime of learning.

About the University The University of Alabama is located in Tuscaloosa, Alabama, named one of Travel + Leisure’s 25 Best College Towns and Cities in the U.S. As one of the nation’s premier universities, UA offers bachelor’s, master’s

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UCalifornia LosAngeles
DirectorQCBIO

The Institute for Quantitative and Computational Biosciences at UCLA is recruiting its next director. Please see recruit.apo.ucla.edu/JPF10007 for more information. Deadline is Friday Feb 7.

Nandita Garud, PhD Associate Professor Department of Ecology and Evolutionary Biology Department of Human

Genetics, DavidGeffen School of Medicine University of California, Los Angeles 621 Charles E. Young Drive South Los Angeles, CA 90095-1606

Lab website:<https://garud.eeb.ucla.edu> Nandita Garud <ngarud@g.ucla.edu>

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UCalifornia SanDiego ResTech EvolutionaryEcol

The Rennison laboratory (rennisonlab.com) at University of California San Diego seeks one Research Technician to support research on evolutionary ecology of threespine stickleback. The work is part of a broader research center we are establishing on the neurobiology of changing environments.

Job Description

The Staff Research Associate will assist the Principal Investigators and other lab members in research on the effects of climate change on neurological phenotypes in threespine stickleback (*Gasterosteus aculeatus*).

Incumbent is responsible for the experimental care and maintenance of the stickleback colony and associated facility (feeding, cleaning, breeding, cataloguing, maintaining), and will assist with molecular biology tasks including cloning, embryo injections, genotyping, nucleotide extraction (DNA/RNA), quantification and library preparation, molecular labeling.

There will also be tasks related to specimen preparation and curation including histology, staining, dissection and photography. The Staff Research associate will perform routine laboratory duties such as ordering and maintenance of lab equipment, supplies and records; serve as lab safety coordinator; maintain cleanliness of lab; prepare buffers, media, and solutions; and perform other general lab duties as needed. Incumbent will train lab members on fish husbandry and lab safety protocols.

Job link:

<https://employment.ucsd.edu/staff-research-associate-133990/job/28794130> Diana J. Rennison PhD Assistant Professor, Ecology, Behavior & Evolution Section Division of Biological Sciences University of California San Diego Office: 2212 Muir Biology Building Office Phone 1-858-246-5412 Website: rennisonlab.com

drennison@mail.ucsd.edu

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UMaryland EcoEvoMicrobes

The Department of Biology at the U of Maryland, College Park invites applications from individuals studying fundamental questions in ecology and evolutionary biology using microbial systems for a tenure-track or tenured position at any rank:

<https://bit.ly/ecoevomicro-open-rank-umd> Research areas of particular interest include the use of microbial systems to explore: eco-evolutionary dynamics, community ecology, ecosystem functioning, and environmental and human health. Apply by January 31, 2025 for best consideration.

Joshua Weitz - jweitz@umd.edu

“Joshua S. Weitz” <jweitz@umd.edu>

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UNacionalAutonomaDeMexico IntergrativeBiol Botany

Faculty Position. Integrative Biology. Evolutionary Patterns and Processes Underlying Plant Biodiversity Institute of Biology. Universidad Nacional Autonoma de Mexico

<https://tinyurl.com/27jwrzne> The Universidad Nacional Autonoma de Mexico (UNAM, www.unam.mx) is Mexico’s preeminent public higher-education center. UNAM is among the highest-ranking Spanish-speaking, and Latin American, universities. The Institute of Biology is a research center on the main campus of UNAM in Mexico City, with the missions to discover, describe and systematically document biota; to conduct scientific research about its evolutionary origin and maintenance, composition, relationships, distribution and interactions; and to conserve and develop sustainable use for the well-being of society and the planet. The Institute of Biology houses the National Biological Collections of Mexico,

including ten zoological collections, and the National Herbarium. The faculty at the Institute of Biology has a long tradition, expertise and leadership in taxonomic and systematic research on various groups of plants, animals, and fungi; their composition, distribution, and traditional uses in Mexico. In recent decades, phylogenetic estimation of relationships among organisms, including the generation and use of genomic data, has proliferated. Nevertheless, research about higher-level evolutionary patterns and processes that underlie and determine the different dimensions of diversity and distribution of biota, that transversally integrate different types of organisms, are few and incipient.

The Institute of Biology aims to promote research about higher-level evolutionary patterns and processes that cause and determine biodiversity, and invites applications for one tenure-track full-time position as Research Scientist in Integrative Biology (equivalent to Investigador/a Asociado/a C) with emphasis in botany. This full-time position will be assigned to the recently created Unit for Synthesis in Systematics and Evolution (UniSSE).

CANDIDATE'S PROFILE We seek candidates capable to propose and develop integrative research lines about patterns and processes that cause and determine different dimensions of plant biodiversity. Candidates with research interests based on analyzing and synthesizing data from biological collections, biotic inventories, and/or cybernetic databases, and whose research proposes transversal approaches among different types of organisms, and the link between taxonomic and inventory research with their macroevolutionary context, are encouraged to apply.

Ideal candidates should have: 1. The ability to integrate key concepts among several of the following disciplines: systematics, comparative phylogenetics, biogeography, evolution, or similar lines within and among different groups of organisms, with a focus on plants. 2. The ability to propose and develop integrative research on evolutionary patterns and processes that underlie biodiversity, a. preferably including the use of data from biological collections, biotic inventories and/or biodiversity databases at a global level; b. preferably encouraging transversal interactions with and among specialists in taxonomy and systematics of different types of organisms; c. fostering students in this line of research through direct mentorship and teaching. 3. Experience in methods for handling large volumes of biological (e.g., biological collections, genetic/genomic, morphological, ecological), environmental, and/or geographical data to address questions about the evolutionary processes underlying different dimensions of biodiversity. 4. The ability to analyze different types of information (e.g.,

phylogenetic, biotic, environmental, geographic), and temporal and spatial scales. 5. The ability to interact with specialists on different taxonomic groups and fields within Biology. 6. The ability to mentor students in emerging research topics.

REQUIREMENTS 1. Doctorate or Ph.D. degree in science. 2. Professional experience of at least five years (including graduate education) in integrative research on evolutionary patterns and processes underlying plant biodiversity. 3. Preferably with postdoctoral experience. 4. Authorship of research articles on the topic of the position. 5. Because the position is sponsored by UNAM's Subprograma de Incorporacion de Jovenes Academicos de Carrera (SIJA), female candidates should be no older than 39 years old, and male candidates should not be older than 37 years old at the time of hiring approval by the Technical Council of Scientific Research. 6. Non-native speakers must be fluent in the Spanish language.

APPLICATIONS AND SUPPORTING DOCUMENTS To apply, please send the following documents to sacademica@ib.unam.mx, with a copy (Cc:) to secacad_vl@ib.unam.mx. 1. Curriculum vitae (CV), including academic degrees and

— / —

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

UNewMexico Parasitology Curator

We invite applications for an endowed professorship, the Robert L. Rausch Chair of Parasitology. The Chair will be an Assistant or Associate Professor of Biology with a concurrent appointment as Curator of Parasites at the Museum of Southwestern Biology (MSB), a natural history collections facility within the Department of Biology of the University of New Mexico (UNM).

We seek a colleague with demonstrated commitments to (1) collecting and curating natural history specimens; (2) using specimens to address questions in evolution, systematics, and ecology; (3) pursuing a vigorous, externally-funded research program; (4) advancing the integration of specimens into parasitology, including helminthology; (5) achieving excellence in teaching and

mentoring; and (6) supporting diversity, equity, inclusion, and student access within a diverse community.

UNM is a research-intensive (Carnegie R1), minority-majority institution located in Albuquerque, a city with a rich cultural heritage in a biodiverse, scenic landscape. The Department of Biology is a family-friendly academic community of 35 tenure-track faculty members (<https://biology.unm.edu/core-faculty.shtml>), ~1500 undergraduate majors, 100+ graduate students, and a vibrant portfolio of extramurally funded research.

The MSB (<https://msb.unm.edu/>) includes eight collections (more than 5 million specimens), each headed by a faculty curator, full-time collection manager, and shared mission: to collect and curate biodiversity specimens and information that advances scientific understanding of Earth's biota over time and space. MSB contributes to more than 400 scientific publications annually and leads globally in the development and dissemination of informatics resources (<https://arctosdb.org/>). MSB's cryo-collections comprise more than 700,000 samples that document global change, emerging diseases, and evolutionary processes.

The MSB Division of Parasites (<http://www.msb.unm.edu/divisions/parasites/index.html>) holds the third-largest helminth collection in North America, including extraordinary collections from Robert and Virginia Rausch, Eric Hoberg, and ongoing fieldwork by MSB personnel. The Rausch Endowment will support a faculty member to continue building and investigating these collections to address fundamental questions in host-parasite symbioses, with a preferred focus on helminthology.

Minimum Qualifications: 1. PhD in Life Sciences or a related field by date of appointment (August 1, 2025). 2. Evidence of primary specialization in Parasitology

Preferred Qualifications: We seek colleagues with demonstrated commitments to 1. Collecting and curating natural history specimens 2. Using specimens to address fundamental questions in evolution, systematics, and ecology 3. Pursuing a vigorous, externally funded research program 4. Advancing the integration of specimens into the fields of parasitology 5. Achieving excellence in teaching and mentoring 6. Post-doctoral experience by the start of the appointment 7. A demonstrated commitment to diversity, equity, inclusion, and student success, as well as working with broadly diverse communities

Only applications submitted through the official UNMJobs site will be accepted. If you are viewing this job advertisement on a 3rd party site, please visit UNMJobs to submit an application: <https://unm.csod.com/>

[ux/ats/careersite/18/home/requisition/31287?c=unm&referralToken=d5EFuqUeSE6kXs8qWZX1Kw](https://unm.csod.com/ats/careersite/18/home/requisition/31287?c=unm&referralToken=d5EFuqUeSE6kXs8qWZX1Kw)

Please attach the following: Cover letter Curriculum vitae Three representative publications Four two-page statements addressing past, present, and future efforts in (1) research, (2) curation, (3) teaching, and (4) diversity, equity, and inclusion. Contact information for at least three professional references.

Applicants who are appointed to a UNM faculty position are required to provide an official certification of successful completion of all degree requirements prior to their initial employment with UNM.

For best consideration, please apply by 1/31/2025. This position will remain open until filled.

– Christopher Witt (he/him) Professor of Biology Director & Curator of Birds Museum of Southwestern Biology University of New Mexico <https://www.unmornithology.org/> Zoom <https://unm.zoom.us/j/7376030834> 505-918-7199

cwitt@unm.edu

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UNotreDame DatabaseManager AmboseliBaboonProject

A full-time database and lab manager position is available in Dr. Beth Archie's research group at the University of Notre Dame, focused on data from the Amboseli Baboon Research Project (ABRP; <https://amboselibaboons.nd.edu/>). The manager will support ABRP faculty, students, and staff by maintaining and growing BABASE, an extensive PostGreSQL database that serves as the repository for the Amboseli baboon project's long-term data. Tasks and skills include data entry, database design, data analysis, problem solving, communication, and teamwork. The manager will also contribute to administration and organization in the Archie lab at Notre Dame, including purchasing, organizing supplies, training students in data-related tasks, and administrative support.

CANDIDATE PROFILE. The ideal candidate will have excellent attention to detail, experience curating high quality data sets to support scientific research, experience in coding (especially SQL, R, or Unix), strong communication and problem-solving skills, and initia-

tive on data and lab management-related projects. The position can be tailored to suit different educational levels (Bachelor's to PhD) and backgrounds (e.g., ecology, anthropology, evolution, computer science etc.). Salary is commensurate with experience.

LAB ENVIRONMENT. The Archie lab offers a congenial research environment that encourages scientific inquiry, intellectual curiosity, friendliness, and fun. We provide an inclusive and equitable environment, and we encourage all applications regardless of gender, race, ethnicity, country of origin, immigration status, age, religion, sexual orientation, socioeconomic status, other aspects of identity, and their intersections. Notre Dame is committed to creating work and learning environments that are free from harassment and discrimination.

BACKGROUND ON THE AMBOSELI BABOONS. Founded in 1971, the ABRP is among the longest-running studies of wild primates in the world. We are a highly collaborative, supportive, international team, with members in North America, Europe, and Kenya. We collect detailed and wide-ranging data on baboon ecology, diet, social interactions, reproduction, and survival. The ABRP is directed by Beth Archie at University of Notre Dame, in collaboration with Susan Alberts (Duke University) and Jenny Tung (Max Planck Institute for Evolutionary Anthropology/Duke University). The full team includes field researchers, data managers, students, postdocs, and other trainees who interact frequently. The ABRP has had a considerable impact on biology, primatology, and evolutionary anthropology, contributing over 300 peer-reviewed papers over the years. Our research is greatly facilitated by BABASE, which the data manager will play a large role in maintaining and growing, together with project leaders and managers at Duke and Max Planck.

TO APPLY. To apply, please email Beth Archie at earchie@nd.edu and include a CV, cover letter, and the names and contact information for three references. Informal inquiries are also welcome. Applications will be accepted until 1 March, 2025. Review of applications will begin immediately.

Elizabeth Archie (she/her) Notre Dame Collegiate Professor Department of Biological Sciences University of Notre Dame Notre Dame, IN Tel. (574) 631-0178 Office. 179 Galvin <http://blogs.nd.edu/archielab/> Beth Archie <Elizabeth.A.Archie.2@nd.edu>

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UOslo NHM Curation

Associate Professor in Zoology

A permanent position as an Associate Professor in Zoology is available at the Natural History Museum, University of Oslo. The appointment is a fulltime position with a start date of January 1, 2026 or by agreement.

The Natural History Museum (NHM) in Oslo houses the largest natural history collections in Norway, including extensive zoological collections of vertebrates and invertebrates. The Department of Research and Collections is currently organized in nine thematic research groups, four of them with a research focus on animals. The wet collections (ethanol/formalin) include significant collections of annelids, arthropods, bryozoans, chordates (fishes, amphibians, reptiles and birds, but also tunicates), cnidarians, echinodermites, flatworms, molluscs and sponges. NHM has a current focus on strengthening curation and research of its wet collections, and the appointed candidate will be expected to take responsibility for one or more of these collections according to the candidate's taxonomic research profile and interests. NHM has a strategic goal of strengthening cutting edge research on museum specimens and to integrate the scientific collections better in education and outreach activities. It is also a strategic priority to modernize the collections in accordance with new research needs.

To further develop and strengthen NHM's position at the forefront of modern biodiversity research, we seek an active researcher with a relevant and strong track record in zoology. Areas of expertise that we are looking for include, but are not limited to, evolutionary biology, comparative genomics, transcriptomics, systematics, and population genomics. We are especially interested in candidates who combine high-quality research with the use and development of museum collections, and who have the potential to attract external research grants for collection-based research. We are also seeking a candidate with complementary expertise to the current scientific staff who can contribute to ongoing research initiatives. Candidates whose research is multi- or inter-disciplinary are encouraged to apply.

An attractive start-up package is available. However, the successful applicant will be expected to obtain extramural research funding, and a proven record of acquiring such funding is a competitive advantage. NHM has a

collaborative agreement with the Department of Biosciences on teaching and supervision of students at the bachelor and master's level, and with the Faculty of Mathematics and Natural Sciences in the education of doctoral candidates. NHM also hosts an international research school in biosystematics (ForBio). The successful candidate is expected to participate in teaching at all levels and be a capable and enthusiastic supervisor of master's and PhD students. Relevant background in working with museum collections will be an advantage. Up to 50% of the working time will be devoted to curating collections (main activity), teaching and supervision of students, outreach and administrative tasks at NHM. Lectures are given in Norwegian and English. Foreign language speakers are expected to be able to teach in a Scandinavian language within three years after being hired.

Qualification requirements

The successful applicant must have - A PhD or an equivalent doctoral degree in biology - A postdoctoral research profile with relevant experience in zoology - Demonstrated expertise in collections-based research - Demonstrated expertise in zoological systematics and/or taxonomy of the taxonomic group of their research focus - Excellent English language skills (written and spoken)

The successful candidate should have - Curatorial experience with natural history collections - Proven ability to attract external research funding - Teaching and supervision skills of master's and PhD students - Leadership experience from research groups or projects - Team-working and networking skills - Command of a Scandinavian language

For more information, see here: <https://www.jobbnorge.no/en/available-jobs/job/268410/-associate-professor-in-zoology> Application deadline February 23rd 2025

Hugo de Boer, Prof Research Director

University of Oslo Natural History Museum Phone: +47 98126030 <+4798126030> Mail: h.de.boer@nhm.uio.no Adresse: Postboks 1172 Blindern, 0316 Oslo Visiting address: Tøyen Hovedgård, Sars gate 1, Oslo

Hugo de Boer <h.de.boer@nhm.uio.no>

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USFWS Pennsylvania Mussel Geneticist

Summary

This position is a Geneticist, GS- 0440-11 working in Lamar, Pennsylvania for the R5-Lamar NFH and Northeast Fishery Center.

This is a term position expected to last 13 months but may be extended up to a total of 4 years at management's discretion.

Duties The Northeast Fishery Center, located in Lamar, Pennsylvania. Lamar is located in a rural area surrounded by agriculture, state forest and game lands, high-quality fishing streams, and near college towns including State College, PA, the home of Penn State University, and Lock Haven, PA where Lock Haven University is located.

The Northeast Fishery Center includes both the Lamar Fish Technology Center and Lamar Fish Health Center. The Lamar Fish Technology Center provides research capabilities and technical expertise in areas including fish culture, population dynamics, and conservation genetics. The Conservation Genetics Lab works closely with partners in the FWS and elsewhere to apply genetic methods to issues conservation, and focuses on population genetics, environmental DNA, and genomics applications. The Conservation Genetics Lab works with partners to develop, conduct, and interpret genetics projects. Genetic projects include monitoring estimates of genetic diversity, defining populations, identifying species, and conducting environmental DNA analysis and research in the lab and field.

The duties for this position include, but are not limited to:

- * Conducts environmental DNA projects focused on freshwater mussels but including other freshwater organisms.
- * Provides overall technical coordination of complex molecular genetic analyses for a variety of projects working with different aquatic species and genetic analysis methods.
- * Develops and uses DNA markers and automated DNA analyzers/sequencers to collect genotypic, gene frequency, and DNA sequence data on aquatic species.
- * Collects eDNA samples or tissue and/or blood samples from living or dead aquatic organisms in natural or environments as well as water samples.
- * Performs statistical analyses and generates graphical

representations of study results, maintains results in databases, and incorporates these data into written reports, scientific publications, and oral presentations. * Works as a team leader or as a member of a team to conduct complex molecular genetic analyses for a variety of projects working with environmental samples, aquatic organisms, and genetic analysis methods.

Open & closing dates: 01/17/25-01/31/25

Pay scale & grade: GS-0440-11 (TERM)

\$73,939.00 to \$96,116.00 Per Year

Announcement number: R5-25-12668216-LL-DE

<https://www.usajobs.gov/GetJob/ViewDetails/-828751900> Stacey Nerkowski, PhD

Regional Geneticist Northeast Fishery Center Complex
U.S. Fish and Wildlife Service 308 Washington Ave.
Lamar, PA 16848

work: 570-726-4247 ext 50138 cell: 570-927-0073

stacey_nerkowski@fws.gov

Pronouns: she/her

stacey_nerkowski@fws.gov

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W K Kellogg Michigan Biological Station Director

A great administrative opportunity at a great place! Questions can be addressed to me or the Search Committee Co-Chairs, Dr. Richard Kobe (kobe@msu.edu) and Dr. Andrea Case (caseand4@msu.edu).

Jeff Conner

Director and Professor W.K. Kellogg Biological Station
Michigan State University

Position:

Michigan State University seeks a resident Director for the W. K. Kellogg Biological Station (KBS) to provide leadership and promote a creative environment that fosters innovation and excellence in the Station's research, education, and outreach programs in ecology, evolution, agriculture, and conservation biology.

KBS is one of the world's leading biological field stations and one of MSU's AgBioResearch Centers, enabling un-

paralleled application of fundamental ecological and evolutionary research to environmental problems. With its large year-round resident faculty, KBS is unique in its ability to integrate laboratory and field research, with over 1,800 hectares of natural and managed aquatic and terrestrial habitats, as well as a 60,000 square foot modern research building. In addition to faculty laboratories, major research facilities at KBS include: a genomics lab, more than 50 growth chambers and ultracold freezers, 4800 sq ft of greenhouse space, and specialized field labs including an experimental pond facility. KBS is home to an NSF Long-Term Ecological Research (LTER) site and a USDA Long-Term Agroecosystem Research (LTAR) site, and also hosts sustainability research for the DOE Great Lakes Bioenergy Research Center. The Kellogg Farm, Bird Sanctuary, and Kellogg Conference Center play critical roles in supporting the Station's research, education, and outreach missions.

Located in southwest Michigan, 65 miles southwest of the MSU main campus, KBS has a community of 13 year-round resident faculty, ~25 graduate students, ~20 postdoctoral scholars and academic specialists, and ~100 support staff. In addition to graduate training, KBS has a vibrant summer undergraduate program and a year-round professional development program for K-12 teachers. KBS faculty grant expenditures are ~\$5.5M per year. KBS has the equipment and staff to conduct small- to large-scale field experiments for both KBS labs and a large number of visiting researchers from MSU and other institutions (156 PIs in the last five years). KBS programs are fully integrated into the academic and outreach programs of MSU. All KBS faculty hold academic appointments in departments on the MSU campus, and they participate in campus teaching and departmental and interdepartmental graduate programs. Additional information about KBS can be found at www.kbs.msu.edu. Specific responsibilities: The Director provides visionary leadership for KBS research, education, and outreach programs and is expected to maintain and enhance a creative and productive environment for faculty, students, and both academic and non-academic staff. The Director serves as the principal representative of KBS with authority and responsibility for administrative decisions. The Director reports directly to the Deans of the College of Agriculture and Natural Resources and the College of Natural Science at MSU. This is an administrative leadership position with opportunities and support to continue a research or outreach program and/or engage in teaching. Key responsibilities of the Director are carried out with the support of faculty, specialists, and administrative staff. These responsibilities include:

Providing visionary and strategic leadership for advanc-

ing and articulating the mission of KBS, promoting national and international prominence in ecology, evolution, agriculture, and conservation biology

Overseeing the research, outreach, and education programs at KBS with the Associate Director and coordinating these programs with campus departments (including Earth & Environmental Sciences; Entomology; Fisheries and Wildlife; Forestry; Integrative Biology; Plant Biology; and Plant, Soil, and Microbial Sciences), as well as the Ecology, Evolution, and Behavior program, MSU AgBioResearch, and MSU Extension

Developing and supporting undergraduate research and learning experiences with the KBS Academic Programs Coordinator

Mentoring and evaluating the development of KBS faculty in collaboration with the chairs of their campus departments

Fostering a culture of inclusion, collaboration, creativity and mentorship; working with the KBS DEI Advocate and the KBS Culture and Inclusion Committee to create an environment where diverse faculty, staff, and students can meet their full potential and thrive

Overseeing the large and complex KBS budget and working with the KBS Assistant Director for Finance and Operations to ensure fiscally responsible implementation

Leveraging the work of the Bird Sanctuary, Kellogg Farm and Conference Center to support the KBS mission and outreach activities

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ASN StudentResearchAwards

Apply for the ASN Student Research Awards by March 14, 2025!

The ASN Student Research Awards support research by student members that advances the goals of the society: the conceptual unification of ecology, evolution, or behavior. Each award consists of a \$2,000 check to the candidate. An applicant must must hold a bachelor's

degree or equivalent, must have passed to candidacy in a Ph.D. program or equivalent, and must be at least one year from completing the Ph.D at the time of the award. Projects in all types of research (i.e., laboratory, field, theory) are encouraged. A total of ten proposals will receive awards. Proposals will be judged on originality, strength, and significance of the questions being addressed, prospects for significant results, and the match between the proposed research and the ASN mission. If not already a member of the ASN (student membership is international and US\$20), awardees are expected to join ASN at the time of the award.

Applications include four elements: (1) a two-page pro-

posal describing the research project for which support is requested; (2) a budget with justification (one page); (3) a short curriculum vitae (two pages); (4) a short reference questionnaire filled out by their academic supervisor. For detailed instructions, or to apply, please click here!

Sonal Singhal Associate Professor

ssinghal@csudh.edu www.singhallab.org Sonal Singhal
<ssinghal@csudh.edu>

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Award Excellence Scientific Collections Research

Dear EvolDir community,

I'm pleased to announce the call for the 6th edition of the CETAF E-Score Award, which is open until March 30th 2025.

The E-SCORE Award - Excellence in Scientific Collections-based Research - is a celebration of the new generation of scientists who have shown dedication to the use of collections that help document, describe and understand life on Earth and the processes that have shaped it. The award also celebrates the United Nations-endorsed International Day for Biological Diversity, which falls annually on the 22nd of May to commemorate the 1992 adoption of the Convention on Biological Diversity.

This year, the award is exclusively dedicated to PhD students (no early career researchers).

More information and access to the application portal can be found here: <https://cetaf.org/template-activities/cetaf-initiatives/escore/> Best wishes Eva

Dr. Eva Häffner Wissenschaftliche Koordinatorin
Botanischer Garten Berlin

Telefon: +49 30 838 59964 Mobil: +49 176 183 850 63
e.haeffner@bo.berlin

Freie Universität Berlin ZE Botanischer Garten und
Botanisches Museum Berlin Köpenicker Straße 6-8
14195 Berlin

#BoBerlin Internationales Wissenszentrum der Botanik
"Häffner, Eva" <E.Haeffner@bo.berlin>

(to subscribe/unsubscribe the EvolDir send mail to

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

Biology letters

Biology Letters Early Career Researcher competition opened for entries with a deadline of 30 April 2025 - further details can be found at <https://royalsociety.org/journals/authors/early-career-researchers/bl-ecr-paper-prize>. In 2022, Biology Letters launched the Early Career Researcher Competition to highlight the best research papers published in the journal by early career researchers (ECRs). We are delighted to announce that the 2025 competition is now open until Wednesday 30 April. The overall winner will receive £1000 and two runners-up will receive £500 each (or currency equivalent). We hope the prizes are particularly helpful for funding new research and/or attending conferences. Please see our terms and conditions before entering or contact the editorial office with your questions.

You don't have to be an ECR to submit to the journal! Take a look at our Information for Authors page for more information on what we publish and how you can get involved.

Felicity Davie Royal Society Publishing

T +44 20 7451 2647

The Royal Society 6-9 Carlton House Terrace London
SW1Y 5AG

<http://royalsocietypublishing.org> Registered Charity
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Call Papers Dispersal Evolutionary Ecology

Dear all,

We would like to announce that the deadline for papers to be included in a Special Issue of Evolutionary Ecology, "Dispersal in Small Organisms" has been extended to May 1, 2025. This Special Issue will appear on the 50th Anniversary of the publication of D. O. Wolfenbarger's "Factors Affecting Dispersal Distances of Small Organisms" and will cover dispersal in viruses, bacteria, plants, fungus, and insects. This solicitation calls for

papers on behavior, ecology, genetics, and evolution that deal with factors promoting and restricting dispersal. The effects on dispersal for landscape connectivity, distributions, invasions, host diversity, and speciation are of particular interest. Publication is expected in late 2025, but accepted articles will be made available Online First on an ongoing basis. Pre-submission enquiries are welcome.

Find more information here:

<https://link.springer.com/journal/10682/updates/-26984662> Best,

Frank and Aurélie

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

Aurélie Coulon Muséum National d'Histoire Naturelle Centre d'Ecologie et des Sciences de la Conservation (CESCO), Paris, France and Centre d'Ecologie Fonctionnelle et Evolutive (CEFE), Montpellier, France
aurelie.coulon@mnhn.fr

ESEB UnderRepresented ECR Achievement Award Deadline Jan 31

ESEB Under-represented ECR Achievement Award

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

DEADLINE: 31 January 2025

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

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DEADLINE: 31 January 2025 ELIGIBILITY

1. The award is open to PhD students, postdoctoral scientists or non-tenure-track research fellows who do not hold a permanent academic position and have achieved their research while facing difficult circumstances. Note that researchers based in any country are eligible, irrespective of GDP status, and not just in Europe.
2. Applications may be submitted by the person benefiting from the grant, or by a colleague/supervisor when a letter is included from the nominee approving their nomination.
3. The person submitting the application must be an ESEB member, or become a member immediately after receiving the award (to become a member of ESEB, please visit our membership page <<https://eseb.org/society/eseb-membership/>>).
4. Applicants who have previously received this award are not eligible.
5. The award stipend (2000 euro) can be spent at the discretion of the nominee. Nominees will be required to write a short summary of their achievement to be highlighted on the ESEB Equal Opportunities website and ESEB newsletter.
6. ESEB understands that some applicants are concerned about personal and professional risks of exposure. In such cases, the EO board will work with the recipient of the award to increase visibility of underrepresented backgrounds in Evolutionary Biology while also protecting the individual's safety.

APPLICATION PROCEDURE Applications should be sent as a single PDF file to Ute Friedrich at the ESEB office, office@eseb.org with the subject line: 2025 EUEA Award.

Applications should include: 1. A cover letter with the nominee's name, current status and institution, PhD start date, duration and reason for any career

breaks, and a signed statement on what the nominee has achieved and why it is considered the nominee achieved it under difficult circumstances. The difficult circumstances are primarily, but not solely, disabilities, social/cultural/political discrimination, refugee status, single parenting or other caring responsibilities. The letter should not exceed 2 pages. 2. A short CV of the nominee (1-2 pages). 3. Proof of the nominee's achievement: this can be for instance a PhD diploma, a publication, or an outreach initiative. 4. A letter of support from the nominee's host institution or a colleague.

Applications should arrive no later than Friday, 31 January 2025. Please take care to limit the size of attachments (total < 10 MB) in any one email.

Applications will be evaluated by the Equal Opportunity Committee chaired by Anne Charmantier, and awardees will be informed around the end of February. The award recipients are encouraged to attend the next ESEB congress in Barcelona, Spain (August 17-22, 2025), where they will be invited to speak about their work and/or equal representation in the field of evolution. In cases where professional exposure poses risks to an awardee's safety and well-being, the EO committee will collaborate with the award recipient to identify alternative actions that promote visibility for underrepresented groups while ensuring their protection. ESEB will contribute to the travel expenses and registration fees.

Previous awardees can be seen here: <https://eseb.org/-prizes-funding/equal-opportunities-initiative/eseb-under-represented-ecr-achievement-award/> Camila Beraldo, EO committee member On behalf of the ESEB Equal Opportunities Committee

“Souza Beraldo, Camila” <camila.beraldo@helsinki.fi>
(to subscribe/unsubscribe the EvoDir send mail to golding@mcmaster.ca)

ICZN Commissioner Election Registration

Dear Zoologist,

On 22 January 2025, the International Commission on Zoological Nomenclature sent out an announcement for its Election of Commissioners to be held over a 24-hour period on 17 February 2025. The announcement can be found on the ICZN homepage (<https://www.iczn.org/>).

Registration to participate in the election is now open. To self-register, you must fill out the registration form here (registration form). Please note that only those who completely fill out the form will be allowed to vote. Self-registration will close on 12 February 2025.

Sincerely

ICZN Secretariat

Dr. Alex Figueroa

Research Fellow/Executive Secretary

International Commission on Zoological Nomenclature
(ICZN) Secretariat

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JMolEvol Zuckerkandl Prize

This year marks the sixth straight year that the reinstated Zuckerkandl Prize has been awarded. This is an award in honor of Founding Editor Emile Zuckerkandl for the top paper published in the Journal of Molecular Evolution to appear in a print issue during the calendar year, as judged by a committee. The award committee

consisted of Ugo Bastolla, Kerry Geiler-Samerotte, and Maeva Perez this year.

The panel focused in on four finalists and struggled to choose among these excellent papers to decide upon a prize winner. The four finalist papers spanned the gamut of molecular evolution from sex chromosome evolution to enzyme evolution, to methods focused on mutational scans of membrane proteins and to ancestral sequence reconstruction.

We are pleased to announce that the 2024 winner is “Stochastic Epigenetic Modification and Evolution of Sex Determination in Vertebrates” by Braciamore et al. (2024). Throughout vertebrate evolution, there have been multiple independent transitions from environmental to genetic sex determination, with many proposed mechanisms for these transitions involving antagonistic selection. Through a modelling approach that does not rely on deterministic selection, this paper proposes a mechanism whereby the stochastic epigenetic silencing of a sex determination gene can influence the dynamics of fixation of silencing mutations within the locus. The authors show that this process maintains an equilibrated sex-ratio and is sufficient to enable the evolution of heteromorphic sex chromosomes from a homomorphic state. This extends conceptually to a general mechanism through which epigenetic modifications can influence genetic evolution.

The three runner up papers are “Scaling up Functional Analyses of the G Protein-Coupled Receptor Rhodopsin” by Scott et al. (2024), “Frustration can Limit the Adaptation of Promiscuous Enzymes Through Gene Duplication and Specialisation” by Schmutzer et al. (2024), and “Extant Sequence Reconstruction: The Accuracy of Ancestral Sequence Reconstructions Evaluated by Extant Sequence Cross-Validation” by Sennett and Theobald (2024).

Scott et al. (2024) and Chen et al. (2024) from the same research group developed methods including a fluorescence assay to characterize the effects of mutations on the function of membrane proteins. A clever experimental design that tied membrane protein function to downstream expression of a fluorescent protein enabled the scale up in exploration of sequence space. They applied the method to rhodopsin receptors, belonging to the large family of G-protein coupled receptors, scaling up the exploration of their sequence space and extending some general results on mutational effects already known for globular proteins.

Schmutzer et al. (2024) presents a theory of enzyme evolution based on the tradeoffs between different reactions catalyzed by the same promiscuous enzyme, which suggests that frustration that may result from reactions

that cannot be simultaneously selected may be an important factor in the evolution of enzyme families, including through gene duplication and sub-functionalization. Their theory predicts the observed bimodal distribution of promiscuous enzymes with peaks of specialist and of generalist enzymes.

Sennett and Theobald (2024) provide a first solution to a key limitation of ancestral sequence reconstruction; how to assess the accuracy of the reconstructions? Their approach proposes to cross-validate ancestral sequence reconstruction methods by predicting extant sequences according to an evolutionary model. The paper establishes an important role for model selection in ancestral sequence reconstruction, as different models yield varying performance levels.

The Journal of Molecular Evolution is proud to congratulate the authors of all of these works and the winners of the award, which includes a US\$250 cash prize to the first author of the winning paper. The journal is proud to have published these papers in 2024 and looks forward to receiving more outstanding submissions in 2025.

Braciamore, S., Rodin, A.S. & Riggs, A.D. Stochastic Epigenetic Modification and Evolution of Sex Determination in Vertebrates. *J Mol Evol* 92, 861-873 (2024). <https://doi.org/10.1007/s00239-024-10213-9>
Chen, S.K., Liu, J., Van Nynatten, A. et al. Sampling Strategies for Experimentally Mapping Molecular Fitness Landscapes Using High-Throughput Methods. *J Mol Evol* 92, 402-414 (2024). <https://doi.org/10.1007/s00239-024-10179-8>
Schmutzer, M., Dasmeh, P. & Wagner, A. Frustration can Limit the Adaptation of Promiscuous Enzymes Through Gene Duplication and Specialisation. *J Mol Evol* 92, 104-120 (2024). <https://doi.org/10.1007/s00239-024-10161-4>
Scott, B.M., Chen, S.K., Van Nynatten, A. et al. Scaling up Functional

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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>

LouisianaStateU
PostbaccTrainingProgram Mar16

Applications for the Louisiana Graduate Network in Applied Evolution (LAGNiAppE) are now open!

The year-long program, funded by NSF and offering paid opportunities, enables scholars to conduct original research under the guidance of two faculty members from LSU and partner universities. Participants will engage in professional development activities and acquire sought-after technical skills essential for a wide range of STEM careers. LAGNiAppE actively encourages applicants without extensive research backgrounds, especially those from underrepresented communities.

The application deadline for our upcoming cohort is March 16, 2025. For more details and to apply, please visit our website < <https://www.lsu.edu/science/biosci/-programs/postbacc-research/index.php> >.

We would greatly appreciate your help in sharing this opportunity with your network to ensure it reaches potential candidates. Attached, you'll find a program flier suitable for display at your institution and a PowerPoint slide that can be shared with students in advanced biology courses.

If you have any questions or need further information, please don't hesitate to reach out to evo_lagniappe@lsu.edu

LAGNiAppE Network <evo_lagniappe@lsu.edu>

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but don't have specimens, please ask other colleagues who do have material to get involved. We select finalists based on several factors, including general coolness, the scientific need, our wish to support groups (of people and molluscs) that do not have access to genome sequencing.

https://docs.google.com/forms/d/e/1FAIpQLSdSI5SQV4kYwOGArJyAmcH5SXdnUDUJ8sW0NVqi90aEF/viewform?usp=sf_link Nominations are open through 22 January!

Happy new year,

Julia Sigwart & Carola Greve

Prof Dr Julia Sigwart Head of Section, Malacology Senckenberg Research Institute and Museum

@sigwarta | bit.ly/SMFMalacology

You could... - Watch how species get named! <https://www.youtube.com/watch?v=yn7kUDRVcVM> - Download my book! bit.ly/whatspeciesmean - Join the Molluscalist email listserve www.listserv.dfn.de/sympa/-subscribe/molluscalist - Join the Senckenberg Ocean Species Alliance sosa.senckenberg.de

Julia Sigwart <j.sigwart@qub.ac.uk>

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MolluscOfTheYear NominationDeadline Jan22

Dear all

We are delighted to announce we will be continuing the International Mollusc of the Year competition sponsored by Senckenberg in 2025! Nominate your favourite unappreciated mollusc now

This is how it works YOU nominate any mollusc species for the prize, as long as you can (help to) arrange specimens suitable for genome sequencing. Our panel selects the top 5 species from the nominated molluscs The final winner is selected by a public online vote – and as a prize for the winning mollusc, we sequence its complete genome

The species can be the subject of your research, or just a mollusc that you happen to know and love. But in order to be eligible for the final prize, we do need specimens. Although this is a competition, we love it when teams work together, so if you know a deserving species

NSF REU Internship InsectBehavior

NSF Research Experiences for Undergraduates (REU) Positions Available in Insect Behavior & Biomechanics

Location: University of Florida, Gainesville, FL Program Dates: Summer 2025. Ten weeks of work between May and early August, with some flexibility in start/end dates. Contact: Dr. Salerno, salernoc@ufl.edu. In subject line include “REU application 2025 (Evol-dir)”

Deadline to Apply: February 14th, 2025

Stipend: \$600/week for 10 weeks plus a contribution towards living expenses of \$150/week.

We are interested in individuals at any stage of their undergraduate career, however, REU students must be enrolled as undergraduates through at least August 2025 (i.e., cannot be graduating in May 2025) and be US citizens or full-time residents. Students from underrepresented groups in science are strongly encouraged to apply.

REU students will work directly with Drs. Christina Salerno, Noraly van Meer, and Janice Yan under the guidance of Phil Hahn (University of Florida) and Christine Miller (University of Cambridge, UK) in the summer of 2025 to: (1) receive training in behavioral ecology research, (2) receive guidance to develop an independent project within the context of ongoing NSF funded research. We are a supportive group of researchers united by our enthusiasm for behavioral ecology. We work hard and have fun!

REU students will work onsite in Gainesville, Florida where they will interact with a diverse group of researchers to gain experience with experimental design, field work, data collection, data analysis, and scientific writing and presentation. Additionally, with guidance from their mentors, students will develop an independent project and contribute to larger project goals to further hone their research skills. These activities potentially include conducting field work to collect host plants, insect rearing, insect behavioral trials, insect photography/digital measurements.

Applicants should be hard-working, inquisitive, dedicated, and responsible, with a keen interest in animal behavior. This is an excellent opportunity for students interested in pursuing graduate school or careers in science, particularly in ecology and evolutionary biology.

Please send the following documents to Dr. Christina Salerno at salernoc@ufl.edu with the subject line "REU Application 2025 (Evol-dir)": 1) a cover letter (1 page max) describing your research experience and general interests in animal behavior 2) resume or CV including relevant coursework, and 3) list of three references. Please combine all documents into one pdf and include your last name in the file name. We will begin reviewing applications February 14th, so please consider applying soon.

www.millerlab.net <https://entnemdept.ufl.edu/people-directory/phil-hahn/> "Miller, Christine W." <cwmiller@ufl.edu>

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OklahomaStateU PostbacResearchProgram

Dear EvolDir members,

I am pleased to announce that the Oklahoma Network-Research and Mentoring for Post-Baccalaureates (ON-RaMP) applications are open! This includes opportunities to work with multiple faculty that specialize in Evolutionary Biology

This program offers mentored research experiences for recent graduates in the biological sciences and related careers. This is a one-year fully paid position, funded by NSF, focused on exploring anthropogenic impacts upon different biological systems.

The aim of our program is to provide research experiences in biology to individuals with a bachelors degree but who have limited previous research experience. Please pass on this opportunity to any students who may potentially be interested (e.g. your classes). This is a well-funded program with generous support for research expenses and travel, along with the opportunity to be mentored on an independent research project.

Link to apply <https://etap.nsf.gov/award/475/-opportunity/10302> If you want to learn more about this opportunity, please visit <https://cas.okstate.edu/-onramp/> The deadline for the applications is February 28, 2025, at 11:59 pm EST.

Please feel free to contact our program coordinator Celeste Luna for more information: celesteluna@okstate.edu.

Best wishes,

Michael Reichert Associate Professor Department of Integrative Biology Oklahoma State University 524 Life Sciences West Stillwater, OK 74078 USA <https://reichertlab.com/> "Reichert, Michael" <michael.reichert@okstate.edu>

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SSE Evolution Education Award Deadline Feb 1

The Society for the Study of Evolution (SSE) Education and Outreach Committee is pleased to announce the call for applications for the 2025 T.H. Huxley Award, named in honor of Darwin's very public supporter: <https://shorturl.at/dziho> This award recognizes and promotes the development of high-quality evolution education resources. If you have an interesting project or educational activity to share, consider applying for this award. You must be an SSE member to apply. Graduate students and postdoctoral fellows are encouraged to apply.

This award provides funding for the recipient to present an evolution education resource at an education-focused session or conference approved by the Huxley Award Committee (e.g., education session at the annual Evolution meeting or the annual National Association of Biology Teachers conference).

Applications are due February 3, 2025.

Learn more and apply here: <https://shorturl.at/dziho> *Kati Moore*she/her *Communications Manager* *Society for the Study of Evolution* communications@evolutionsociety.org www.evolutionsociety.org SSE Communications <communications@evolutionsociety.org>

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SSE Grants AmerInstBiolSciences visits

The Society for the Study of Evolution (SSE) Public Policy Committee invites SSE members to apply for funds to attend the American Institute of Biological Sciences (AIBS) 2025 Congressional Visits Day.

The event will take place in Washington, DC and includes a free half-day training session on April 29 and meetings with lawmakers on April 30. There is also the option to also attend the Communications Boot Camp for Scientists on April 28-29.

SSE members at all career stages who are interested in communicating the importance of federal investments in scientific research and education to lawmakers are encouraged to apply. Funding can be used to cover the cost of the Communications Boot Camp and contribute toward travel and lodging.

SSE members interested in using these funds for other advocacy opportunities are also welcome to apply. Email policy@evolutionsociety.org for more information.

Learn more about the AIBS Congressional Visits Day here: <https://www.aibs.org/news/2024/241213-congressional-visits-day#subheader> Apply for SSE funding here: <https://docs.google.com/forms/d/e/1FAIpQLScFE5TRpIJUD3dXq6TmQLAODHzBYJuR1wR4c9xqCIr6Rf/viewform?usp=header> Deadline: February 17, 2025

*Kati Moore*she/her *Communications Manager* *Society for the Study of Evolution* communications@evolutionsociety.org www.evolutionsociety.org SSE Communications <communications@evolutionsociety.org>

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Survey Research Conceptualization

You are invited to participate in a study on how ecologists and evolutionary biologists think about their research with respect to the patterns and mechanisms they study. Please consider participating by completing the survey linked below, which consists of 7 primary questions (plus some optional ones) and takes approximately 5 minutes to complete.

<https://z.umn.edu/personasquantified> If you have any questions or concerns about your participation in this study, please contact Allison Shaw (ashaw@umn.edu<<mailto:ashaw@umn.edu>>) or Maria Servedio (servedio@email.unc.edu<<mailto:servedio@email.unc.edu>>).

Thank you for your consideration! Allison Shaw and Maria Servedio

UConnecticut Research Opportunity Genomic Novelty

I am thrilled to share information about the UConn RaMP (Research and Mentoring for Postbaccalaureates) Program on Genomic Novelty; a year-long, paid NSF-funded postbaccalaureate research training program based at the University of Connecticut. The purpose of the program is to offer a mentored research experience and professional development opportunities to individuals historically underrepresented in STEM (including underrepresented ethnic groups, people with disabilities, veterans, and first-generation college students) or those who did not have sufficient access to research during their undergraduate careers (college graduates of lower-resourced institutions). RaMP provides an intensive research experience, with salaries comparable to an entry level job.

Scholars will:

* Conduct original biological research on the theme of genomic novelty under the mentorship a faculty members and graduate student mentor * Participate in profes-

sional development activities, attend conferences and networking events * Expand high demand technical skills in preparation for a diverse array of STEM careers and/or graduate school

Program Overview: Where: UConn, Storrs Campus
When: Program runs from August 2025-July 2026

No research experience required!

Our website and application information can be found here: <https://genome-postbac.biology.clas.uconn.edu/>. Applicants are encouraged to visit the website to learn more about the program and review potential research projects/mentors. The application deadline for the 2025 cohort is February 21st. Please feel free to share this opportunity with others in your network.

If you have any further questions, please feel free to contact me (teisha.king@uconn.edu).

Best, Teisha King

Teisha King, PhD RaMP Educational Program Coordinator University of Connecticut Dept of Ecology and Evolutionary Biology Applications for the 2024 cohort are open!!! Apply < <https://etap.nsf.gov/award/617/-opportunity/3466> > today RaMP Website: <https://genome-postbac.biology.clas.uconn.edu/> “King, Teisha” <teisha.king@uconn.edu>

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ArizonaStateU PrimateEvolutionaryGenomics

Postdoctoral position in primate evolutionary genomics at Arizona State University

The Jensen and Pfeifer Labs at Arizona State University are searching for a joint postdoctoral researcher to study the evolutionary genomics of non-human primates, supported by NIH MIRA and NSF CAREER awards.

Research in the Pfeifer Lab is centered around mutation and recombination rate inference (<http://spfeiferlab.org/>), and in the Jensen Lab around demographic and selection inference (<http://jjensenlab.org/>). This position will combine the development of novel population-level genomic datasets with these computational inference approaches. As such, researchers with a background or interest in primate genomics generally, or in the study of any of these individual evolutionary processes specifically, are particularly encouraged to apply.

Research topics are open to discussion and mutual interest, though should align with the general theme. The start date is flexible, and the beginning salary will be on NIH-scale (~\$61,000 per year).

Both labs are based in the School of Life Sciences and are associated with the Center for Evolution and Medicine (<https://evmed.asu.edu/>) and the Center for Mechanisms of Evolution (<https://biodesign.asu.edu/mechanisms-of-evolution/>), which further provides for a strong intellectual environment including frequent seminars and journal clubs (<http://asupopgen.org/>).

Interested applicants should contact Jeff Jensen <jeffrey.d.jensen@asu.edu> and Susanne Pfeifer <susanne@spfeiferlab.org> for informal inquires, and/or to send an application (including a CV, names of 3 references, and a cover letter describing your interests and fit for the position). The evaluation of

applications will begin January 25, and will continue until a suitable candidate has been found.

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

Susanne Pfeifer <susanne@spfeiferlab.org>

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Barcelona Bioinformatics

The Evolutionary and Functional Genomics Lab at the Institut Botànic de Barcelona (CSIC) is looking for a bioinformatics postdoctoral researcher. The postdoctoral researcher will be part of a team carrying out a research project that aims at understanding the genomic basis of adaptation to natural environments. The selected candidate will analyze -omics data to discover and annotate transposable element insertions and to understand what determines their abundance, diversity, activity, and functional effects on gene expression and transcriptome diversification across species. Genomic sequences are already available and more -omics data sets will be generated within the project.

Desired Skills and Expertise

Experience with computing programming Experience with modeling, statistical analysis and/or machine learning. Experience with high-performance computing or use of clusters (SLURM). Knowledge on evolutionary processes is desirable. Knowledge on transposable element biology is desirable. Strong organizational skills. Good scientific writing and oral communication skills. Ability to work as part of a team

Contract duration and benefits 2 year contract. Full time: 37,5 hours/week. Position available immediately, starting date is negotiable. The candidate will join a research team that has expertise both in experimental

and bioinformatics methodologies (www.gonzalezlab.eu). Several projects are currently ongoing in the laboratory which allows for collaborative opportunities. The Evolutionary and Functional Genomics lab also offers extensive networking opportunities as we are co-leaders of the European Drosophila Population Genomics Consortium (<https://droseu.net>) that brings together 74 research labs across 28 countries. We are also co-leading the CSIC Genomics Hub (<https://conexion-genoma.csic.es>) that brings together 156 research groups based in Spain. We are also members of the Spanish excellence network in Adaptation Genomics (<https://adaptnet.es>), the CSIC LifeHub network (<https://lifehub.csic.es>), and the TE hub initiative (<http://tehub.org/>).

Required Information and Contact Send your CV and a brief letter of motivation explaining qualifications and interest in the position to Dr. Josefa González at josefa.gonzalez@csic.es. Please include “Bioinformatics postdoc position” in your e-mail subject. Deadline: 28 February 2025.

Josefa González | CSIC Research Scientist Institut Botànic de Barcelona, IBB, CSIC-CMCNB Passeig del Migdia s/n. 08038, Barcelona. Spain. www.gonzalezlab.eu |

@GonzalezLab.BCN

Co-organizer of the European Drosophila Population Genomics Consortium (DrosEU) Coordinator of CSIC GENOME Hub Vice President of the European Society for Evolutionary Biology Associate Editor for GBE Science Outreach La Ciència Al Teu Món

melanogaster.eu

Most recent preprints/publications: Gene-TE chimeras Genome Res | TEs context dependent effects Mol Biol Evol | TE library curation Genome Res | TE & Epigenetics bioRxiv

“GONZALEZ PEREZ, JOSEFA”
<josefa.gonzalez@csic.es>

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Bolzano Italy

InsectPhytoplasmaGenomics

A Postdoctoral position is offered at the Free University of Bozen-Bolzano (Italy) in the lab of Hannes Schuler. The position is funded for three years and aims to study

different factors that are influencing the transmission of phytoplasmas by psyllid species.

Phytoplasmas are bacterial pathogens that cause hundreds of plant diseases affecting many important vegetables and fruit crops, thus being responsible for high yield losses worldwide. These pathogens reside in the plant’s phloem and transmission among plants is mainly mediated by phloem-sucking insects. Apple proliferation is a disease caused by the phytoplasma ‘Candidatus *Phytoplasma mali*’. While several phloem feeders occur on apple, only a small number of species are able to acquire and transmit phytoplasmas. We aim to unravel different phytoplasma transmission pathways in different insect vectors using a population genetic approach.

We are looking for an enthusiastic candidate with a strong background in next-generation sequencing and bioinformatic analyses. The candidate will be responsible to investigate factors affecting transmission efficiency of *Phytoplasma mali* by the two main vectors *Cacopsylla picta* and *Cacopsylla melanoneura* by performing population genetic analyses of the insects and the phytoplasma.

The project is funded by a joint project of the Province of Bolzano and the Fonds National de la Recherche FNR, Luxembourg and is in close collaboration with Michael Eickermann (Luxembourg Institute of Science & Technology) and Wolfgang Jarausch (RLP Agroscience, Germany). The position will be based at the Free University of Bozen-Bolzano in Northern Italy.

The Free University of Bozen-Bolzano is located in one of the most fascinating European regions, at the crossroads between the German-speaking and Italian cultures. The Schuler lab is member of the Competence Centre for Plant Health, a joint institution which consists of several research groups in the field of Biology, Agricultural Sciences and Engineering. We are a young and dynamic research group studying various aspects of insect-microbe interactions in a collaborative atmosphere <http://hschuler.people.unibz.it> We are looking for an enthusiastic candidate with a strong background in insect ecology and evolution. Competences with molecular genetic methods, next generation sequencing and bioinformatics as well as experience with ecological studies, collection and handling of insects are desired.

General requirements for the position: PhD degree in Agricultural Sciences, Agricultural Biotechnology, Ecology and Evolution with a multidisciplinary profile. The candidate should have excellent communication skills and should be fluent in English.

The project is expected to start in April 2025, but the starting date is negotiable. Application deadline is

08.01.2025 (noon)

For informal inquiries, and for questions about the hiring process, please contact Hannes Schuler hannes.schuler@unibz.it

All documents for the application procedure can be found here: <https://www.unibz.it/de/home/position-calls/positions-for-academic-staff/7504-allgemeine-und-angewandte-entomologie-prof-schuler-hannes-pos-1?group=> Prof. Hannes Schuler Competence Centre for Plant Health Faculty of Agricultural, Environmental and Food Sciences Free University of Bozen-Bolzano Universitätsplatz 5 I-39100 Bozen-Bolzano Tel: +39 0471 017648 <http://hschuler.people.unibz.it> Schuler Hannes <Hannes.Schuler@unibz.it>

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BrownU VirtualPostdocPreviews

The Office of University Postdoctoral Affairs (OUPA) is excited to announce a Virtual Postdoc Preview for individuals interested in learning more about postdoctoral training at Brown University. This event is scheduled for Wednesday, March 12, 2025, from noon to 2:00 p.m. Eastern Time via Zoom.

This event is aimed at advanced PhD students and current postdoctoral scholars within 1-2 years of doctoral degree completion.

The agenda will include:

Noon EST - Overview by the OUPA: An introduction to research and teaching excellence at Brown, the postdoc training structure, resources available to postdocs, strategies for identifying fellowship opportunities, the availability of training grant slots, open positions, and a general overview of the region.

12:45 p.m. EST - Postdoc Panel: Current postdoctoral appointees will provide an overview of the Brown Postdoc Council's mission and contributions and share their perspectives about the postdoc experience at Brown and life in the Providence area.

1:15 p.m. EST - Faculty Panel: Representatives overseeing postdoc programs and fellowships and those involved in training postdocs will address topics ranging from identifying a good fit for a postdoc mentor to answering specific inquiries about Brown's research and training environment. Panelists include Rose McDermott, Chris

Rose, Robert Miranda, and Diane Lipscombe.

1:45 p.m. EST - Q&A with Associate Dean Audra Van Wart, Director of OUPA.

More information available at: <https://biomeddeansoffice.cmail19.com/t/r-l-theyukdtdwktydlt-y/> Click here to register: <https://biomeddeansoffice.cmail19.com/t/r-l-theyukdtdwktydlt-t/> If you have any questions, please contact OUPA by emailing postdoc-affairs@brown.edu.

“Weinreich, Daniel” <daniel.weinreich@brown.edu>

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Czechia BCCAS FreshwaterBacteriaGenomics

OPEN POSTDOC POSITION at the Laboratory of Microbial Cultivation and Ecogenomics, Department of Aquatic Microbial Ecology, Institute of Hydrobiology, Biology Centre CAS, Aeské BudĀjovice, Czech Republic.

A postdoc position is open to study the mechanisms of growth and survival of oligotrophic freshwater bacteria by using (meta-)transcriptomics, (meta-) genomics, and culture experiments.

Background A recently granted project by the Czech Science Foundation aims to study the mechanisms of growth and survival of freshwater oligotrophs (MEGASO, GACR grant 25-15813S). Freshwater lakes are numerically dominated by oligotrophic bacteria that are adapted to low nutrient conditions, however, the reasons for their success are still not well understood. We plan to study the mechanisms of growth and survival of oligotrophs by comparing them to fast-growing copiotrophs. We will systematically compare strains from three oligotrophic model genera (Fonsibacter, Planktophila, Methylopumilus) to meso- and copiotrophs from our large culture collection based on genomic and growth characteristics. Lab experiments combined with seasonal and diurnal metatranscriptomics will identify growth limitations and in situ gene expression to pinpoint fundamental reasons for the overall success of oligotrophs in lakes. We will further investigate a widespread strategy for harvesting light energy, rhodopsin-based photoheterotrophy, by monitoring seasonal and diurnal changes, experiments, and co-expression analyses to identify potential benefits. Fi-

nally, we address one of the main mortality factors of aquatic microbes in experiments aiming to resolve the long-standing conundrum if oligotrophs are less affected from grazing by protists than copiotrophs.

Requirements Applicants should hold a PhD in Biological Sciences (e.g., Limnology, Microbiology, Ecology) and must be strongly motivated to continue their work in an ecogenomics laboratory. Prior experience in one or more of the following areas is favorably considered: - (meta-)genomic and (meta-)transcriptomic analyses - shell/perl/python/R programming - experience in working with bacterial cultures (maintenance, experiments) Candidates must be proficient in English. Please submit a professional CV, a brief statement of your research interests and work performed (max. 1 page), a list of publications and the names and contact information of two-three professional references. Preferably combine all this information into a single PDF file and send via email with the subject 'position' to michaelasalcher@gmail.com. The position is available from July 2025 and will remain open until a suitable candidate is found. The position is funded till December 2027 with a possibility of prolongation.

Infrastructure and Benefits Position includes standard health insurance and social security and five weeks of holiday yearly. Postdocs have access to accommodation in dormitories at the campus shared by the Biology Centre and the University. Czech courses are available for foreign staff and students to reach a basic level of proficiency in everyday situations. The Biology Centre provides assistance in the visa application process for foreigners.

About the employer The Department of Aquatic Microbial is an internationally recognized high-class institution for studying freshwater microbes. The Institute of Hydrobiology is the principal institution in the Czech Republic devoted to complex freshwater research of man-made reservoirs and natural lakes and is one of the institutes associated in the Biology Centre of the Czech Academy of Sciences in Āeské BudĀjovice. The Laboratory of Microbial Cultivation and Ecogenomics has a large culture collection of environmentally relevant freshwater microbes (>7000 axenic strains, >500 genome-sequenced) and the team is experienced in in-situ and laboratory experiments and (meta-)genomics.

About the location Ceske Budejovice is a medium-sized town ca. 150 km south of Prague with 100,000 inhabitants, a relaxed atmosphere, and a growing expat community at the Biology Centre and the University. Both the town and the surrounding countryside provide numerous opportunities for research and leisure activities. Living costs are low by international standards.

Contact Please don't hesitate to contact me for further information about the position: michaelasalcher@gmail.com

Dr. Michaela Salcher Laboratory of Microbial Cultivation and Ecogenomics Department of Aquatic Microbial Ecology Institute of Hydrobiology Biology Centre CAS, v.v.i. Na Sadkach 702/7 37005 Āeské BudĀjovice, Czech Republic

Links Biology Centre CAS: <https://www.bc.cas.cz/en>
 Institute of Hydrobiology: <https://www.hbu.cas.cz/en/>
 Department of Aquatic Microbial Ecology: <https://www.hbu.cas.cz/en/structure/ame/>

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FieldMuseum Chicago SmallMammalFunctionalMorphology

Post Doc Research Scientist Department: Negaunee Integrative Research Ctr, Field Museum of Natural History Location: Chicago, IL

Our Mission: Since the 1893 World Columbian Exposition, our organization has aimed to connect people to the natural environment and human history.

Join our team and enjoy a benefits package that truly supports your well-being and lifestyle:

Comprehensive Health Coverage: Including medical, dental, vision plans, and even pet insurance. **Financial Security:** Life and disability benefits plus a 403(b) savings plan to help you plan for the future. **Work-Life Balance:** Generous paid time off, paid sick leave, and paid holidays to ensure you have time to recharge and spend with loved ones. **Exclusive Perks:** Enjoy great employee discounts and complimentary general admission to participating cultural institutions.

We're dedicated to enhancing your life both at work and beyond!

We are accepting applications for a 1.5 year postdoctoral fellowship at the Field Museum of Natural History, investigating the functional morphology and evolution of the vertebral columns of mammals in the clade Eulipotyphla (shrews, moles, hedgehogs, and solenodons).

Our postdoc will join a collaborative NSF-funded research project (IOS-2223964/5, https://www.nsf.gov/awardsearch/showAward?AWD_ID=2223964), and will conduct research concerning the shape, function, and evolution of the lumbar spine at small body sizes, using eulipotyphlans as a model system. The selected candidate will report to Drs. Stephanie Smith and Kenneth Angielczyk (Field Museum), and will have the opportunity to collaborate with Dr. Tristan Stayton, the PI of a collaborative grant at Bucknell University. The postdoc will be allowed to develop their own research within the scope of the funded project.

Resources available for this position include: access to the Field Museum modern and fossil mammal collections, including a huge variety of eulipotyphlan skeletal and fluid-preserved specimens; a library of approximately 150 existing microCT scans of eulipotyphlan lumbar vertebrae executed for the project; an in-house CT scanning facility at the Field Museum for scanning additional relevant specimens; and high-powered 3D imaging workstations with scan segmentation and finite element modeling software. In addition to conducting research, this postdoc will be expected to participate in broader impacts activities, including but not limited to those described in the grant. These include: development of K-12 educational tools related to the grant for dissemination through the Field Museums Harris Learning Collection Experience Boxes; and development of an in-gallery scavenger hunt for tiny animals in Field Museum galleries, aimed at engaging visitors with the biomechanical adaptations for being small.

WHO SHOULD APPLY: Candidates must hold a Ph.D. by the start of the position; soon-to-graduate Ph.D. candidates are encouraged to apply. Applicants should have experience with multivariate statistics and R programming. Further, applicants should be interested in and have experience with some combination of: phenotypic evolution, skeletal biology, functional morphology, biomechanics, mammalogy, geometric morphometrics, CT imaging, body size evolution, and/or 3D data processing and analysis.

OTHER LOGISTIC DETAILS: Start date is negotiable but should be early 2025. Position is eligible for fringe benefits, and will remain open until filled.

HOW TO APPLY: Please email Stephanie Smith (sm-smith@fieldmuseum.org) with a CV (including publication list), names and contact information of three references, and a cover letter including the following:

A description of past research experience relevant to this position
A short description of one or more projects that you would like to carry out that fit into the scope of the funded project
A description of relevant experience

with scientific outreach

Pay: \$48,000/Annually

The Field Museum is an equal-opportunity employer. We are committed to providing a workplace free from discrimination, embracing diversity, and fostering mutual respect. We value the unique perspectives each team member brings, which empowers our ability to innovate and overcome challenges.

At the Field Museum, we are dedicated to making our career website and recruitment process accessible to everyone. If you encounter any difficulty when using or accessing our online application, or if you need a reasonable accommodation for completing your application, participating in interviews, or any other part of the selection process, please reach out to us at accessibility@fieldmuseum.org.

Stephanie M. Smith, Ph.D. (she/her < <https://pronouns.org/she-her> >) Research Scientist XCT Lab Manager - FMNH XCT Portal

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FloridaAtlanticU EvolutionaryGenomics

The Assis group (<http://assisgroup.fau.edu/>) at Florida Atlantic University is currently recruiting a highly motivated postdoctoral scholar to work on NIH- and NSF-sponsored projects.

Our group develops and applies machine learning approaches to address questions about the evolution of adaptive and disease-associated traits. A major focus of our work is on structural variations (SVs), which arise from duplications, deletions, inversions, and translocations of large genomic segments. We are currently designing novel machine learning methods for understanding the evolutionary and disease implications of different types of SVs by determining how they modify gene expression patterns, protein structures, and molecular interactions. We are also interested in predicting associations between SVs and diverse traits, including antibiotic resistance.

The ideal candidate will have a strong computational background and will be given extensive freedom in choosing their research direction within the broad scope of research areas covered in the group.

The position will also offer a competitive salary and is located in the beautiful beachside city of Boca Raton, FL.

If interested in applying, please send a current CV to Raquel Assis (rassis@fau.edu).

rassis@fau.edu

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Halmstad Sweden PopulationGenetics

We are announcing a postdoc position in population genetics at Halmstad Uni, Sweden Project is to investigate population structure of salmonoid fish at different scales, using a variety of methods. One goal is to evaluate eDNA a tool for population genetics.

Supervised by Johanna Sjöstedt and Martin Lind

Apply here (deadline Jan 20): <https://hh.varbi.com/en/-what:job/jobID:779665/iframeEmbedded:0/where:4>
Martin Lind

Associate Professor | Senior Lecturer Dept of. Environmental and Biosciences Halmstad University Sweden

Also active as:

Researcher Animal Ecology Dept. of Ecology and Genetics Uppsala University Norbyvägen 18D 752 36 Uppsala Sweden

<http://www.martinlind.org/> Martin Lind
<martin.i.lind@gmail.com>

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Hannover PlacozoaEvolution

Postdoctoral position available immediately (one year, renewable) in the Schierwater lab for a motivated young

investigator to undertake molecular genetic analyses in or more of the following areas: Polarity/cancer research on the placozoon Trichoplax, evolutionary systematics of Placozoa, conservation genetics of dragonflies and/or environmental genomics of marine ecosystems.

Interest in fundamental questions of evolutionary adaptation and speciation is essential. Experience with functional genomics and/or transcriptome analysis and/or eDNA and bioinformatics is highly desirable. The successful candidate will have ample opportunity to pursue additional projects and define his own project within the broad molecular ecology/evolutionary genetics scope of the lab. We provide excellent working conditions.

Salary is according to the German E13 salary scale.

Please email CV, brief statement of research interests and experience and list of 2 references to Bernd Schierwater (bernd.schierwater@ecolevol.de).

Bernd Schierwater

Professor & Director Institute of Ecology & Evolution
TiHo Hannover, Foundation Buenteweg 17d D-30559
Hannover Germany

Bernd Schierwater <bernd.schierwater@ecolevol.de>

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INRAE France AnalysisGenomicData

Dear colleagues,

We are proposing a two-year post-doctoral fellowship, co-supervised by AgroParisTech (Palaiseau, France) and CBGP in Montpellier, to develop inference methods for the joint analysis of population dynamics and population genetics data, in order to estimate the local and recent demographic functioning of populations.

We are looking for a motivated researcher, with a PhD in population genetics, population dynamics, probabilities or statistics applied to genetics.

The project is detailed below.

Sincerely,

Camille Coron, Sophie Donnet, Raphaël Leblois, Miguel De Navascues

Two-year post-doctoral position at AgroParisTech - INRAE (France)

We are offering a 2-year postdoctoral position aimed at understanding how combining demographic and genetic data could improve the inference of a population's demographic history. We are looking for a motivated researcher, with a PhD in population genetics or in probabilities or statistics applied to genetics.

Localisation : AgroParisTech - INRAE (Palaiseau, France) Duration : 2 years Beginning : September 2025 at the latest

Subject : To study the demographic dynamics of a population, two types of data and approaches are generally used: on one hand, count data, and on the other hand, data from genetic sequencing. These two types of data require different mathematical techniques to infer the demographic parameters of the populations under consideration.

The aim of this postdoctoral position is to propose probabilistic models to jointly represent count data, coming from capture-mark-recapture protocols or from citizen science programs, and genetic sequencing data. The properties of these models will be studied and these models will be used to infer the demographic dynamics of the considered population. These probabilistic models could range from the Wright-Fisher model to more complex birth-and-death models with interaction and spatial structure. Different modes of genetic transmission will also be considered. Some of these models could be studied using the SLiM program, which allows for the simulation of individual-based models and associated genetics.

The associated biological challenges are the study of a population's demographic dynamics, and more specifically, understanding the decline and displacement of certain populations due to climate warming, as well as the control of proliferating species.

The mathematical approaches envisaged are (1) the joint probabilistic modeling of population dynamics and datasets from different protocols, containing count data on one side and genetic data on the other. These models may have a natural hierarchical structure and must integrate the different acquisition protocols for the different types of data. (2) The inference of these models parameters, by combining inference by simulation and by maximum likelihood estimation. Finally, these models could be confronted to real data, for example, concerning the monitoring of fishery stock dynamics or the control of pest insect populations (i.e., disease vectors, crop pests), in collaboration with the CBGP (Montpellier).

Supervisors : - Camille CORON (INRAE, Mathématiques et Informatiques Appliquées de Paris-Saclay) - Sophie DONNET (INRAE, Mathématiques et

Informatiques Appliquées de Paris-Saclay) - Raphael LEBLOIS (INRAE, Centre de Biologie pour la Gestion des Populations, Montpellier) - Miguel DE NAVASCUES (INRAE, Centre de Biologie pour la Gestion des Populations, Montpellier)

Searched profile : PhD in theoretical population genetics or in probability or statistics applied to population genetics. A strong interest for modeling and applications is required.

For more informations and to apply : camille.coron@inrae.fr, raphael.leblois@inrae.fr, miguel.navascues@inrae.fr

Send a resume, a motivation letter, and at least one recommendation letter.

Linked references : [1] Giraud et al. 2016 Capitalizing on opportunistic data for monitoring relative abundances of species. *Biometrics* 72:649-658 [2] Benjamin C Haller, Philipp W Messer, SLiM 3: Forward Genetic Simulations Beyond the 1 Wright-Fisher Model, *Molecular Biology and Evolution*, Volume 36, Issue 3, March 2019, Pages 632-637 [3] Navascués et al. 2009 Characterization of historical demographic expansions from pairwise comparisons of haplotypes using linked microsatellites. *Genetics* 181:1013-1019 [4] Raynal et al. 2019 ABC random forests for Bayesian parameter inference. *Bioinformatics* 35:1720-1728 [5] Rousset et al. 2024 Better confidence intervals in simulation-based inference. *BioRxiv* [6] Stoehr & Robin 2024 Composite likelihood inference for the Poisson log-normal model. *ArXiv*

raphael.leblois@inrae.fr

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JagiellonianU AmphibianDiseaseEvolution

Postdoc position in Amphibian Disease Ecology

We are seeking for a postdoctoral researcher in amphibian disease ecology and evolution to work in the Genomics and Experimental Evolution group at the Institute of Environmental Sciences, Jagiellonian University, Krakow, Poland. The position is part of the National Science Centre (NCN) grant "The role of blood parasites in emerging disease dynamics and biodiversity loss in amphibians".

Background. Understanding the interactions between pathogens, as well as between pathogens and their hosts, is essential for inferring the evolution of disease dynamics, host immunity, and pathogen virulence. This knowledge is particularly critical for endangered taxa like amphibians. In this project, we aim to assess the role of hematic parasites in amphibian decline, as these parasites have been shown to significantly impact other taxa.

Job description. The postdoc will conduct an experiment to investigate the impact and costs associated with infection by blood parasites in amphibians. This experiment will be carried in Dr. Netherlands' lab in South Africa (<https://www.ufs.ac.za/natagri/faculty-of-natural-and-agricultural-sciences-home/general/-staff?pid=HyjqNLMuYYE%3D>). The position will involve experimental laboratory work and statistical modelling. (S)he will work together with the PI, Dr. Netherlands, and other team members, including a network of international collaborators.

Requirements. The suitable candidate will have a PhD degree obtained no earlier than in 2017 (extensions for parental leave apply), be fluent in English and have a strong interest in disease ecology and evolutionary biology. The candidate should have experience in experimental biology and data analysis, ideally with R; a background in blood parasites or emerging amphibian diseases will be an advantage. Employment: full-time research for nine months. Salary: approx. 7800 PLN gross (before tax, including benefits).

How to apply. The application—(one single pdf file) should include: cover letter, CV with the list of publications, contact details of two referees and a scan of the PhD certificate. Please send the application by e-mail to: gemma.palomar.garcia@gmail.com by 20th February 2025 at the latest. Selected candidates will be invited for live or Skype interviews. Preferred starting date April-May 2025.

Gemma <gemma.palomar.garcia@gmail.com>

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JagiellonianU Krakow BarkBeetleGenomics

A reminder that only one week left to apply!

We are looking for a postdoc to work on the project

'Genomics of eco-evolutionary dynamics in the spruce bark beetle'. The main objective of the project is to address several hypotheses about the nature of rapid adaptation by analyzing changes in allele frequencies and inversion haplotypes over time in different populations of the spruce bark beetle. Our international team is based at the Institute of Environmental Sciences at the Jagiellonian University in Krakow (Poland).

We are looking for a person with a strong interest in evolution, molecular ecology, population genomics as well as experience in bioinformatics; proven experience in working with NGS data and their multi-step analysis (experience in pool-seq analysis preferred); strong English language, communication and organizational skills. The position is for 3 years (after successful probation) and the salary is 140k PLN/year before tax.

If interested, please send a cover letter explaining your background, skills, and interest in the project, CV, and contact information of two academics willing to provide references to Dr. Krystyna Nadachowska-Brzyska (krystyna.nadachowska@uj.edu.pl).

Review of applications is ongoing; please apply by January 15, 2025 to ensure full consideration. The start date of the position is 03.06.2025 (but may be negotiable!). A short summary of the project is available below or at <https://genomicsofoutbreaks.com/>. Krystyna Nadachowska-Brzyska

More details on the project

One of the central goals of evolutionary biology is to understand how natural selection works and how it operates at the genomic level. In particular, rapid adaptation, where strong selection leads to drastic phenotypic changes within a few generations, has been at the center of recent scientific debate. In part, this is because while identifying the molecular basis of rapid and often polygenic evolutionary responses at the phenotypic level has proven difficult, several recent studies have suggested that genome-wide rapid adaptation can be detected and quantified using temporal genomic data and appropriate statistical analyses. In addition, an increasing number of recent studies have suggested that polymorphic inversions may be key drivers of rapid adaptation. This changing perspective, but also methodological advances, indicate that there is an urgent need to revisit long-standing questions in the field of evolutionary genetics and eco-evolutionary dynamics, such as: Can populations continuously adapt to changing environments (via adaptive tracking)? What is the genomic architecture of such adaptation? Or, does fluctuating selection acting on multiple loci across the genome play a critical role in rapid adaptation?

The main goal of this project is to address several hypotheses about the nature of rapid adaptation by characterizing the temporal genome-wide dynamics of allele frequencies in multiple populations of the spruce bark beetle. In particular, we will test whether the bark beetle is under temporally fluctuating selection, whether it is more frequent than directional selection, and whether it affects large parts of the species genome. We aim to identify sets of SNPs that show significant changes in allele frequencies over short periods of time, and to identify genes and pathways associated with directional and fluctuating selection. In addition, we will take advantage of the extremely complex genomic landscape of polymorphic inversions discovered in the spruce bark beetle and test whether polymorphic inversions are important drivers of rapid adaptation within the species. We will also identify potential abiotic factors that generate fluctuations in selection and force specific genomic regions to continuously respond to environmental changes (outside and inside inversions). Finally, we will quantify the effect of linked selection on linked neutral sites on ecological timescales, the effect of which is particularly understudied on short temporal scales.

To address the main questions of the project, we will use extensive temporal data sets from several spruce bark beetle populations collected over the course of several generations, we will use a combination of short-read pooled sequencing and long-read nanopore sequencing approaches, and we will apply state-of-the-art population genetics and statistical analyses. The results of the project will shed light on fundamental evolutionary questions regarding the role and prevalence of adaptive tracking of rapidly changing environments, the role of polymorphic inversions in rapid adaptation, and the genomic scale of fluctuating selection in natural populations. We believe that this proposal is a unique example of research that aims to shed light on multilocus fluctuating selection in the context of an extremely inversion-rich genome, and as such will have a high impact on the advancement of the field.

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JYU Finland ExptEvolutionGenetics

Post-doctoral researcher position is available in the group of Ilkka Kronholm at the department of Biological and Environmental Sciences at the University of Jyväskylä. Starting earliest on 3rd of March 2025, but no later than 1st September, for a fixed term of three years.

The genetics, epigenetics, and evolution group lead by Ilkka Kronholm studies the properties of mutations, broadly defined, including properties of epistatic interactions and epigenetic changes. Our research questions are focused on understanding how different intrinsic and extrinsic factors affect evolutionary adaptation. As model systems we use the filamentous fungus *Neurospora crassa* and fission yeast.

The post-doctoral researcher will join an ERC-funded project that studies the properties of epistatic interactions. Epistatic interactions are known to play an important part in certain aspects of evolution, such as speciation. However, the properties of epistatic interactions are not very well known. In this project, we will estimate the probability that a pair of fixed mutations will exhibit a negative epistatic interaction, and are there some genes in the genome that are more often involved in epistatic interactions than others due to their place in the protein-protein interaction network for example. We plan to address these questions using transposon insertion libraries that will be constructed in different genetic backgrounds, and estimating the fitness effects of different insertions using population sequencing. We have different genetic backgrounds that we have obtained by a mutation accumulation experiment in fission yeast, and yeast populations that have adapted to different environments. Furthermore, the postdoc will participate in a long term experimental evolution project that further explores these questions.

Examples of recent work from the group includes developing mutation accumulation lines for the filamentous fungus *Neurospora crassa*, and analysis of how chromatin modifications affect mutation rate, see: Villalba de la Peña et al. 2023. Chromatin structure influences rate and spectrum of spontaneous mutations in *Neurospora crassa*. *Genome Research* 33: 1-13 <https://doi.org/10.1101/gr.276992.122> To be eligible, the candidate needs to have a doctoral (PhD) degree in evolutionary biology, population genetics, genetics, or a

related discipline with strong interest in evolutionary genetics. Experience with yeast genetics, analysis of NGS data, and good command of statistics can be an advantage. While previous experience with yeast is not mandatory, please note that previous laboratory experience is required.

While the postdoctoral researcher is expected to contribute to the current project, and supervise students jointly with the PI, there is also the possibility to develop your own interests within the framework of the project or to participate in teaching if the researcher so wishes.

The salary for a Postdoctoral Researcher is determined based on the task-specific demand level 5-6 of the university salary system for teaching and research staff. The salary range will be approximately 3500-4800 euro/month (gross income), depending on the qualifications and experience of the candidate.

Finland has a high standard of living, with free schooling (also in English), affordable childcare, good family benefits, and healthcare. Jyväskylä is located in central Finland in the Finnish lakeland, and has excellent opportunities for different nature, outdoor, and sports activities. The city of Jyväskylä is a major educational center and the city has a large student population. As such there is a vibrant cultural scene in the city.

To find useful information about the University of Jyväskylä, the City of Jyväskylä and living in Finland, see the international staff guide: <https://www.jyu.fi/en/workwithus/international-staff-guide> Please attach the following documents to the online application form:

1. Curriculum vitae, including contact information of two people willing to provide a reference
2. Cover letter explaining your motivation, research interests, and career plans.
3. List of publications
4. Relevant certificates / diplomas

Please submit your application at the latest by 28th of February 2025 by using the link found on page: <https://ats.talentadore.com/apply/postdoctoral-researcher-in-experimental-evolution-and-genetics/8pWaJM> or using the tiny url link: <https://tinyurl.com/bdeajwxf> Informal inquiries are welcome and should be directed to Ilkka Kronholm email: ilkka.kronholm@jyu.fi lab website: ikronholm.net twitter: @kronholmmlab

Ilkka Kronholm



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LundU PollinatorLandscapeGenomics

We have a post doc opening within the project “Evaluating effects of green infrastructure on pollinator functional connectivity using landscape genomics”, funded by the strategic research environment BECC “Biodiversity and Ecosystem services in a Changing Climate”. This project aims to deploy landscape genomic methods to evaluate the importance of green infrastructure for gene flow and connectivity. The project will use whole genome data and advanced landscape genomic analyses and simulations to address to which extent the prevalence of green infrastructure increases functional connectivity. The project will be supervised by Anna Runemark and Maj Rundlöf at Department of Biology, Lund University, and performed in collaboration with postdoctoral fellow Isolde van Riemsdijk, University of Copenhagen. The work will be set within the SPeciation, Adaptation and Co-Evolution group at the Division of Biodiversity and evolution and the BECC environment at Lund University.

Please see the announcement at <https://lu.varbi.com/en/what:job/jobID:785801/> or contact Anna.Runemark@biol.lu.se for further information. Last day for application: February 20th.

The Lund University biology department offers an interactive environment with many strong research groups and a high proportion of international post docs, doctoral students, and researchers. The department hosts weekly seminars with invited speakers, and there is also an active department pub, floor hockey, board game evenings and division breakfasts making it a social interactive research environment. The SPACE environment with 4 PIs and several post docs, PhD-students and students provides a forum for discussion and collaboration, and the BECC environment provides both workshops, courses, funding opportunities and is an excellent interface for interdisciplinary research and interactions with stakeholders.

Anna Runemark <anna.runemark@biol.lu.se>

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Madagascar Palynology sedaDNA

Postdoctoral position in Palynology and Sedimentary DNA Analysis to Understand the History of Malagasy Landscapes and Populations Over the Last Millennia

Scientific Context Located just 200 km from East Africa, Madagascar represents a unique intersection of Austronesian populations from Asia and Bantu populations from Africa. These groups introduced agricultural practices, plants, domestic animals, and diverse cultural expressions, leaving visible traces of this blending to this day. The MADEOGEN project aims to reconstruct the timeline of these colonizations, the diffusion of populations, and their various influences on the island's landscapes over the past 3,000 years. This research adopts an interdisciplinary approach, combining paleoecology, human genetics, and ethnoecology, to understand long-term socio-ecological dynamics.

Postdoctoral Objectives The postdoctoral researcher will focus on paleoecological research using two complementary approaches: 1. Fossil pollen analysis to reconstruct vegetation dynamics. 2. Sedimentary DNA analysis to identify specific plant and animal species. These methods will be applied to sediment cores collected from various sites across Madagascar.

Expected Outcomes The work is expected to result in at least two scientific publications based on data obtained during the 24-month contract.

Desired Profile **Scientific Skills** - Expertise in tropical palynology or willingness to train in the flora of Madagascar. - Interest in sedimentary DNA analysis techniques, with aptitude for laboratory work and bioinformatics. **Personal Qualities** - Motivation for fieldwork in Madagascar. - Ability to work in interdisciplinary teams and collaborate effectively. - Capacity to supervise students (Masters level).

Working Conditions - Primary location: ISEM in Montpellier (palynology and sedimentary DNA). - Secondary location: EDYTEM in Bourget-du-Lac (sedimentary DNA). - Duration: 24-month contract, starting in April 2025. - Training: Introduction to coring equipment before field missions. - Salary: From €3021.50 gross per month, adjustable according to experience. - Contact: Laurent Bremond (laurent.bremond@umontpellier.fr)

This project, funded by the French National Research Agency (ANR) with CNRS credits, offers a unique

opportunity to contribute to understanding the socio-ecological dynamics of Madagascar, an island exceptional for its biodiversity and human history.

Deadline for applications: 28/02/2025

More information such as research program: <https://emploi.cnrs.fr/Offres/CDD/UMR5554-LAUBRE-003/Default.aspx?lang=EN> Christelle TOUGARD <christelle.tougard@umontpellier.fr>

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MissouriBotanicalGarden PlantConservation

Postdoctoral Fellow - Design of ex situ plant collections for conservation

The Center for Conservation and Sustainable Development at the Missouri Botanical Garden (MBG) seeks to hire a full-time postdoctoral scholar to work on a project funded by Institute of Museum and Library Services to investigate strategies to conserve intraspecific variation in ex situ collections of imperiled plants. The candidate will 1) identify loci or phenotypic traits that may show signatures of local adaptation using genomic and phenotypic data that was already collected from common garden experiments with North American plant species of conservation concern, 2) design ex situ collections that optimally conserve neutral and adaptive intra-specific variation under real-life constraints (e.g., maximum number of individuals in a collection) by applying multi-objective optimization approaches (e.g., simulated annealing algorithms); 3) determine whether trade-offs exist that limit the ability to represent different forms of intra-specific variation in ex situ collections (e.g., among neutral and adaptive genotypic and phenotypic variation); 4) assist MBG scientists with coordinating grant-funded activities including mentoring students, organizing and participating in outreach events and workshops, and presenting lectures to professional organizations, and 5) prepare and submit manuscripts for publication.

The position will be based in St. Louis (MO) and the candidate will work closely with MBG scientists active in conservation genetics, conservation biology, ecology, and horticulture/living collections management and will also actively engage with collaborators and colleagues at MBG and in the broader St. Louis Ecology, Evolution,

and Conservation community.

Candidates should have completed a Ph.D. in Ecology and Evolutionary Biology, Botany, Genetics, Environmental Science, Conservation Biology, or a related field before the start date. The ideal candidate will have prior experience in several of the following: ex situ sampling techniques, plant phenotyping, quantitative genetics, multi-objective optimization, bioinformatics, statistical analysis of phenotypic or population genomic data, and spatial (e.g., landscape) analysis of phenotypic or genomic data.

Review of applications will begin January 27, 2025 and will continue until the position is filled. Ideal start date is spring 2025 (March – June), but start date is negotiable. The term for this grant-funded position will be up to 2 years, with renewal in the 2nd year contingent on satisfactory performance. Salary will be commensurate

For more information and to apply: <https://jobs.dayforcehcm.com/en-US/mbg/-CANDIDATEPORTAL/jobs/3813> Iván Jiménez <<http://www.mobot.org/MOBOT/Research/curators/-jimenez.shtml>> Scientist Center for Conservation and Sustainable Development <<http://www.mobot.org/plantscience/ccsd/>> Missouri Botanical Garden <<http://www.mobot.org/plantscience/default.asp>>

P.O. Box 299 St. Louis, MO 63166

Ivan Jimenez <Ivan.Jimenez@mobot.org>

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Missouri Botanical Garden Biodiversity Scanning

Supervisor, Hyperspectral Scanning

Apply at: <https://jobs.dayforcehcm.com/en-US/mbg/-CANDIDATEPORTAL/jobs/3842> Postdoctoral Fellow, Biodiversity Data, Herbarium

The Missouri Botanical Garden (MBG) seeks to hire a full-time Postdoctoral Fellow to work in the lab of Dr. Matthew Austin on a project investigating how hyperspectral scans of Herbarium specimens can be used for taxonomic identification and trait prediction. The candidate will (1) collect hyperspectral data from taxonomically diverse Herbarium specimens, (2) use machine learning to analyze the resolution of taxonomic identification and accuracy of trait prediction that can be achieved with hyperspectral data, (3) prepare and submit

manuscripts for publication, and (4) assist MBG scientists with other research-related activities, including mentoring of students and technicians, participating in outreach events and workshops, and presenting research lectures. This person will also have the opportunity to explore other novel applications of hyperspectral data in the biodiversity sciences.

This position is part of MBG's Revolutionizing Species Identification (RSI) project. The RSI project - made possible by an anonymous \$14.4 million grant - is digitizing MBG's entire herbarium (of nearly 8 million specimens) and is harnessing specimen data to develop new technology to automatically identify herbarium specimens. The successful candidate will work closely with MBG scientists and colleagues to carry out this groundbreaking initiative.

The position will be based in St. Louis, which is home to a collaborative community of ecologists, evolutionary biologists, and data scientists that interact through partnerships among MBG, Washington University in St. Louis, the University of Missouri - St. Louis, Saint Louis University, and other area institutions. This position is based in the Herbarium, a department within MBG's Science and Conservation Division, which manages MBG's world-class Herbarium and conducts specimen-based research in the furtherance of biodiversity conservation and ecosystem restoration.

Apply at: <https://jobs.dayforcehcm.com/en-US/mbg/CANDIDATEPORTAL/jobs/3818> Matt Austin <maustin@mobot.org>

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Norwich UK Bioinformatics

Hello,

We have a postdoctoral vacancy in my group at Quadram/Earlham Institutes, Norwich UK, that I wanted to bring to the attention of EvolDir, as the data and scientific questions are about evolution of microbes in communities, and in relation to dispersal strategies and persistence in the human host.

The infrastructure for this project is excellent (novel datasets, 3rd gen deep sequencing of metagenomes, plenty of evolution, bioinformatic & microbiology focused groups at both the Quadram + Earlham Institutes). The post is for 2 years, funded by an ERC grant,

application deadline would be 27th Jan:

Research Scientist (Metagenomics) - Quadram Institute
< <https://quadram.ac.uk/vacancies/research-scientist-metagenomics-2/> >

Please do not hesitate to write me with further questions.

Kind regards,

Falk

Dr Falk Hildebrand PI at Quadram Institute Bioscience & Earlham Institute Norwich Research Park www.falk.science "Falk Hildebrand (QIB)" <Falk.Hildebrand@quadram.ac.uk>

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PrincetonU EvolutionaryBiology

The Department of Ecology and Evolutionary Biology (EEB) at Princeton University invites applications from postdoctoral research associates or more senior researchers for the EEB Postdoctoral Fellows Program. The Program recognizes and supports outstanding early-career scientists who can make important research contributions in the areas of ecology, evolution, and/or behavior, while also contributing to Princeton University's excellence and diversity, broadly defined. The Program is intended to foster the onward scientific careers of the Fellows by providing research support, mentoring, advocacy, and community.

The Term of appointment is based on rank. Positions at the postdoctoral rank are for one year with the possibility of renewal pending satisfactory performance and continued funding; those hired at more senior ranks may have multi-year appointments. Appointments will be at most three years in duration and will include a research fund. The expected starting date is autumn 2025, although this is flexible. Fellows will be thoroughly integrated into the life of the EEB department. Furthermore, the Office of the Dean of the Faculty will offer programming to provide Research Fellows from across the university with professional development, mentorship, and community building opportunities.

A Ph.D. in a related field is required. Applicants must apply online at <https://puwebp.princeton.edu/AcadHire/apply/application.xhtml?listingId=37241> and include a curriculum vitae, a two-page statement of re-

search experience, interests, and vision (i.e., long-term research plans and goals), and a cover letter that includes an explanation of why the candidate is interested in the EEB Postdoctoral Fellows Program, plus names and contact information for three references. We encourage potential applicants to identify at least 2 EEB faculty members who could be suitable collaborators and mentors on their independent work. Applicants are welcome to contact those faculty members to discuss possibilities: <https://eeb.princeton.edu/people/faculty> All applications received by 17 January 2025, 11:59 pm ET will be fully considered, but applications will continue to be accepted until the position is filled. Thanks!

All the best, Andrea

Andrea L. Graham Professor of Ecology & Evolutionary Biology Faculty Director of the Stony Ford Center for Ecological Studies Associated Faculty Member of the Center for Health and Well-Being Associated Faculty Member of the High Meadows Environmental Institute Princeton University Princeton, NJ 08544 USA

External Faculty of the Santa Fe Institute Santa Fe, NM 87501 USA

Tel: (+1) 609-258-6703 E-mail: algraham@princeton.edu Graham Group: <http://algraham.princeton.edu/> @grahammunology.bsky.social algraham@princeton.edu

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QMUL London AmphibianMicrobiome

The Bates Lab at The Blizard Institute (QMUL) is seeking a 3-year Postdoctoral Researcher as part of a recently funded BBSRC project investigating glycan - microbe interactions using amphibian models. The post holder will use state-of-the-art omics methods and experimentation to dissect how microbiome assembly processes shape host resistance to the deadly fungal pathogen *Batrachochytrium dendrobatidis* (Bd). To date, Bd has driven at least 500 amphibian species into decline globally, equating to one of the worst diseases of wildlife on record. The PDRA will benefit from a close collaboration with the world-leading Glycosciences Laboratory at Imperial College London and the ZSL Institute of Zoology.

For more details: <https://qmul-jobs.tal.net/vx/-appcentre-ext/brand-4/candidate/so/pm/1/pl/3/-opp/5038-Post-Doctoral-Research-Associate/en-GB>

Lab website: <https://sites.google.com/view/bateslab>
Kieran Bates <k.bates@qmul.ac.uk>

Dr. Kieran Bates Lecturer in Microbiome Science Centre for Immunobiology The Blizard Institute Bart's and The London School of Medicine and Dentistry Queen Mary University of London 4 Newark Street, London E1 2AT

Kieran Bates <k.bates@qmul.ac.uk>

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Roslin Edinburgh Evolutionary Genomics

Post doc positions in evolutionary genomics

Two post-doctoral researcher positions are available that will play key roles in delivering an exciting new 4-year multi-partner BBSRC research project focussed on understanding genome evolution following whole genome duplication (WGD, i.e. polyploidy) events across the Tree of Life (please see rediploidisation.org). The researchers, based at the Roslin Institute, will lead and deliver ambitious scientific objectives as part of a highly integrated multi-partner consortium, for example using cutting-edge comparative single cell transcriptomics and whole genome alignment approaches to reconstruct genetic and functional changes that follow WGD events in diverse eukaryotic taxa.

One post focusses on comparative single cell transcriptomics and is available full-time (35 hours per week) for three years with potential for extension up to 4 years. This post will involve both lab work and bioinformatic analyses.

One post focusses on bioinformatic analyses of genome evolution following whole genome duplication events. This post is available either full-time (35 hours per week) for two years (with potential for extension up to 3 years) or part-time (e.g. 0.5 FTE, 0.75 FTE) for a longer period, accommodating candidates seeking part-time working arrangements.

Both posts will be based primarily on campus at the Roslin Institute; however, we are open to considering flexible working patterns (on a contractual basis) and

requests for hybrid working (on a non-contractual basis) that combine a mix of remote and regular on-campus working.

For informal enquiries, please get in touch with Professor Dan Macqueen (daniel.macqueen@roslin.ed.ac.uk)

For more details about the project in which these post docs are embedded see <https://www.rediploidisation.org/> For more information about Professor Macqueen's research group - see <https://www.macqueenresearchgroup.com/> Please see the full advert and apply here:

https://elxw.fa.em3.oraclecloud.com/hcmUI/-CandidateExperience/en/sites/CX_1001/job/11979

The salary for these posts is UE07 40,247 to 47,874 per annum (pro rata if part time).

Your skills and attributes for success:

PhD in relevant discipline of biology
Extensive experience in comparative or evolutionary genomics and bioinformatics
Proven skills in a range of advanced omics technologies
Demonstrated interests in genome evolution
Proven track record of publishing first author papers in high quality journals
Potentially skills in lab work required to produce high quality omics datasets

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Dan Macqueen <daniel.macqueen@roslin.ed.ac.uk>

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SMNK Germany Bee eDNA

As a member of the DNFS (Deutsche Naturwissenschaftliche Forschungssammlungen e.V.), the State Museum of Natural History Karlsruhe (SMNK) is one of the largest research museums and collections in Germany and presents permanent and special exhibitions on over 5000 m², including the largest living coral reef in Germany. With extensive analog and digital offerings, it attracts more than 200,000 visitors every year. As a nationally and internationally active research museum in the fields of geosciences and biosciences, the museum enjoys recognition far beyond the region. The SMNK has a well-developed research infrastructure with molecular laboratories and imaging facilities. Based on

its extensive collections and the taxonomic expertise of its curators, the museum is also an important point of contact for the general public, schools and the press interested in plant, fungal and animal species in south-western Germany and for experts in the region, as well as a cooperation partner for national and international institutes.

The Natural History Museum Karlsruhe is looking for a Postdoc for environmental DNA (eDNA) research on bees, 100%, limited to 2.5 years, at Naturkundemuseum Karlsruhe, Karlsruhe, Germany, starting 1.4.2024

We are living in a biodiversity crisis of unprecedented extend. Many species are on the brink of extinction and important ecosystem services are at risk, including pollination. Pollinators and their interactions are the focus of the Beenergia project. In particular, the conflict between managed pollinators, especially honey bees, and wild bees will be investigated. In a multidisciplinary consortium, Beenergia aims to understand the ecological balance between commercial and wild pollinators, assess threats and develop solutions that ensure both pollinator protection and food security.

This subproject aims to develop innovative methods for gentle sampling and monitoring of wild bees based on molecular methods. Therefore, we are looking for a committed, motivated, communicative and team-oriented person with a strong interest in molecular ecology and sequencing methods to participate in developing eDNA-based methods for the detection and monitoring of pollinators in cooperation with the project partners in Germany and Switzerland and to test them in field trials.

We expect: - PhD in biology, or similar disciplines with a focus on biodiversity, ecology or evolutionary biology - In-depth knowledge of eDNA methods and various sequencing techniques - Interest in the realization and testing of prototypes - Basic knowledge of bees and wild bees and their ecology - Good language skills in English (project language) - Bioinformatics knowledge is a plus

We offer - Payment will be in EG 13 TV-L - dynamic collaboration in an international team - the opportunity to work at a nationally renowned research museum with recognized collections and an attractive exhibition - a workplace in the center of Karlsruhe, with excellent public transport connections to several attractive natural areas and the Black Forest National Park - flexible work time and family-friendly working hours (39.5 h/week); possibility of mobile working - participation in company health management, job ticket and job bike subsidized by the state of Baden-Württemberg

The SMNK aims to increase the proportion of women in

areas in which women are underrepresented and therefore expressly asks qualified women to apply. Severely disabled applicants will be given priority if equally qualified. Please include a note to this effect in your cover letter and enclose proof of disability. Please send your informative electronic application with CV, list of publications, certificates and references to bewerbung@smnk.de by 31.01.2025, quoting reference number 01_2025.

If you have any questions, please contact the Scientific Director Prof. Dr. Martin Husemann: martin.husemann@smnk.de.

Please note that the application documents will be forwarded to the persons involved in the recruitment process. Unfortunately, costs for interviews cannot be covered or reimbursed. Further information on the State Museum of Natural History Karlsruhe can also be found on the Internet at www.smnk.de Data protection notice for applicants The protection of your personal data is an important concern for the Staatliches Museum für Naturkunde Karlsruhe and is guaranteed at all times. All personal data collected and processed as part of an application is protected against unauthorized access and manipulation by technical and organizational measures. Your data will only be used to process your application within the Natural History Museum and will be treated in strict confidence in accordance with legal regulations. If you send your application by e-mail, please note that confidentiality risks and unauthorized access by third parties cannot be ruled out when communicating by unencrypted e-mail.

— / —

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

Sweden EvolutionaryBiology

SciLifeLab PULSE: Postdoc program for Future Leaders in Life Science Academia and Industry Visit <https://www.scilifelab.se/research/pulse/> for more details.

Join SciLifeLab PULSE (Program for future leaders in Life Science) to move your research career forward.

Why PULSE?

* Empowering Diversity in Science: PULSE is committed to fostering diversity and creating inclusive envi-

ronments. * Flexible and Supportive: Tailored training and career development designed to balance professional growth with personal commitments. * State-of-the-art Research: Engage in cutting-edge, high-density data-driven research that impacts academia, industry, and policy worldwide.

About the Programme

* Fellowship: each participant will benefit from a 36-month postdoctoral training. * Two tracks to align with your goals: Choose between the academic or the entrepreneurial path. * Global Collaboration: Opportunities for secondments at 24 renowned research institutions, infrastructures, and industry partners across Europe and beyond. * Host Universities: Collaborate with one of nine leading Swedish universities.

Research Areas

Academic track

* Cell & Molecular Biology * Precision Medicine & Diagnostics * Epidemiology & Infection biology * Evolution & Biodiversity.

Entrepreneurial track

* Machine Learning/AI * Therapeutic Oligonucleotides * Display and Selection technologies * Proximity Inducing Agents

What You get

* Transferable Skills: E.g. Open science, FAIR, communication, entrepreneurship and leadership training, to develop expertise to address related challenges. * Technology and methodology skills: Research methodology and technology training, according to an individually designed career development plan. The program integrates international, interdisciplinary, and intersectoral elements to provide a well-rounded educational experience. * Networking Opportunities: Build lasting relationships through secondments at any of the PULSE partners; international industries, institutions, and research infrastructures. * Leadership Development: Become one of the 48 future leaders equipped to move forward towards their goals within molecular life sciences. * Competitive salary and benefits, including access to the Swedish social security system, to support work-life balance.

Our Commitment to Inclusivity

PULSE follows the European Charter for Researchers and the Code of Conduct for Recruitment of Researchers, ensuring an open, fair, and transparent selection process. We encourage applications from women and individuals of all backgrounds to enrich the future of Life Sciences.

Application Period: The first call for 24 postdoctoral

positions is open between January 7 and March 31, 2025, and welcomes candidates of all nationalities under MSCA eligibility criteria.

Visit <https://www.scilifelab.se/research/pulse/> for more details. Contact: pulse@scilifelab.se

SciLifeLab PULSE Management Team

Ni_i¹/₂r du har kontakt med oss p_i¹/₂ Uppsala universitet med e-post s_i¹/₂ inneb_i¹/₂r det att vi behandlar dina personuppgifter. F_i¹/₂r att l_i¹/₂sa mer om hur vi g_i¹/₂r det kan du l_i¹/₂sa h_i¹/₂r: <http://www.uu.se/-om-uu/dataskydd-personuppgifter/> E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: <http://www.uu.se/en/-about-uu/data-protection-policy> Maria B_i¹/₂ckstr_i¹/₂m <maria.backstrom@scilifelab.uu.se>

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Sweden LifeScienceFellowships

SciLifeLab PULSE: Postdoc program for Future Leaders in Life Science Academia and Industry Visit <https://www.scilifelab.se/research/pulse/> for more details. Join SciLifeLab PULSE (Program for future leaders in Life Science) to move your research career forward.

Why PULSE?

Empowering Diversity in Science: PULSE is committed to fostering diversity and creating inclusive environments. Flexible and Supportive: Tailored training and career development designed to balance professional growth with personal commitments. State-to-the-art Research: Engage in cutting-edge, high-density data-driven research that impacts academia, industry, and policy worldwide.

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Machine Learning/AI Therapeutic Oligonucleotides Display and Selection technologies Proximity Inducing Agents What You get

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SciLifeLab PULSE Management Team

Page Title

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UBristol eDNA of Parasitic Bees

Title: Using eDNA to study the impact of parasitic bees on a key tropical pollinator community

Application deadline: 23 February 2025

We are offering a 3-year Postdoctoral Research Associate position at the University of Bristol funded by the Leverhulme Trust to investigate the impacts of parasitic bees on a tropical pollinator community.

Bees are key pollinators in the tropics, yet they also face multiple threats. One major threat is the parasitic robber bee *Lestrimelitta*, which damages and often kills bee colonies. However, how robber bees impact tropical bee communities (especially stingless bees) and their pollination services is not well understood. This project will use an emerging molecular tool, DNA metabarcoding of environmental DNA (eDNA), in combination with behavioural and ecological surveys to investigate how parasitic robber bees select and exploit host colonies, and how they affect vital pollinator communities in tropical ecosystems.

Beneficial skills & experience

- Ecological fieldwork in tropical habitats
- DNA barcoding or metabarcoding of eDNA, molecular tools to assess colony densities and foraging ranges (microsatellites, SNPs)
- Expertise in behaviour and ecology of bees or social insects

Team and research environment

The team includes Dr. Christoph Gr½ter and Dr. Emily Bell at the University of Bristol and collaborators Prof. Klaus Hartfelder, Prof. Eduardo Almeida and Prof. Fabio Nascimento at the University of Si½o Paulo, Brazil.

The successful applicant will join an international and interactive scientific environment with access to state-of-the-art facilities at the University of Bristol. Bristol is a vibrant city known for its thriving academic community and rich cultural scene. Bristol University has a strong commitment to sustainability and diversity and offers excellent opportunities for professional and personal

growth in an engaging and supportive environment.

Starting salary: $\ddot{y}_i \frac{1}{2} 37,999 - \ddot{y}_i \frac{1}{2} 42,632$, depending on experience & qualifications

Preferred starting date: 1 May 2025

How to apply: Apply via the University of Bristol Jobs Portal, Reference Number: ACAD107912

Link: <https://tinyurl.com/568zbx9u> For informal enquiries, please contact Dr. Christoph Grueter (c.grueter@bristol.ac.uk).

Dr. Christoph Gr \ddot{u} ter (he/him) Associate Professor in Animal Behaviour & Ecology School of Biological Sciences University of Bristol 24 Tyndall Avenue |BS8 1TQ | UK Tel: 0117 455 6234 Office: 302

Virtual Office: <https://tinyurl.com/55a2zdh> Web: www.socialinsect-research.com Christoph Grueter <c.grueter@bristol.ac.uk>

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UCalifornia Berkeley EvolutionaryGenomics

The Nachman lab is hiring a postdoc as part of an NIH-funded project to study the genomic basis of environmental adaptation in house mice. House mice are native to Western Europe and were introduced into the Americas in association with humans during the last few hundred years. In this short time, mice have adapted to different environments through changes in morphology, behavior, and physiology. We seek to understand the genetic basis of this variation using a variety of approaches, including whole-genome sequencing of wild-caught mice across North and South America, studies of gene expression and chromatin accessibility, and genetic crosses using wild-derived inbred strains of mice from different environments. We are also using long-read data to study the role of structural variation, including insertions of transposable elements, in adaptation. The postdoc will work on existing projects in the lab and also have the opportunity to develop new projects in the context of our research program. Please direct questions about this position to Michael Nachman: mnachman@berkeley.edu. For complete details and to apply, please see <https://aprecruit.berkeley.edu/JPF04754>. Michael Nachman Director, Museum of Vertebrate Zoology Professor, Department of Integrative Biology 3101 Valley Life Sciences

Building University of California, Berkeley Berkeley, CA 94720-3160 (510) 642-1792, mnachman@berkeley.edu

Michael Nachman <mnachman@berkeley.edu>

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UCalifornia Davis PlantGenomics

The laboratory of Dr. Xiaosa (Jack) Xu in the Department of Plant Biology at the University of California, Davis, wishes to employ a 100%-time Postdoc who will contribute to plant developmental genetics and/or single-cell genomics research.

Apply link: <https://recruit.ucdavis.edu/JPF06904> Feel free to contact PI, Xiaosa (Jack) Xu, xjkxu@ucdavis.edu for specific questions regarding the position.

Position description:

The candidate will work closely with the PI and other lab members to design and implement a variety of cutting-edge projects focused on plant development and evolution, single-cell genomics, genome editing, and genetics.

Research (90%): The Postdoc will work closely with the PI and lab members, as well as collaborators at UC Davis and other institutions, to conduct single-cell genomics and spatial transcriptomics experiments, perform data analysis, and validate findings through genome editing. The candidate will have the opportunity to be involved in: 1) Conducting single-cell genomics and spatial transcriptomics experiments by extracting DNA and RNA from single cells and plant tissue sections, and preparing libraries for next-generation sequencing; 2) Performing cutting-edge single-cell genomics and spatial transcriptomics data analysis using packages in Linux, R, Python, etc; 3) Genotyping plant mutations and conducting molecular, cell biology, and biochemistry experiments, such as building CRISPR gene-editing constructs, imaging fluorescent plants, extracting proteins from bacteria and plants, and performing immunoprecipitation and western blot analysis for proteins of interest; 4) Propagating and caring for plants in the field, greenhouse, and growth chambers.

Professional Competence and Activities (5%): The candidate is expected to work semi-independently with oversight from the principal investigator. The candidate will assist in preparing data figures, tables, and summaries of results for progress reports to the funding agency.

The candidate will keep a detailed laboratory notebook or digital notebook, including experimental methods and results. The candidate will write research results for publication by drafting sections of the manuscript and assisting with editing the full manuscript. The candidate will attend seminars on topics related to fields of interest, participate and present in lab meetings and journal clubs, and engage in scientific discussions with collaborators. The candidate will present research findings at suitable external scientific meetings, either on campus or elsewhere, depending on the availability of funds. Additionally, the candidate may participate in training programs to enhance knowledge and skills, depending on their long-term goals.

University and Public Service (5%): The Postdoc will actively contribute to lab activities through meetings and unit/campus presentations, participate in public outreach activities, and assist with mentoring graduate and undergraduate students or student interns.

Qualifications

Basic qualifications (required at time of application)

- Ph.D. in the area of Biology, Plant Biology, Computational Biology, Developmental Biology, Genetics, Evolution, Molecular and Cell Biology, or Systems Biology (Applicants do not need to have their PhD degree at the time of application but must have it before starting the position).
- Experience in molecular protocols, DNA or RNA focused.
- Experience in molecular cloning and/or CRISPR genome editing.
- Efficient utilization of computer clusters and programming experience with Linux, R, Python, or similar tools to analyze genomics data using bioinformatics packages and databases.
- Excellent written and verbal communication skills.
- Highly motivated and can manage multiple projects.

Preferred qualifications (other preferred, but not required, qualifications for the position)

- Experience in building NGS libraries.
- Experience in designing, maintaining, and harvesting large-scale experiments in fields, greenhouses, and chambers.
- Demonstrated knowledge of imaging with microscopies such as DIC and confocal.
- Experience in single-cell genomics

Application Requirements

Document requirements

Curriculum Vitae - Your most recently updated C.V.

Cover Letter

Statement of Research

Statement of Teaching (Optional)

Statement of Contributions to Diversity, Equity, and Inclusion - Contributions to diversity, equity, and inclusion documented in the application file will be used to evaluate applicants.

Visit <https://academicaffairs.ucdavis.edu/faculty-equity-and-inclusionfor> guidelines about writing a statement and why one is requested.

List of Publications

Reference requirements

3-5 letters of reference required

Xiaosa Xu <xjkxu@ucdavis.edu>

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UCalifornia Irvine PlantEvoGenomics

The Gaut lab at the University of California, Irvine has positions for one or two motivated postdoctoral fellows to study aspects of plant evolutionary genomics and population genetic inference.

One postdoc will contribute to an NSF-funded project that is designed to study the evolutionary forces that act on secondary and tertiary structures in maize genomes. The project is a collaborative effort with the lab of Dr. JJ Emerson, who is also at UC Irvine, and builds on previous epigenetic work from the Gaut lab. This position requires a strong bioinformatic background, with experience in genomic analyses and familiarity with evolutionary principles.

The second position, if funded, will explore aspects of spatial population genetics, utilizing simulations and methods of inference based on machine-learning methods. Computational efforts will be complemented by empirical population genetic analyses across a range of model systems. The goal is to understand the processes that shape the distribution of genetic variation across geographic space and to enhance the performance of metrics that measure the climate-genotype interface.

The lab is a part of the UCIDepartment of Ecology and Evolutionary Biology, which houses a vibrant community of evolutionary geneticists including Drs. Tony Long, Grace Lee, Kevin Thornton, JJ Emerson, Jose Ranz, and Adriana Briscoe. The department also has an amazing community of microbial ecologists,

most of whom are interested in evolutionary questions. This group includes Maria Rebolleda-Gomez, Alejandra Rodriguez-Verdugo, Tobin Hammer, Adam Martiny and Jennifer Martiny.

The University of California, Irvine is an Equal Opportunity/Affirmative Action Employer advancing inclusive excellence. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age, protected veteran status, or other protected categories covered by the UC nondiscrimination policy.

Feel free to contact Brandon Gaut (bgaut@uci.edu) with questions. Informal inquiries are most welcome!! Formal applications can be submitted to <https://recruit.ap.uci.edu/JPF08999> . Brandon Stuart Gaut <bgaut@uci.edu>

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UCalifornia LosAngeles PopulationGenetics

Postdoctoral research position at UCLA in population genetics

The Garud lab is seeking a postdoc to join our group (<https://garud.eeb.ucla.edu>) in the Department of Ecology and Evolutionary Biology at the University of California, Los Angeles. Our lab focuses on quantifying evolutionary dynamics in natural populations, with an emphasis on the human gut microbiome. We are primarily a population genetics group using computational and statistical techniques to gain an insight into the dynamics of evolution. The position may be either 100% in the Garud lab or joint with Kirk Lohmueller's group, also at UCLA.

The successful candidate will have substantial input in the specific nature of their research project. However, the project should broadly fit within the lab's goals of learning about evolution in natural populations. There are a wide range of projects to choose from, including developing fundamental population genetic theory, as well as application of theory and models to metagenomic data. The candidate is also welcome to work on other study systems besides human microbiomes, including *Drosophila* and Humans.

Candidates should have a Ph.D. in biology, genetics, computer science, bioinformatics, statistics, computational biology, or a related field. A background in population genetics/evolutionary genomics is preferred. As this is a computational position, proficiency in programming in R, Perl, or Python, and shell scripting is essential. Preference will be given to candidates with a strong publication record, evidence of substantial research productivity, and ability to successfully communicate scientific information.

Interested candidates should send to Nandita Garud at ngarud@ucla.edu the following:

- A letter describing your background and motivations pursuing a postdoc in the Garud Lab
- CV that includes a brief 1-2 sentence description of your contribution to past research projects.
- Contact information for two referees who can provide references upon request

The University of California is an equal opportunity/affirmative action employer.

Nandita Garud, PhD Associate Professor Department of Ecology and Evolutionary Biology Department of Human Genetics, David Geffen School of Medicine University of California, Los Angeles 621 Charles E. Young Drive South Los Angeles, CA 90095-1606

Lab website: <https://garud.eeb.ucla.edu> Nandita Garud <ngarud@g.ucla.edu>

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UGent Belgium Two PlantGenomeEvolution

FWO-UGent funded bioinformatics postdocs - Unveiling the significance of gene loss in plant evolution

We are seeking two highly motivated postdoctoral researchers to join our research team based in the Van de Peer lab, under the supervision of Dr. Zhen Li, Assistant Professor at Ghent University/VIB Staff Scientist.

The two positions are funded through an FWO research grant awarded to Dr. Zhen Li and will focus on the evolutionary significance of gene loss in shaping plant adaptation, speciation, and biological innovations. This project aims to redefine our understanding of gene loss alongside gene gain in plant evolution, focusing on de-

veloping novel genomic approaches to analyze gene loss across diverse plant lineages and their evolutionary consequences. To this end, the initial focus will be developing a novel genomic approach integrating homolog identification and multiple genome alignment to identify gene loss in plants and investigating its links with species divergence and adaptive traits in various plant clades, e.g., Orchidaceae, Poaceae, Solanaceae, Brassicaceae, and Fagales.

Research Focus Areas While the two positions will work closely together and share many responsibilities, they have slightly different initial focus areas: **Position 1:** Computational Genomics and Method Development - Develop novel genomic frameworks for detecting gene loss in plant genomes - Implement approaches to distinguish DNA deletion from pseudogenization - Analysis of gene loss patterns across diverse plant lineages - Explore graph-based algorithms for multiple genome alignment and ancestral karyotype reconstruction

Position 2: Evolutionary Analysis and Network Biology - Analysis of cross-species/-ecotype co-expression and gene regulatory networks - Study of molecular mechanisms underlying how gene loss affects biological network rewiring - Integration of phenotypic data with omics analysis - Explore machine learning and network analysis methods

We Offer The VIB-UGent Center for Plant Systems Biology is a world-leading science institution in Ghent, Belgium. Ghent University is among the top 100 global universities according to several international rankings. - A fully funded, full-time postdoctoral position for one year (with possibility of a two-year extension after positive evaluation) in a stimulating and supportive international research environment - Access to state-of-the-art tools and computational infrastructure, including CPU/GPU clusters - Opportunity to contribute to cutting-edge research in plant evolution and genomics - Support for attending international conference and developing professional networks - Comprehensive training in academic, technical, and career skills through VIB and Ghent University

Motivated candidates are asked to apply online via the VIB application procedure.

A complete application file (English) should contain the following documents: - A cover/motivation letter (max. 2 pages) stating career goals, experience, and how these relate to your preferred position 1 and/or 2 - A detailed CV, including a list of your scientific publications - Contact information of at least two academic references

For detailed information, please visit <https://jobso.id/>-

ko16 For inquiries about the positions, please mail to zhen.li@psb.vib-ugent.be

Zhen Li <zhen.li@psb.vib-ugent.be>

(to subscribe/unsubscribe the EvoDir send mail to gold-ing@mcmaster.ca)

zhen.li@psb.vib-ugent.be

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UGlasgow ReproductiveModeEvolution

University of Glasgow: Postdoctoral researcher position open in evolutionary genomics

We have a research opportunity at the University of Glasgow in the team of Kathryn Elmer in collaboration with Oscar Gaggiotti (St Andrews), Maureen Bain (Glasgow), Mike Ritchie (St Andrews) and project partners in Slovenia (Recknagel) and France (de Villemereuil, Le Galliard)

We are seeking a motivated, skilled, creative and enthusiastic postdoctoral researcher for a project on the evolution of oviparous and viviparous reproductive modes, funded by an ambitious NERC Pushing the Frontiers grant.

Our aim is to show how and why transitions between egg-laying and live-bearing evolve. To accomplish this, we will pinpoint the functional traits that matter, determine their genetic basis, and illuminate their evolutionary mechanisms and outcome. This project leverages a distinctly informative oviparous-viviparous common lizard hybrid zone (see e.g. Recknagel et al 2021 Nature Ecol Evol). This project involves a multi-year in situ experiment to track individual fitness and phenotypes across life stages and reshuffle oviparous-viviparous-hybrid genomes through directed genetic crosses. We will identify the genetic basis of i) eco-physiology and reproductive traits and ii) fitness components using genome-wide approaches. With that, we will build fitness landscapes based on the most important genetic variants, and identify if and how these differ between males and females. Drawing together this new information, we will carry out a simulation study to explore the evolutionary genetic conditions under which the transition between oviparity and viviparity could have taken place, and evaluate the impact of different model pa-

rameters (mating, selection, genomic architecture, gene flow) on outcomes.

The PDRA will make a leading contribution to the genomic and evolutionary analysis of empirical data (genomic and phenotypic), selection and fitness landscape analysis, and evolutionary modelling of parity mode evolution (in SLiM or similar). The position is primarily focussed on data analysis and interpretation, with the on-site experiment and data collection being conducted by the field- and lab-based team members. The PDRA will be based in Glasgow and work closely with co-Is in St Andrews, with some travel between sites expected.

Applicants must have a PhD in evolutionary biology, genetics, computational biology, or a closely related field. Prior experience with analyses of genomic data and computational skills are essential and expertise in population genetics is strongly preferred. Previous experience should demonstrate a commitment to research, positive work ethic, computational skills, organisational ability, and publication productivity. A strong track record of evolutionary genomics and/or computational biology is necessary, and on vertebrates (especially squamates) is a benefit. Ability to work well both independently and in a team are a must.

The postdoc will join University of Glasgow's School of Biodiversity, One Health & Veterinary Medicine. Elmer's research group studies the evolution of major adaptive traits by bringing together expertise in evolutionary biology, genomics and gene expression, and organismal biology in environmental context.

The position is for 3 years and start date is somewhat flexible; preferably by spring 2025. The position is open at grade 6 (early postdoc; research assistant) or grade 7 (experienced postdoc; research associate). See the specific criteria for these grades in the Univ. Glasgow advert for this position.

International applicants should be eligible for a UK work visa sponsored by the University of Glasgow. Please see the Univ Glasgow advert for details. The University, School and PIs are strongly committed to supporting early career researchers and their professional development. We strive to be a supportive environment and welcome a diversity of applicants!

The University of Glasgow ranks in the world's top 100 universities and recently won the Top University award from the Times Higher Education. The city of Glasgow is lively and cultural, and sits on the doorstep of the great outdoors of the Scottish Highlands, islands, and coast.

The official job description and application requirements are available on the University of Glasgow homepage

under current vacancies, <https://www.jobs.gla.ac.uk/-/job/research-assistant-slash-research-associate> vacancy reference 163613

We do not expect candidates to meet all criteria under "Knowledge, Qualifications, Skills and Experience", but in your application to the position do please outline how you meet EACH of the essential/desirable criteria listed in the job advert and any other relevant experience and skills.

The advertisement closes 12 Feb 2025

Informal email inquiries to Kathryn in advance are very

— / —

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>

UGuelph Two GenomeLevelEcology

Postdoc in genome-level ecology, University of Guelph <https://graduatestudies.uoguelph.ca/postdoctoral/-postdoctoral-fellowship-genome-level-ecology> Description of the Topic of Research:

We are seeking two postdoctoral researchers to collaborate on an interdisciplinary project in genome-level ecology. This field takes a novel approach to genomics, focusing primarily on transposable genetic elements (TEs) rather than on conventional genetic or epigenetic components of the genome. More specifically, our project views TEs as ecological agents inhabiting an intra-cellular environment. The aim is to explain patterns in the abundance and diversity of TE communities by applying ecological concepts, models, and methods at the genomic level. Suitable candidates will have experience in at least one of the following areas.

Philosophy of biology. An aptitude for clarifying scientific concepts and applying them outside their conventional domains. Expertise in either the philosophy of ecology, the philosophy of biological agency, or the philosophy of genomics (all broadly construed) is an asset.

Comparative genomics. Ideally, research expertise in analyzing whole-genome sequence data with a focus in bioinformatics. Experience working with TEs or some knowledge of their biological interactions within the genome is an asset.

Community ecology. Ideally, research expertise in analyzing community-level data (e.g. species diversity and abundance or spatial ecology) to discern likely ecological processes, such as competition or niche partitioning.

Computational modeling. Ideally, research expertise in agent-based modeling working with high performance computing clusters (HPC). Experience working on multi-species interactions within ecological communities or interactions among multiple genetic elements within genomes is an asset.

Description of Group:

These positions are funded by the John Templeton Foundation as part of a grant awarded to Dr. Stefan Linquist entitled, "Transposable Genetic Elements as Ecological Agents." Other members of the core research team include Dr. Ryan Gregory (evolutionary genetics), Dr. Stefan Kremer (computer science), Dr. Karl Cottenie (community ecology), Dr. Ford Doolittle (philosophy and evolutionary biology), Dr. Brent Saylor (bioinformatics), and Dr. Tyler A. Elliott (evolutionary genomics). Successful candidates will work in collaboration with the entire research team. There will be opportunities for learning new research skills and theoretical approaches associated with the various dimensions of this project.

General Outline of Duties:

Specific Duties will depend on the candidates' expertise. However, we require people able to co-author theoretical and empirical research papers, to analyze patterns in genomic data, and to develop individual based models. There will be opportunities for training in these fields. Postdoctoral fellows will be involved in the organization of two international workshops.

Required Qualifications:

Successful candidates should have a PhD in a discipline relevant to the project (e.g. philosophy, molecular biology, bioinformatics, ecology, or computer science). It is not necessary for successful candidates to have expertise in all aspects of the project, but an enthusiasm for interdisciplinary collaboration is highly valued. Strong candidates will have expertise in two or more research areas.

Start Date & Duration of Appointment: May 2025 through May 2027

Anticipated Hours/Days of Work (at time of posting): 35

Salary Range (Minimum): \$65,000 - \$70,000 CDN

Other Salary Information: There will be an opportunity to teach one course per year in the Department of

Philosophy at the University of Guelph for additional remuneration, if so desired by the successful candidates.

Benefits: <https://graduatestudies.uoguelph.ca/-postdoctoral/benefits-services> Application Requirements Documents Cover letter CV

Supervisor: Stefan Linquist

Contact Information: Mrs. Elanor Baldwin, Administrative Assistant baldwinelanor@gmail.com

At the University of Guelph, fostering a culture of inclusion is an institutional imperative. The University invites and encourages applications from all qualified individuals, including groups that are traditionally underrepresented in employment, who may contribute to further diversification and inclusion.

Posting Date: Tue, 12/17/2024

Closing Date: Sat, 05/31/2025

Dr. T. Ryan Gregory | Professor | Department of Integrative Biology | University of Guelph | SSC 1450 | 50 Stone Rd. E. | Guelph, ON | N1G 2W1 | 519-824-4120 Ext. 58053 | rgregory@uoguelph.ca | [he/him](#)

Ryan Gregory <rgregory@uoguelph.ca>

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UMainz EvolutionInCommunity

Position Details Start Date: March 1, 2025, or earlier, depending on the candidate's availability.

Duration: Initial funding for three years, with the possibility of extension.

Project Focus: Organisms interact in nature and form multitrophic communities. How do species evolve in a complex community? How does the evolutionary process affect community functions? In this ERC funded project, the successful candidate, together with a collaborative team, will deploy cutting-edge multi-omics approaches to address these two fundamental questions by studying real-time evolution of the duckweed and its interacting organisms in a natural community.

Key Requirements

We seek a highly motivated researcher with a doctoral degree (or equivalent) in one of the following fields: biology, evolutionary genetics, bioinformatics, or computer science. The ideal candidate will:

Demonstrate the ability to design, execute, and manage research projects independently.

Have a strong background in bioinformatics, evolutionary genetics/genomics, or community ecology.

Possess experience in statistics and genomics; expertise in computational modeling is advantageous.

Be proficient in both spoken and written English.

Why Join Us

Supported by a collaborative research team (<https://plant-x.uni-mainz.de/>), this project will provide the candidate with opportunities to enhance their scientific skills, gain independence in project planning and management, and develop leadership abilities. The candidate may also supervise PhD and Master's students, with the potential to establish their own research group. The University of Mainz is home to numerous outstanding scientific institutions (<http://www.uni-mainz.de/eng/>) and fosters a vibrant academic environment. Mainz is a historic city located on the Rhine River, offering a rich social and cultural life, and is home to a dynamic student population.

Application Requirements Applications must be written in English and include the following documents: **Motivation Letter:** A statement of research interests and how they align with the position, addressing the specified requirements (maximum 2 pages). **Curriculum Vitae:** A detailed CV, including academic achievements, research experience, and extracurricular activities. **PhD Abstract:** A concise summary of the doctoral thesis. **Referees:** Contact details for at least two references. Compile all documents into a single PDF file and send the application to Prof. Shuqing Xu via email at shuqing.xu@uni-mainz.de with the subject line: "EvolCommunity Postdoc Position - [Your Name]". **Application Deadline** The review of applications will begin on January 31, 2025. The position will remain open until filled.

Prof. Dr. Shuqing Xu Institute of Organismic and Molecular Evolution (IomE) Johannes Gutenberg University Mainz Biozentrum I Hanns-Dieter-Hüsch-Weg 15 D-55128 Mainz Germany Phone: +49 6131 39 26907 E-mail: shuqing.xu@uni-mainz.de

Shuqing Xu <shuqing.xu@uni-mainz.de>

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UMaryland EvolQuantGenomics

The Fritz Lab is seeking a postdoctoral scholar who will develop and execute research to determine the evolutionary history of structural variants involved in rapid insect adaptation.

Location: University of Maryland Institute for Advanced Computer Studies, College Park, MD

Supervisor: Principal Investigator (PI) Megan Fritz

Salary: \$62,000 plus University benefits (<http://uhr.umd.edu/benefits/>)

Category Type: Non-tenured, continuing contract (12 mo.)

Duration: 24 months, contingent upon performance

Project Topic: Structural variants and their role in rapid adaptation to human-imposed selection.

Position Description: The postdoctoral project leader will conduct experiments to quantify nucleotide sequence and structural changes across the genome over time, as well as characterize haplotypic variation in adaptive genomic regions from long-read data. The postdoc will be responsible for collection and analysis of data, reporting, communication of results at conferences and through peer-reviewed manuscripts, as well as mentorship of graduate and undergraduate researchers.

Minimum Requirements: Ph.D. in Biology, Genetics, Entomology, or related fields. Candidates must have experience using standard molecular techniques (e.g. DNA isolation, PCR, gel electrophoresis) and substantial experience conducting population and evolutionary genomic analyses.

Preferred Qualifications: Analysis of large genomic datasets (Illumina short reads, Oxford nanopore long reads), familiarity with Linux command line, and use of R and/or Python.

For best consideration apply by February 21, 2025. Interested applicants should send a cover letter, CV/resume, and a list of 3 references to Megan Fritz (mfritz13@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 affiliation, and gender identity or expression. Minorities and women are encouraged to apply.

Megan Fritz

Associate 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: www.meganfritzlab.com Twitter Handle: @MosquitoDoc she/her

Megan Lindsay Fritz <mfritz13@umd.edu>

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UOldenburg Evolution Antibiotic Resistance

Postdoctoral fellow in the Institute of Medical Microbiology and Virology

The School VI of Medicine and Health Sciences comprises the fields of human medicine, medical physics and acoustics, neurosciences, psychology and health services research. Together with the four regional hospitals, School VI forms the University Medicine Oldenburg. Furthermore, the university cooperates closely with the University Medicine of the University of Groningen.

In the research laboratory (location: Philosophenweg) of the Institute of Medical Microbiology and Virology (Director: Prof. Dr. Axel Hamprecht), Medical Campus of the University of Oldenburg, we are engaged in clinically-oriented and fundamental microbiological research with a focus on antibiotic resistance, resistance mechanisms and multidrug-resistant pathogens in human and veterinary medicine and the environment.

Your tasks

• The scientific activity includes the supervision of research projects from conception, acquisition of third-party funding to the publication of results.

• You will actively participate in the development and organization of the research laboratory.

• Active participation in the planning and implementation of teaching.

Your profile

Required qualifications:

• Completed university degree (Master or equivalent) in biology, biochemistry, human biology, human or veterinary medicine or a related field with completion of a PhD, MD or equivalent.

• Expertise in microbiological and biomolecular methods.

• Experience in documentation of research results, data management and analysis.

• Ability to prepare, present and publish scientific data.

• Excellent communication skills in English, knowledge of German (B2-level)

• High level of commitment, an independent way of working and the ability to work in a team.

Preferred qualifications:

• Knowledge of bioinformatic methods and whole genome sequencing (WGS).

• Experience in genetic engineering work

We offer

• A friendly environment with opportunities to develop your own research focus and projects.

• Active participation in the development of our research unit.

• Payment in accordance with collective bargaining law (special annual payment, public service pension scheme, asset-related benefits) incl. 30 days annual leave

• Support and guidance during your onboarding phase

• A family-friendly environment with flexible working hours (flexitime) and the possibility of pro-rata mobile work

• Benefits from the university's health promotion programme

• The possibility of personal scientific qualification (post-doctoral thesis/habilitation)

• An extensive and free further education programme as well as programmes geared toward the promotion of early career researchers (<https://uol.de/en/school6/early-career>)

Our standards

The University of Oldenburg is dedicated to increase the percentage of female employees in the field of science. Therefore, female candidates are strongly encouraged to apply. In accordance to § 21 Section 3 NHG, female candidates with equal qualifications will be preferentially considered. Applicants with disabilities will be

given preference in case of equal qualification.

Further information

There is the possibility of personal scientific qualification (post-doctoral thesis).

Contact

For further information please contact Prof. Dr. Axel Hamprecht, sandra.schoebel@uol.de, 0441/403 2160.

Apply now

Please send your application via e-mail by 22.02.2025 to sandra.schoebel@uol.de

Please send your application documents (description of your motivation, curriculum vitae, references) as one PDF document.

This ad was sent in by Timo van Eldijk, timo.jakob.benjamin.van.eldijk@uni-oldenburg.de

Timo van Eldijk <timovaneldijk@gmail.com>

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UppsalaU AntibioticResistance

Postdoc position in microbiology with a focus on antibiotic heteroresistance

At the Department of Medical Biochemistry and Microbiology, Uppsala University.

Time-limited postdoc stipend 100% during 2 years beginning as soon as possible.

Research group: Prof. Dan Andersson's research group is part of the Department of Medical Biochemistry and Microbiology and we work on bacterial genetics and evolution with a special focus on evolution of antibiotic resistance. The group presently consists of 15 people. More information can be found at: <https://www.uu.se/en/department/medical-biochemistry-and-microbiology/research/andersson-dan-i> Research project: The overall aim of this project is to understand the dynamics and fitness effects of gene copy number variation in bacteria. Of special interest is heteroresistance, a phenotype where in a main population of susceptible bacteria there exists a small resistant sub-population. We have previously shown that four different mechanisms can cause a transient increase

in the copy number of antibiotic resistance genes and generate the resistant sub-population. These gene copy number (GCN) increases carry fitness costs that can be genetically ameliorated by compensatory stable resistance mutations that are less costly than the original copy number increase. These findings led to the novel hypothesis that heteroresistance mediated by GCN changes can facilitate and precede the evolution towards stable resistance. In this project, we want to understand the mechanisms underpinning the fitness costs of increased GCNs and whether the compensatory evolution also can be observed in antibiotic-treated patients.

Qualifications: We are looking for a postdoc that has a PhD in microbiology, molecular biology, evolutionary biology or similar. The project will involve physiological and genetic analysis of bacteria (mainly *E. coli*), experimental evolution and WGS. We want a person with high creativity, ability to independently plan experiments as well as excellent analytical and practical skills. You should have high skills in written and spoken English and the ability to work in an interdisciplinary team.

Instructions for application: Please send your application compiled in a single pdf file to Prof. Dan I. Andersson (Dan.Andersson@imbim.uu.se) before 31 Jan 2025 and include in your application.

- A short letter that describes your research interests and a motivation for why you would be suitable for this position (maximum 2 pages)
- Curriculum vitae including publication list
- Copy of proof of passed PhD exam
- Names, email addresses and telephone numbers to three references

Dan I. Andersson, PhD Professor in Medical Bacteriology Director Uppsala Antibiotic Center (www.uac.uu.se) Uppsala University Dept. of Medical Biochemistry and Microbiology Box 582, SE-751 23, Uppsala, Sweden phone: +46 (0)18 4714175 email:dan.andersson@imbim.uu.se

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Page Title

När du har kontakt med oss på Uppsala universitet med e-post innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: <http://www.uu.se/-om-uu/dataskydd-personuppgifter/> E-mailing Uppsala University means that we will process your personal data. For more information on how this is

performed, please read here: <http://www.uu.se/en/-about-uu/data-protection-policy> “Dan I. Andersson” <dan.andersson@imbim.uu.se>

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Department of Animal Ecology Evolutionary Biology
Centre Uppsala University Norbyvägen 18D 752 36 Uppsala Sweden

Phone: +46-(0)18-471 2639 <https://clausrueffler.github.io/> Claus Rueffler
<claus.rueffler@posteo.net>

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UppsalaU EcologyGeneticsEvolution

Reminder: Deadline for application February 9, 2025

The Department of Ecology and Genetics at Uppsala University, Sweden, invites applications for postdoctoral fellowships through the Birgitta Sintring Foundation.

For details see here <https://www.uu.se/en/department/-ecology-and-genetics/research/the-birgitta-sintring-foundation> Scholarships are handed out for up to 2 years, with the possibility for prolongation with a third year. Scholarships are handed out to young scientists (defined as up to 7 years after their PhD degree; career breaks, e.g., for child care and sick leaves, can be deducted from the total time).

Interested candidates should contact a group leader of their choice to discuss potential projects and obtain their support as a host (for a list of all group leaders see the tab PIs available as postdoc hosts or collaborators on the above website).

Uppsala University is a comprehensive research-intensive university with a strong international standing. Our ultimate goal is to conduct education and research of the highest quality and relevance to make a long-term difference in society. Our most important assets are all the individuals whose curiosity and dedication make Uppsala University one of Sweden’s most exciting workplaces. Uppsala University has over 54,000 students, more than 7,500 employees and a turnover of around SEK 8 billion. The Department of Ecology and Genetics is an international environment with staff and students from all over the world. Research at the Department of Ecology and Genetics spans from evolutionary ecology and genetics to studies of ecosystems. For more information, see <https://www.uu.se/en/department/-ecology-and-genetics> Please submit your applications by 9 February 2025.

Applications have to be submitted through this the link on the above website

Decision are taken in May 2025.

Claus Rueffler Associate Professor

UppsalaU HumanPopgen

Postdoctoral position in Population Genetics at the Center for the Human Past

Uppsala University is a comprehensive research university with a strong international position. The mission is to conduct research and education of the highest quality and to interact with society in various ways. Our most important asset is all the individuals who with their curiosity and commitment make Uppsala University one of the most exciting workplaces in the country. Uppsala University has 54,000 students, 7,500 employees, and a turnover of nearly 8 billion SEK.

Research will be conducted within the Human Evolution Program within the Department of Organismal Biology (Evolutionary Biology Center, Uppsala University, Sweden). The program has extensive interests in population genetics and human evolution, providing numerous opportunities for collaboration with postdocs and PhD students working on related projects. The research environment is international, with English as the working language. For more information on the Human Evolution Program, visit: <http://www.iob.uu.se/research/-human-evolution>. The postdoc will also be associated with the Center for the Human Past.

Center for the Human Past: The CHP is a pioneering initiative that unites the three research areas of archaeology, genetics, and linguistics. Each discipline has accumulated significant amounts of information and developed many different research methods to analyze these. Researchers at the center will focus on bringing together these unique types of data and methods to strengthen the interdisciplinary development of the field. A central goal for the center is to train a new generation of students and doctoral candidates with skills and insights into the various theoretical models and analytical methods used across these research areas, as well as the ability to work with the databases that are under

development. The aim of the center is to illuminate and understand various aspects of human development over the past 10,000 years, thereby creating a comprehensive picture of human prehistory regarding language, culture, and genetic evolution in Africa, Oceania, and Eurasia.

We are seeking a postdoctoral researcher in population genetics who will contribute to the center's overarching goal to illuminate and understand various aspects of human development over the past 10,000 years. The postdoctoral researcher will work with computer-based analysis methods and large databases to develop theory and method for using aggregated data from genetics, archaeology and linguistics, thereby developing innovative interdisciplinary research on human history. Based on population genetic perspectives, the postdoctoral project will illuminate various aspects of human history, at the interface between questions of genetic, culture and language evolution.

Qualification requirements: A doctoral degree in population genetics, bioinformatics, archaeogenetics or a related area or a foreign degree assessed as equivalent to a doctoral degree. The degree must have been obtained by the time the employment decision is made. Primarily, those who have graduated no more than three years ago are eligible. In calculating the three-year period, the reference point is the last application date. If there are special reasons, such a degree may have been awarded earlier. Special reasons include leave due to illness, parental leave, trust duties within trade union organizations, etc.

Proven experience and ability to work with computer-based analysis methods and information in large databases with complex aggregated data is a requirement. The applicant should have demonstrated independence and high research quality through high-quality research publications. Very good oral and written skills in English are required. Being able to work independently as well as in collaboration with others is necessary. Great emphasis will be placed on personal characteristics, hence interviews and reference checking may be included in the selection process.

Desirable/Additional qualifications: Previous studies in population genetics and/or archaeogenetics involving Africa, Oceania, and Eurasia, or a combination of studies from these areas are desirable. Knowledge and skills in working with database curation, model testing, simulation-based studies, and spatial genetic analyses will be highly regarded. Additionally, a background in mathematics, computational methods, and statistical training will be advantageous. Demonstrated ability to contribute to the principles of open science, especially regarding the production of open and reusable

research data. Experience of working in international and interdisciplinary research contexts is desirable.

About the employment The position is temporary for two years according to the central collective agreement. The extent is full-time. The position may include teaching and supervision up to 20% of full time.

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

USaoPaulo Two GenomicsClimateAdaptation

2 Postdoctoral Fellowships in Ecology, Evolution and Genomics of Climate Adaptation

Universidade de São Paulo (Brazil)

We have two FAPESP postdoctoral fellowships available to work at Rodrigo Cogni' lab at the Ecology department, Biosciences Institute, Universidade de Sao Paulo in Brazil. The postdoctoral fellow will work on some of the following projects: (1) Clinal adaptation in South American *D. melanogaster* populations at the phenotypic and genomic levels, (2) Climate adaptation in Neotropical drosophilid species from the Atlantic Forest and the Cerrado savannah, (3) The influence of gut bacteria and the endosymbiont *Wolbachia* on climate adaptations, (4) The interactions among Neotropical drosophilids, *Wolbachia* and viruses.

Overall in the next few years our group will be working on a project that have five main innovative features: (1) the use of modern next-generation sequencing technologies integrated with laboratory and field studies on natural populations, (2) the use of extensive material that has been in storage for 20 years, to understand long-term genome wide responses to global warming, (3) our project is the first study to investigate clinal variation in natural populations of *D. melanogaster* in South America over a broad geographical range, (4) we will investigate climate adaptation in a highly integrated way, from genomes and transcriptomes to phenotypes, including a very innovative mapping approach, and the influence of gut microbiota and the symbiont *Wolbachia*, and (5) we will use natural population of extremely diverse neotropical drosophilids and their

interactions with *Wolbachia* and viruses to understand climate adaptation and evolution of ecological interactions.

Fellows will have the opportunity to guide the direction of the research depending on their interests and to collaborate on other projects at the Cogni's lab.

The initial fellowship would be for two years, with the possibility of renewing it for an additional two years. There is also the possibility to apply for a Research Abroad Fellowship to spend an additional year in one of our international collaborators or any research group abroad. FAPESP pays 12,000.00 reais/month (tax free), relocation costs and 14,400 reais/year for training, conferences, and research expenses.

We are seeking highly motivated candidates who have a deep interest in this area of research. Previous experience of some of the approaches that will be used in the project is preferable but not required. Applicants must have a PhD in evolutionary biology, ecology, genetics, or related fields. To be considered, please submit the following material by email to Prof. Rodrigo Cogni (rcogni@usp.br):

1. Cover letter outlining your interests and suitability for the position
2. Curriculum vitae
3. Up to three examples of published papers
5. Names and contact information of two references.

Application deadline: January 26th, 2025.

Start date: Ideally early 2025, but flexible.

Address questions about the application/nomination process to Prof. Rodrigo Cogni (rcogni@usp.br)

We support diversity and encourage applications from women and groups under-represented in science.

Rodrigo Cogni

Associate Professor, Department of Ecology, Universidade de São Paulo

Rua do Matão 321, Trav. 14 (sala 358) Cid. Universitária, São Paulo-SP CEP: 05508-090 Brazil E-mails: rcogni@usp.br and rodrigocogni@gmail.com <http://ecologia.ib.usp.br/ecoevo/> Rodrigo Cogni <rcogni@usp.br>

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USouthFlorida EvolGenomics

POSTDOCTORAL RESEARCHER

University of South Florida

Department of Integrative Biology

We are seeking a postdoctoral researcher for August 1, 2025 (or sooner) to work on genomics, transcriptomics, and machine learning in Tasmanian devils and devil facial tumor disease (DFTD). The NSF-funded international collaboration builds on 20+ years of research tracking the spread of this unique transmissible tumor across Tasmania and consequent endangerment of the iconic Tasmanian devil. A chromosome-level reference genome assembly is available for the devil, and population genomic data have already been collected for >3500 Tasmanian devil individuals. The successful applicant will have an unprecedented opportunity to analyze thousands of devil and tumor samples taken throughout epizootic progression to use GWAS, eQTL mapping, machine learning, and other approaches to understand the repeatability and predictability of the genotype-phenotype relationship in wild populations.

The position is centered in the lab of Dr. Mark Margres (<https://www.margreslab.com>) at the University of South Florida in close collaboration with Dr. Andrew Storfer (<https://labs.wsu.edu/storfer/>) at Washington State University. The University of South Florida offers genomic core facilities with state-of-the-art equipment, high-performance computational facilities, and staff support.

Review of applications will begin immediately and continue until the position is filled. A Ph.D. in Biology or a related discipline, combined with genomics and bioinformatics experience, is required. Desired qualities also include a background in machine learning, infectious disease evolution, and/or cancer genomics. Start date is negotiable. Salary and benefits are competitive. Position is for 1 year, with continuation for an additional year pending satisfactory progress. To apply, please send in pdf format a CV, statement of interest, up to three representative reprints, and names, addresses and emails for three references via email to: Mark Margres (margres@usf.edu).

Mark J. Margres, Ph.D. Assistant Professor Department of Integrative Biology University of South Florida Tampa campus (813)-974-4576 www.margreslab.com

Mark Margres <margres@usf.edu>

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UTurku Finland Three HumanDiversity

The Human Diversity consortium at the University of Turku, Finland (sites.utu.fi/humandiversity/) is looking for three postdoctoral researchers:

Postdoctoral Researcher in Archaeogenomics (<https://tinyurl.com/archgen>)

Postdoctoral Researcher in Evolutionary Health (<https://tinyurl.com/evolheal>)

Postdoctoral Researcher in Evolutionary Language Sciences (<https://tinyurl.com/evolangsci>)

The Human Diversity research consortium studies human diversity from the perspectives of language, genetics, culture and health. The central questions of the consortium are how human contacts, environmental factors and communication networks have produced the past and current human diversity, and what it will be like in the future.

Application deadline is on 31 January 2025 at 16:00 (Europe/Helsinki). The employment begins in February 2025 at the earliest or upon agreement, and lasts until the end of December 2026. See the tinyURLs above or bedlan.net/news/three-postdoc-positions/ for further information about the positions.

Mirkka Lahdenperä, $\frac{1}{2}$ <mirkka.lahdenpera@utu.fi>

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UWesternAustralia BioinformaticsGenomics

Postdoctoral Research Associate - Bioinformatics (Evolutionary/Conservation)

Employer: University of Western Australia

Duration: 1-year

Brief Position Description: We are looking at the evolutionary genomics of fragmented populations of lizards in relation to phenotype, habitat change and population structure. We have whole genome sequences for ~300 lizards across a spread of discrete populations from over 25 years, and we are looking for a bioinformatician with skill strengths in estimating mutation load (SnPEff) and/or genomic parameters from WGS. The successful candidate will work under the supervision of Dr Natasha LeBas, Prof Leigh Simmons (Centre for Evolutionary Biology) and Professor Dave Edwards (Applied Bioinformatics Group). Remote working may be considered. We are keen to fill and commence soon, please contact us for further information.

Bioinformaticians working in other disciplines welcome to apply.

Key Responsibilities: Estimate genomic parameters of interest (mutation load, GWAS, GEA) from whole genome sequences and prepare data for analysis, analyse data and contribute to manuscript preparation.

Centre for Evolutionary Biology

<https://www.uwa.edu.au/.../centre-for-evolutionary-biology> Centre for Applied Bioinformatics

<https://www.uwa.edu.au/.../centre-for-applied-bioinformatics> Contact email: natasha.lebas@uwa.edu.au

Natasha Lebas <natasha.lebas@uwa.edu.au>

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UZurich PopulationGenomics Human Plants

The Shimizu group invites applications for a Postdoctoral Researcher in population genomics to study the demography of humans and domesticated crop species related to language evolution at the University of Zurich, Switzerland. The details with full links here: <https://jobs.uzh.ch/job-vacancies/postdoc-in-population-genomics/40227b73-2360-4e79-8924-844e5f5ed4c0>

Your responsibilities Similarities between genetic and linguistic evolution were first pointed out by Charles Darwin. Supported by the NCCR Evolving Language (www.evolvinglanguage.ch), we used human population genomic data at a global scale to explore the extent of matches and mismatches between genes

and languages, with the database GeLaTo (Genes and Language TOgether) (Barbieri et al. PNAS 2023, <https://evolvinglanguage.ch/genes-and-languages-not-always-together/>), and we also explored local case studies in Asia and in South America (Matsumae et al. Science Advance 2021, Arango-Isaza et al. Curr Biol 2023). With the new Postdoctoral Researcher position, we will expand our team on the genetic studies of human and plant diversity with new projects, testing hypothesis on gene-language coevolution, and looking at case studies of language families spreading along with farmers and crop species (farming/language dispersal hypothesis). The position is in the group of Prof. Kentaro Shimizu (Main PI, Department Director, https://www.ieu.uzh.ch/en/staff/member/-shimizu_kentaro.html) in collaboration with other groups.

Your profile

- PhD degree in biology - Background in population genetics, molecular anthropology, or bioinformatics - Experience in genome-wide polymorphism analysis to infer demography, selection or genome-wide association studies (machine learning is a plus) - Interest in human prehistory, linguistics, human and plant genetic diversity
- Proficiency in English

What we offer

The University of Zurich offers a highly international, mostly English speaking and an interdisciplinary collaborative environment. Zurich offers a great quality of life, consistently ranking in the top three cities worldwide. The NCCR is a Swiss National Center of Competence in Research with the goal of creating a new discipline, Evolutionary Language Science, that targets the past and future of language. The center consists of leading scientists from traditionally separated academic domains, which allows us to harvest the diverse expertise from the humanities, social sciences, computational sciences, natural sciences and medicine towards a broadscale interdisciplinary collaboration. The project is carried with supervision from project PI Prof. Kentaro Shimizu (group website <https://www.ieu.uzh.ch/->

[en/research/evolbiol/ecogenomics.html](https://www.ieu.uzh.ch/en/research/evolbiol/ecogenomics.html)), Prof. Chiara Barbieri (Univ. Cagliari & UZH), and in collaboration with NCCR director Prof. Balthasar Bickel (Department of Comparative Language Science), Prof. Andrea Migliano (Department of Evolutionary Anthropology), and a new professor in genetics of language. We expect further occasions to collaborate within and beyond the NCCR.

UZH offers excellent opportunities and strong support for career development. Salaries are internationally competitive. UZH and the NCCR project invest in gender balance and inclusiveness. Employment is at 80% FTE. Link: Salary ranges, guidelines for employees in SNSF-funded projects https://www.snf.ch/media/en/yXApuFw4ml0TPYe2/-Annex_XII_Ausfuehrungsreglement_Beitragreglement_E.pdf The initial contract is for 1 year and renewable during the project timeframe (until May 2028).

Workplace The positions are primarily located at the Department of Evolutionary Biology and Environmental Studies (Prof. Shimizu as the Director <https://www.ieu.uzh.ch/en.html>), Irchel campus. The NCCR supports exchange with other departments in its network.

Start of employment We seek to fill positions as soon as possible. The search will remain open until the position is filled. Earlier or later start points may be negotiated.

Application procedure Please submit your application in a single PDF to judith.baumgartner@uzh.ch. The file should include your past research achievements, a cover letter that highlights your interests in the position, your CV, two or more reference contacts (or reference letters), and one or two samples of your research work. Application from the website is also possible.

Prof. Dr. Kentaro K. Shimizu,

— / —

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

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Arizona Bees Aug15-25

In partnership with the American Museum of Natural History, Cornell University, and the Southwestern Research Station, we are proud to announce the 24th installment of The Bee Course. The Bee Course is a ten-day workshop held at the Southwestern Research Station in Portal, Arizona that will run from August 15th through the 25th, 2025. The course is designed to train students in bee identification and systematics, bee biology and ecology, and faunistics and faunal survey work. The course focuses on wild bees (not honeybees), and we accept applications from people with an academic, land-management, policy, or conservation background. For more information on the course, including instructions on how to apply, a list of this year's instructors, and course testimonials from previous offerings, please visit the new and improved course website at www.thebeecourse.org. Bryan N. Danforth, Professor Department of Entomology 3124 Comstock Hall Cornell University Ithaca, NY 14853-2601 phone: 607-255-3563/FAX: 607-255-0939 email: bnd1@cornell.edu Lab website: <http://www.danforthlab.entomology.cornell.edu/> The Solitary Bees: Biology, Evolution, Conservation <https://press.princeton.edu/titles/13525.html> The Bee Course (2024): <https://www.thebeecourse.org/> Bryan Nicholas Danforth <bnd1@cornell.edu>

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ArizonaStateU EvolutionaryCellBiology Jan13-Apr28

On behalf of Dr. Michael Lynch, who will be teaching a class in Evolutionary Cell Biology in Spring 2025 semester, I'm writing to share the Zoom link (<https://asu.zoom.us/j/86824596554>) of his class. The class is from 9am to 10:15am every Tuesday and Thursday, from the week of Jan 13 to the week of April 28.

The class is open to the public and people who are interested in this topic, and it would be fantastic if EvolDir could help share this info with your members and readers.

—
Please see below for some details regarding the class provided by Dr. Lynch, and thank you for sharing this with your networks.

EvolutionarCell Biology is a new emerging subdiscipline that strives to integrate the fields of cell biology, biophysics, bioenergetics, and evolutionary theory in novel ways, in an attempt to develop a more comprehensive field of evolutionary biology focused at the mechanistic level.

A graduate course will be offered this semester at Arizona State University by Michael Lynch, who also happens to be the author of

Evolutionary Cell Biology: The Origins of Cellular Architecture. Oxford Univ. Press, Oxford, UK, 2024.

In a series of 24 75-minute lectures, the course will cover all of the chapters in this book, and taught at a level

that should be accessible to those with an undergraduate level of understanding of cell and evolutionary biology.

As part of our NSF Biological Integration Institute on Cellular Mechanisms of Evolution, we are providing an opportunity on Zoom for anyone who wishes to link in and listen. The lectures will also be recorded and subsequently made available open-access.

The course will be taught on Tuesdays and Thursdays, 9:00 to 10:15 am (MST), starting on 16 January 2025.

Zoom Link: <https://asu.zoom.us/j/86824596554>
Queries can be addressed to Victor Chai (victor.chai@asu.edu).

Those who wish to attend should also provide Victor with your name and email address, so we can contact you with announcements.

—

Please let me know if you have any questions in the meantime.

Sincerely,

Victor Chai Program Manager

Biodesign Center for Mechanisms of Evolution Biodesign Institute Arizona State University

Mail Code: 7701 Biodesign Institute Tempe, AZ 85287-5001 p: 916-907-4955 email: victor.chai@asu.edu web: biodesign.asu.edu

Victor Chai <Victor.Chai@asu.edu>

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Berlin FreeDemographicResilience Aug7-8

Dear colleagues and friends,— — We have recently developed a new approach to study the resilience of wild animals. We would like to present this approach to you during a 2-day workshop - with no attendance fee - on Aug 7-8th 2025 in Berlin, Germany.

The idea of the workshop is to teach you how to estimate the resilience of your study population and its variation over time. Considering variation over time can provide more fine-tuned estimates of demographic resilience metrics. — This workshop is designed for holders of long-term datasets on free-ranging wildlife populations or those who are considering to work with

similar datasets in future and/or have interest and experience in demographic resilience. The aim of this workshop is also to inspire an exchange between field biologists and quantitative ecologists interested in the quantification of demographic resilience. No previous background in quantitative ecology is required.

The workshop is free of charge*, can host up to 50 persons and will be offered as a hybrid event. We can book up to 40 rooms for our guests at our venue at Bildungszentrum Erkner e. V..

If you are interested, please let us (wilder-project@izw-berlin.de) know by Feb 17th 2025, and indicate whether you 1) would like to join in person or remotely, 2) will come on your own or with your team, and 3) would like to book a room at the venue.

We would appreciate it if you spread this information to other potentially interested colleagues.

The WILDER team: Viktoriia Radchuk, Oliver Höner, Sarah Benhaiem, Adam Clark, Ella White, Julie Louvrier, Ashlee Mikkelsen and Leonie Walter — Webpage: <https://www.leibniz-izw-akademie.com/-seminare/workshop-demographic-resilience> Reference: Capdevila, P., Stott, I., Beger, M., & Salguero-Gómez, R. (2020). Towards a comparative framework of demographic resilience. *Trends in Ecology & Evolution*, 35(9), 776-786.

Material: Louvrier et al. (2025) demres: An R package to study time-varying demographic resilience Louvrier et al. in prep. Assessing time-varying demographic resilience across mammals White et al. (2025) Resilience of a long-lived mammal: time and demographic structure matter

*Costs not covered: travel, accommodation and dinners
“Walter, Leonie” <walter@izw-berlin.de>

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Gabon TropicalFieldResearch JunJul

The Field School in Tropical Ecology (ECOTROP) is pleased to announce a National Science Foundation supported eight-week summer field course in tropical ecology and conservation. This field course will be held in Gabon, Central Africa and will focus on examining the effects of past human settlements on forest ecol-

ogy and biodiversity. This field research opportunity is open to U.S. students at both the undergraduate and graduate level and will provide hands on mentorship in a variety of disciplines: archaeology, ethnobotany, ecology, environmental anthropology, geosciences and wildlife biology. On-line preparatory courses and language training will be held in May and June (2025) and field work will be conducted in Gabon for the month of July (2025).

Application deadline: March 14th, 2025. Applications can be submitted at the following website: <https://www.uno.edu/studyabroad/gabon> Requirements:

- Must be a citizen, national, or permanent resident of the United States
- Must currently be registered as an undergraduate or graduate student, with a minimum GPA of 2.5
- One semester of sophomore level ecology, evolutionary biology or relevant discipline (e.g. geosciences, anthropology or environmental science)
- Preferably one semester of college-level French
- Hold or are willing to apply for a valid passport
- Enjoy working in a multi-cultural setting and learning new skills
- Able to camp and work under physically strenuous conditions

This course is optionally available for six credits for undergraduates (applicable course fees apply).

Prior to departure, student participants will be given six weeks of preparatory online classes in (a) the French language and (b) the fundamental concepts of conservation sciences relevant to this project. Students will then spend one month in Gabon and will work collaboratively with their Gabonese student counterparts and international mentors in the development of team research projects in one or more disciplines. Beyond the classroom, this will foster cultural exchange while allowing students to experience the breathtaking beauty and diverse wildlife of Gabon's rainforests.

Classroom and field instruction will be given by scientists from collaborating institutions including: the University of New Orleans, The University of Michigan, the Universit? des Sciences et Techniques de Masuku, the University of Omar Bongo, the Gabonese National Park Service, the University of Lausanne, as well as the French Research Institute for Development and the Agricultural Research Center for Sustainable Development. On returning to the U.S., a series of professional development workshops will be organized to provide guidance in future career development and networking opportunities.

This overseas research training opportunity is funded through the National Science Foundation's International Research Experiences for Students (OISE 2420103) and is coordinated in the US by PI Nicola Anthony (Univer-

sity of New Orleans) and co-PI Johannes Foufopoulos (University of Michigan).

Costs for all travel and in-country expenses will be provided by the program as well as an eight-week student stipend for summer 2025.

Sincerely,

Nicola Anthony Professor Freeport-McMoRan Chair in Wildlife Sustainability Department of Biological Sciences University of New Orleans New Orleans LA 70148 Email: (nanthony@uno.edu)

Johannes Foufopoulos Associate Professor School for Environment & Sustainability Dana Building University of Michigan Ann Arbor MI 48109 Email: jfoufop@umich.edu

nanthony@uno.edu

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KingsC London PythonForBiologists Jan27-31

Python for Bioinformatics: 5-Day Course Overview

Instructor: Dr. Martin Jones, in collaboration with the Hub for Applied Bioinformatics (KCL).

Audience: Biologists with no prior programming experience who want to learn Python for bioinformatics.

Course Highlights:

Beginner-Friendly: No programming experience required; tailored for complete beginners with a biology background.

Practical Focus: Real-world bioinformatics examples and hands-on exercises.

Comprehensive Resources: Electronic copies of presentations, exercises, data, and scripts provided.

Goal-Oriented: Equip students to apply Python to their research and continue learning independently.

Who Should Attend?

Designed for researchers and technical workers in biology who:

Have a basic understanding of biological concepts (e.g., DNA, protein sequences, translation, introns/exons).

Want to learn programming from scratch.

Requirements: A laptop with Python installed; no advanced computer skills needed.

Course Structure

Session 1: Introduction and Basics

Overview of Python and its benefits for research. Fundamentals: terminals, variables, strings, and error handling. Practical: Simple scripts for sequence manipulation.

Session 2: File Handling and Slicing

Reading/writing files and Python's interaction with the OS. Practical: File processing scripts using slice syntax.

Session 3: Lists and Loops

Handling large datasets with lists and loops. Practical: Working with larger data files.

Session 4: Conditions and Flow Control

Decision-making with conditional tests and Boolean logic. Practical: Filtering challenges with CSV files.

Session 5: Structuring Code with Functions

Writing reusable functions and introducing automated testing. Practical: Creating functions for unit tests.

Session 6: Standard Library and Regular Expressions

Exploring Python's standard library and regex for pattern matching. Practical: Solving bioinformatics problems with regex.

Session 7: Dictionaries

Introduction to key-value data with dictionaries. Practical: K-mer counting and DNA-to-protein translation.

Session 8: File Management

Automating file operations like renaming, moving, and organizing. Practical: Managing DNA sequences by length.

Sessions 9-10: Workshop Time

Recap of key topics or applying Python to personal research.

Contact Information

For questions, email Dr. Martin Jones: martin@pythonforbiologists.com.

For more information: <https://pythonforbiologists.com/introduction-to-python-for-biologists.html> To sign up: <https://estore.kcl.ac.uk/-conferences-and-events/academic-faculties/faculty-of-life-sciences-medicine/applied-bioinformatics/python-for-biologists-with-martin-jones-in-partnership-with-the-hab> Jazmine Portch Operations Assistant for Mathias Gautel Administrator for Hub for Applied

Bioinformatics School of Basic and Medical Biosciences | Faculty of Life Sciences and Medicine

Jazmine Portch <jazmine.portch@kcl.ac.uk>

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MaxPlanckPleon EvolutionaryRescueTheoryExpts Jun30-Jul3

We are happy to announce the second edition of our Evolutionary Rescue workshop series at the Max Planck Institute for Evolutionary Biology in Plön, Germany.

In 2023 we organised a workshop on 'Mathematical models of evolutionary rescue'. In this second edition we now aim to bring modelers and experimentalists together to discuss (1) which theoretical insights should be tested experimentally and how this could be done, (2) which experimental observations could be clarified with the help of theoretical models, and (3) which open questions could be addressed by the co-development of models and experiments. In addition to invited and contributed talks and posters there will be discussion sessions designed to increase cross-talk between theory and experiments.

The workshop will take place from June 30 (evening) to July 3. Before the workshop (June 29-30) we are offering a "pre-school" for those who would like to obtain an introduction to modeling evolutionary rescue.

Registration is open until March 15. We hope that all participants present a talk or poster but it is not mandatory. Registration is free.

For more information see the website: <https://workshops.evolbio.mpg.de/event/128/> Happy new year, Matt Osmond and Hildegard Uecker

Matthew Osmond <mm.osmond@utoronto.ca>

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Online BayesianAnalysis Feb17-21

Dear colleagues,

A few slots are available for the course “Introduction to Bayesian Inference in Practice”. This course is relevant to people working on evolution and doing statistical analysis. (18 participants max).

Dates: February 17th-21st, 2025, from 13:00 to 17:00 (Madrid time zone).

Instructors: Dr. Daniele Silvestro [1] (University of Gothenburg, Sweden) and Tobias Andermann [2] (University of Gothenburg, Sweden)

Course Overview:

This course is based on the assumption that the easiest way to understand the principles of Bayesian inference and the functioning of the main algorithms is to implement these methods yourself.

The instructor will outline the relevant concepts and basic theory, but the focus of the course will be to learn how to do Bayesian inference in practice. He will show how to implement the most common algorithms to estimate parameters based on posterior probabilities, such as Markov Chain Monte Carlo samplers, and how to build hierarchical models.

He will also touch upon hypothesis testing using Bayes factors and Bayesian variable selection.

The course will take a learn-by-doing approach, in which participants will implement their own MCMCs using R or Python (templates for both languages will be provided).

After completion of the course, the participants will have gained a better understanding of how the main Bayesian methods implemented in many programs used in biological research work. Participants will also learn how to model at least basic problems using Bayesian statistics and how to implement the necessary algorithms to solve them.

Participants are expected to have some knowledge of R or Python (each can choose their preferred language), but they will be guided “line-by-line” in writing their script. The aim is that, by the end of the week, each participant will have written their own MCMC - from scratch! Participants are encouraged to bring own datasets and questions and we will (try to) figure them

out during the course and implement scripts to analyze them in a Bayesian framework.

More information and registration at <https://www.transmittingscience.com/courses/statistics-and-bioinformatics/introduction-bayesian-inference-practice/> 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 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:

[1] <https://www.transmittingscience.com/instructors/-daniele-silvestro/>



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Online Comparative Genomics Apr7-11

Dear all,

registrations are now open for the Physalia Comparative Genomics online course in April (7th-11th).

This course will introduce biologists and bioinformaticians into the field of comparative genomics. We will cover a broad range of software and analysis workflows that extend over the spectrum from assembling and annotating small eukaryotic genomes, via the identification of single nucleotide variants (SNVs) and structural variants (SVs) within the population, to the assessment of their likely functional impact of the detected variants in an evolutionary context.

Course website: (<https://www.physalia-courses.org/courses-workshops/course34/>)

Attendees should have a background in biology. There will be a mix of lectures and hands-on practical exercises using command line Linux. We will therefore dedicate one session to introduce basic and advanced Linux concepts for processing data on Amazon cloud (AWS). Attendees should have also some familiarity with genomic data such as that arising from NGS sequencing experiments.

For the full list of our courses and workshops, please visit our webpage: (<https://www.physalia-courses.org/courses-workshops/course68/>)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR
info@physalia-courses.org

“info@physalia-courses.org” <info@physalia-courses.org>

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Online Computational Pangenomics Apr7-9

Dear all registrations are open for the Physalia online course on Computational Pangenomics, taking place from 7-9 April. This course explores the cutting-edge field of pangenomics, equipping participants with the skills to construct and analyse pangenome graphs from whole genome assemblies.

Course website: <https://www.physalia-courses.org/courses-workshops/computational-pangenomics/> By joining this course, you will learn how to build and analyse pangenome graphs, helping to overcome reference bias and improve genomic analyses. Through hands-on exercises with real datasets, you will gain practical experience using powerful tools like ODGI and WFMASH. The course will also explore key applications of pangenomics in comparative genomics and genome assembly. Throughout the three days, expert instructors will guide you through interactive discussions and exercises, ensuring you gain valuable insights and practical skills. This course is designed for biologists and bioinformaticians working with pangenomes, comparative genomics, or genome assembly. A good understanding of Linux command line and genomic data formats (FASTA, VCF, BED) is required.

For the full list of our courses, please visit: <https://www.physalia-courses.org/courses-workshops/computational-pangenomics/> Best regards, Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR info@physalia-courses.org
www.physalia-courses.org “info@physalia-courses.org”
<info@physalia-courses.org>

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Online Deep Learning for Life Sciences Jan27

Hi everyone

Instats is pleased to be offering a 1-day seminar on

Deep Learning for the Life Sciences, running on Jan 27. Led by Dr. Nikolay Oskolkov, this seminar provides an excellent opportunity to explore how deep learning techniques can be applied to solve complex problems in the life sciences. Whether you are new to deep learning or looking to expand your expertise, this course will equip you with the knowledge and tools needed to integrate these cutting-edge methods into your research. Participants will delve into key topics such as neural network architectures, data preprocessing for biological datasets, and practical applications of deep learning in genomics, proteomics, and other areas of the life sciences. With a focus on hands-on learning, the seminar ensures attendees gain practical experience with tools and frameworks commonly used in the field.

<https://instats.org/seminar/deep-learning-for-the-life-sciences2> Don't miss this chance to learn from a leading expert sign up today to secure your spot!

Best wishes

Michael Zyphur Director Institute for Statistical and Data Science instats.org

Michael Zyphur <mzyphur@instats.org>

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

Online DeepLearningPopGenomics Mar31-Apr3

Dear all,

We are excited to announce our upcoming online course: Machine and Deep Learning Methods in Population Genomics and Phylogeography, scheduled from 31 March to 3 April.

Course website: (<https://www.physalia-courses.org/-courses-workshops/deep-learning-in-popgen/>)

This course will focus on using deep learning, specifically Convolutional Neural Networks (CNN), to extract information from genetic data for population genomics and phylogeography inference. The theoretical background for simulating genetic data and developing machine and deep learning architectures will be covered and followed by practical examples, in modules structured over four days. On the first day, the participants will learn how to simulate genetic data under competing demographic scenarios and use ABC for their inference. Day 2 will include an introduction to machine learning and its ap-

plications to evolutionary genomics. In Day 3, deep learning will be introduced and used to compare the demographic scenarios conceived in previous days. Day 4 will be dedicated to the simulation of genomic regions with selective sweeps and using CNN to detect such regions on real genomes. The course is structured to include lectures with discussions of key concepts and practical hands-on sessions, contextualised with research study cases.

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/deep-learning-in-popgen/>)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR
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(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online GenomeAssemblyandAnnotation Mar17-21

Dear all,

We are excited to announce our upcoming online course, Assembly and Annotation of Genomes, scheduled for 17-21 March 2025.

Course website: (<https://www.physalia-courses.org/-courses-workshops/course20/>)

This course provides a comprehensive introduction to de novo genome assembly and annotation, covering the latest sequencing technologies (e.g., Illumina, PacBio, Oxford Nanopore) and scaffolding methods (e.g., Hi-C, optical mapping). Participants will learn hands-on techniques for assembly evaluation, visualization, and feature annotation.

Key highlights:

- Understand the concepts related to de novo genome assembly and annotation for genomes of all sizes, from viruses to mammals
- Learn the strengths and weaknesses of different sequencing technologies, including Illumina short read sequencing, Pacific Biosciences and Oxford Nanopore

long read sequencing, as well as scaffolding technologies including optical mapping and proximity ligation (Hi-C), for de novo genome assembly and annotation.

- Gain hands on experience with common tools for de novo genome assembly, assembly quality evaluation, assembly visualization and manual curation
- Hands on experience of feature annotation (e.g. genes, repeats)

Designed for researchers at all levels no prior sequencing background required.

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/-course20/>)

Best regards, Carlo

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Online IntroCommunityAnalytics Feb26-28

ONLINE COURSE - Community Analytics in Ecology and Evolutionary Biology for Beginners (CAFB01)

<https://www.prstats.org/course/community-analytics-in-ecology-and-evolutionary-biology-for-beginners-cafb01/> Use discount code 'JAN25' to make the most of our Jan sale worth 20% off all courses

26th - 28th February 2025

Instructor-Dr. Antoine Becker-Scarpitta

COURSE OVERVIEW: This community analytics course is designed for students who have recently started their projects or researchers who are starting using the R ecosystem. During this three-day course, we will cover the basic concepts of multivariate analysis and their implementation in R. This course is a complement to the PR Statistic offering allowing also beginners and non-programmers to discover the statistical tools needed to analyze an ecological dataset in research, natural resource management or conservation context. This course is not geared toward any particular taxonomic group or ecological system.

We will cover diversity indices, distance measures and multivariate distance-based methods, clustering, classification, and ordination techniques. We will focus on the concept of the methods and their implementation on R using different R packages. We will use real-world examples to implement analyses, such as describing patterns along gradients of environmental or anthropogenic disturbances, quantifying the effects of continuous and discrete predictors, data mining. The course will consist of lectures, work on R code scripts, and exercises for participants.

PR stats also deliver a more advanced course on analysing community data

ONLINE COURSE - Multivariate Analysis Of Ecological Communities Using R With The VEGAN package (VGNR07)

Please email liverhooker@prstatistics.com with any questions.

January

ONLINE COURSE - Using Google Earth Engine in Ecological Studies (GEEE01) This course will be delivered live

ONLINE COURSE - Time Series Analysis and Forecasting using R and Rstudio (TSAF01) This course will be delivered live

February

ONLINE COURSE - Machine Vision using Python (MVUP01) This course will be delivered live

ONLINE COURSE - Machine Learning using Python (MLUP01) This course will be delivered live

ONLINE COURSE - Species Distribution Modelling With Bayesian Statistics Using R (SDMB06) This course will be delivered live

ONLINE COURSE - Remote sensing data analysis and coding in R for ecology (RSDA01) This course will be delivered live

ONLINE COURSE - Introduction to generalised linear models using R and Rstudio (IGLM08) This course will be delivered live

ONLINE COURSE - Community Analytics in Ecology and Evolutionary Biology for Beginners (CAFB01) This course will be delivered live

March

ONLINE COURSE - Introduction To Mixed Models Using R And Rstudio (IMMR09) This course will be delivered live

ONLINE COURSE - Stable Isotope Mixing Models us-

ing SIBER, SIAR, MixSIAR (SIMM11) This course will be delivered live

ONLINE COURSE - Multivariate Analysis Of Ecological Communities Using R With The VEGAN package (VGNR07) This course will be delivered live

May

ONLINE COURSE - Movement Ecology Using R(MOVE07) This course will be delivered live

June

ONLINE COURSE - Tidyverse for Ecologists and Evolutionary Biologists (TIDY01) This course will be delivered live

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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

Online MassSpecProteomicsWithR Mar17-19

Dear all,

We're excited to announce our upcoming online course, R/Bioconductor for Mass Spectrometry and Proteomics, taking place online from March 17-19, 2025.

Course website: (<https://www.physalia-courses.org/courses-workshops/course58/>)

This hands-on course will guide you through the analysis of mass spectrometry (MS) data using R and Bioconductor. Learn how to handle raw MS data, identify and quantify proteins, and perform statistical analysis for proteomics research.

A basic working knowledge of R (data frames, vectors, syntax) is required. Familiarity with MS or Bioconductor is helpful but not essential, as we provide a comprehensive introduction.

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops/course58/>)

Best regards, Carlo

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Online Metabarcoding Jan20-Feb14

Virtual Metabarcoding course (Jan 20-Feb 14, 2024)

Metabarcoding is a rapidly evolving method for assessing biodiversity from bulk or environmental samples. It has a wide range of applications: biodiversity monitoring, animal diet assessment, reconstruction of paleo communities, among others. DNA metabarcoding relies on molecular techniques such as PCR and next-generation sequencing, and requires bioinformatics and biostatistics competence to analyze sequencing results. This approach integrates several scientific areas and requires a broad range of skills in addition to the basic knowledge related to the considered research topic. This course will provide an overview of the state of current technology and the various platforms used. It consists of a series of online lectures and research exercises introducing different aspects of metabarcoding and other DNA-based approaches. We will also touch on the suite of bioinformatics tools available for sequence analysis and data interpretation. The four-week course is divided into four units and provides 18 hours of (mostly asynchronous) instructional time.

* Unit 01: Next-Generation Sequencing * Unit 02: Metabarcoding and beyond * Unit 03: Metabarcoding Analytics * Unit 04: Applications/Recent Research

Course Start Date: Monday, January 20, 2025 Course End Date: Friday, February 14, 2025 More information and enrolment: <https://courses.opened.uoguelph.ca/search/publicCourseSearchDetails.do?method=-load&courseId=18146&selectedProgramAreaId=16994&selectedProgramStreamId=12732257>

Dr. Dirk Steinke (he/him) | Associate Director, Analytics - Centre for Biodiversity Genomics - University of Guelph Centre for Biodiversity Genomics | University of Guelph dsteinke@uoguelph.ca | <http://biodiversitygenomics.net>
Dirk Steinke <dsteinke@uoguelph.ca>

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

Online Metabarcoding Microbes Feb3-7

Dear all,

we have the last 3 seats available on our online course “Metabarcoding in Microbial Ecology”.

Dates: February, 3rd-7th

Course website: (<https://www.physalia-courses.org/courses-workshops/course30/>)

This course will introduce metabarcoding techniques in microbial ecology. It covers topics like processing next-generation sequencing data and key methods in multivariate statistics. Through a mix of lectures and hands-on exercises, participants will learn the main steps of a metabarcoding study, from analyzing raw sequencing data to performing statistical evaluations. By the end of the course, participants will understand the strengths and limitations of metabarcoding and be able to analyze their own datasets to answer research questions.

If you are specifically interested in multivariate data analysis in R using the R package *vegan*, we have also a specific course on that in February: (<https://www.physalia-courses.org/courses-workshops/vegan/>)

For the full list of our courses and workshops, please visit: (<https://www.physalia-courses.org/courses-workshops-vegan/>)

Best regards, Carlo

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(to subscribe/unsubscribe the EvoDir send mail to gold-ing@mcmaster.ca)

Online NGS Data Analysis Mar31-Apr4

Dear all, We are pleased to announce the Spring School in Bioinformatics, an online course running from 31 March-4 April 2025, designed to introduce researchers to the concepts and practical skills needed for analyzing Next Generation Sequencing (NGS) data.

Course website: (<https://www.physalia-courses.org/courses-workshops/course68/>)

Course Highlights: Comprehensive Training: From quality assessment to genome assembly, RNAseq, differential gene expression, and phylogenomics. Practical Skills: Hands-on sessions using the Linux command line, Docker/Singularity, and AWS for reproducible analyses. Target Audience: We start with foundational Linux skills and progress through genomic, transcriptomic, and phylogenomic analyses. This means that previous experience with NGS data is not required. Learning Outcomes: Confidently handle and analyze NGS data. Understand the strengths and pitfalls of sequencing technologies. Apply state-of-the-art methods to genomic, transcriptomic, and phylogenomic datasets. For the full list of our courses and workshops, please visit our webpage: (<https://www.physalia-courses.org/courses-workshops/course68/>)

Best regards,

Carlo

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Online Phenotypic Evolution Mar10-14

Dear all,

We are thrilled to announce that only a few seats remain for our upcoming online course: Multidimensional Phenotypic Evolution.

Starting in 2025, Physalia offers this course focused on multidimensional phenotypic data analysis and a companion (<https://www.physalia-courses.org/courses-workshops/course22/>) focusing on geometric morphometric data acquisition..

Dates: 10-14 March 2025 Format: Online (to foster international participation) Course website: (<https://www.physalia-courses.org/courses-workshops/mpe/>)

Course Overview: This course delves into the techniques for analysing multidimensional phenotypes, such as morphometric (e.g., geometric morphometrics) and non-morphometric (e.g., gene expression) traits. Participants will gain insights into the challenges and opportunities of studying multidimensional traits, explore foundational and advanced methods, and apply these techniques to datasets at both microevolutionary and macroevolutionary scales.

Who Should Attend? The course is tailored for beginners and intermediate users, including researchers eager to analyse multidimensional phenotypic data or those looking for a structured foundation to enhance their current analyses.

What You'll Learn: Explore morphometric and non-morphometric phenotypes. Master key techniques like PCA, regression, and comparative methods. Analyze multidimensional data in evolutionary and ecological contexts. Use tools and R scripts to study co-variation, modularity, and phenotypic integration. Schedule: Live sessions: 13:00-19:00 (Berlin time). Hands-on exercises: Apply techniques using your own data or example datasets. For the full list of our courses and workshops, please have a look at: (<https://www.physalia-courses.org/courses-workshops/mpe/>)

Best regards, Carlo Physalia-courses Director (<https://www.physalia-courses.org/>) (mailto:info@physalia-courses.org)

“info@physalia-courses.org” <info@physalia-courses.org>

Online RNASeq Analysis Feb4-6

We still have space available in our RNA-seq Analysis workshop (virtual but live instruction - Feb. 4-6). The workshop will go through experimental design, high throughput sequencing basics, quality control, alignment to a reference genome, differential expression analysis, and gene ontology / gene set enrichment. Tools presented are appropriate for researchers working in systems with a reference genome.

Learn more & register here: < <http://bioinformatics.uconn.edu/cbc-workshops/> >

WHERE: Virtual (Zoom)

WHEN: 10:00 AM - 2:00 PM

COST: \$400 (UConn affiliates including UConn Health) \$500 (External participants)

Registration is first come first serve. There is no application process. Sign up as soon as possible to ensure your place in the workshop.

Questions? E-mail cbcsupport@helpspotmail.com

“Gauden, Kathleen” <spu24005@uconn.edu>

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

Online Statistics Feb11-May13

Dear evolDir community,

Spots are still available for Modern Statistical Thinking for Biologists, running online from 11 February till 13 May. The course follows the principle that statistics is not merely applied maths: it is a distinct way of thinking about the world. And it is best learned through honing our logical thinking skills and our intuitions about data, rather than through rote memorisation of tests or through excessive mathematical detail. The course therefore has no prerequisites in terms of maths skills.

Importantly, we will approach statistics through the

Bayesian framework. Even though Bayesian methods are used throughout biology, they are particularly prevalent in ecology and evolutionary biology. This is because this framework is particularly well adapted to the noisy and complex data sets routinely produced in these fields. It is often also considered to be more intuitive for beginners. The course is therefore open both to those who are beginners in any kind of statistics, as well as those who already have a background in frequentist methods and would like to learn about the Bayesian perspective specifically.

The course is composed of weekly Zoom sessions with lots of interaction and lots of group work in breakout rooms. The concepts learned are immediately applied to real data sets from the biological sciences. There are also weekly assignments, to which the participants receive individual written feedback each time. Towards the end of the course, the students will have several opportunities to put what they have learned to the test in realistic research settings. Notably, one session is devoted to a journal club, where we practice reading real papers that use Bayesian methods. There are also two projects: one on data provided by the instructor and another on each participant's own data.

The course takes on 15 participants on a first-come-first-served basis. For registration and for more information, see here:

<https://www.mondegoscience.com/courses/modern-statistical-thinking-for-biologists-online-11-feb-13-may-2025> If you have any questions, don't hesitate to drop me a line on rosina@mondegoscience.com.

Have a lovely week and a lovely 2025,

Rosina.

Rosina Savisaar <rosinasavisaar@gmail.com>

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

<https://www.prstats.org/course/time-series-analysis-and-forecasting-using-r-and-rstudio-tsaf01/> Use discount code 'JAN25' to make the most of our Jan sale with 20% off all courses

Instructor - Dr. RafaelDe Andrade Moral

27th Jan - 5th Feb 2025

Please feel free to share!

In this six-day course (Approx. 35 hours), we provide a comprehensive practical and theoretical introduction to time series analysis and forecasting methods using R. Forecasting tools are useful in many areas, such as finance, meteorology, ecology, evolution, public policy, and health. We start by introducing the concepts of time series and stationarity, which will help us when studying ARIMA-type models. We will also cover autocorrelation functions and series decomposition methods. Then, we will introduce benchmark forecasting methods, namely the naïve (or random walk) method, mean, drift, and seasonal naïve methods. After that, we will present different exponential smoothing methods (simple, Holt's linear method, and Holt-Winters seasonal method). We will then cover autoregressive integrated moving-average (or ARIMA) models, with and without seasonality. We will also cover Generalized Additive Models (GAMs) and how they can be used to incorporate seasonality effects in the analysis of time series data. Finally, we will cover Bayesian implementations of time series models and introduce extended models, such as ARCH, GARCH and stochastic volatility models, as well as Brownian motion and Ornstein-Uhlenbeck processes.

Please email oliverhooker@prstatistics.com with any questions.

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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

Online TimeSeriesAnalysisUsingR Jan27-Feb5

ONLINE COURSE - Time Series Analysis and Forecasting using R and Rstudio (TSAF01)

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.