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# E v o l D i r

June 1, 2022

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

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## Foreword

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

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

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



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### Ancona Italy EvolutionaryBiology Sep4-7

9TH Congress of the Italian Society for Evolutionary Biology (SIBE), 4-7 September 2022, Ancona, ITALY

REGISTRATION AND ABSTRACT SUBMISSION OPEN!

The Italian Society for Evolutionary Biology invites you to register and submit your abstract for its upcoming congress: EVOLUZIONE2022.

Symposia and INVITED SPEAKERS:

1) Biodiversity conservation using genes and genomes - In partnership with the European Reference Genome Atlas (ERGA) consortium CAMILA MAZZONI, Berlin Center for Genomics in Biodiversity Research, Germany; ASTRID VIK STRONEN, University of Ljubljana, Slovenia

2) Dynamics of genomic diversity in domesticated species YVES VIGOUROUX, Institut de Recherche pour le Développement (IRD), France; ROBERTO PAPA, Marche Polytechnic University, Italy

3) Population genetics using modern and ancient data

RASMUS NIELSEN, University of California, Berkeley, US - “Luca Luigi Cavalli Sforza” Award 2022 winner

4) Advances in phylogeography and phylogenomics DAVIDE PISANI, University of Bristol, UK

5) Behaviour and ecology: an evolutionary perspective GIL ROSENTHAL, University of Padova, Italy

6) Evolution of forms from genes to cells to organisms DETLEV AREDNT, European Molecular Biology Laboratory, Germany

7) Microbial genomics and evolution NICOLA SEGATA, University of Trento, Italy

8) Crash course in “Best practices for high quality genome assembly” in partnership with ERGA ROBERT WATERHOUSE, Universität de Lausanne, Switzerland

Details about registration and abstract submission are available at <https://www.sibe-iseb.it/registration> Please note the following dates:

15 June 2022 - Abstract submission closes 30 June 2022  
- Early bird registration closes

Further details are available at <https://www.sibe-iseb.it/ancona-2022> Prof. Emiliano Trucchi | [e.trucchi@univpm.it](mailto:e.trucchi@univpm.it) Italian Society for Evolutionary Biology | <https://www.sibe-iseb.it/> SIBE Office <[info@sibe-iseb.it](mailto:info@sibe-iseb.it)>

EMILIANO TRUCCHI <[e.trucchi@staff.univpm.it](mailto:e.trucchi@staff.univpm.it)>

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## Asilomar California TreeEvolution Jun14-16

\*\*Deadline for short/lightening talks has been extended to Thursday, May 5th\*\*

We are pleased to announce that the inaugural meeting of the North American Forest Genetics Society (NAFGS) will be held on June 14-16, 2022 at the Asilomar Conference Grounds, Pacific Grove, California. (<https://treegenesdb.org/nafgsconference>).

The first meeting is designed to be primarily a strategic session to develop the mission, goals, and functional capacities of the NAFGS, as well as invited and short contributed talks. In this way, the NAFGS will be different from the long-standing meetings in North America for the discipline of Forest Genetics.

The leadership of the NAFGS encourages your participation in this inaugural meeting by bringing your ideas and priorities to the development of the first professional society in North America for the discipline of Forest Genetics. We have chosen the Asilomar Conference Grounds near San Francisco as the venue for this event as the beautiful setting and intimacy of the venue greatly facilitates collegial interactions and creativity.

We sincerely hope to see you at Asilomar in June.

Jill L. Wegrzyn (she/her) Associate Professor

Department of Ecology and Evolutionary Biology Institute for Systems Genomics: Computational Biology Core University of Connecticut 67 N. Eagleville Road Storrs CT 06269-3214

[jill.wegrzyn@uconn.edu](mailto:jill.wegrzyn@uconn.edu) +1 860-486-8742

Research: [plantcompgenomics.com](http://plantcompgenomics.com) CBC Core: [bioinformatics.uconn.edu](http://bioinformatics.uconn.edu) Office: Gant 419W / Lab: Gant 401W Schedule a meeting with me here: <https://calendly.com/jillwegrzyn> [jill.wegrzyn@uconn.edu](mailto:jill.wegrzyn@uconn.edu)

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## Bainbridge Washington SelfishEvolution Jul25-28

AGA2022 President's Symposium - Selfish Evolution: Mechanisms & Consequences of Genetic Conflict

Early-bird registration ends next week! <https://www.theaga.org/agatwentytwentytwo> Registration is FREE for students & postdocs who submit poster abstracts by June 1. Several abstracts will be chosen for oral presentations.

President Lila Fishman will hold the 2022 Symposium, July 25-28, 2022, at the beautiful IslandWood campus on Bainbridge Island near Seattle, Washington (with virtual options for speakers and attendees). The Symposium will open Monday evening with a reception and the AGA Key Distinguished Lecture by David Haig, followed by two days of invited talks, panels, and poster sessions on topics spanning the field of genetic conflict and selfish evolution.

Invited speakers include: David Haig, AGA Key Distinguished Lecturer Yaniv Brandvain Justin Havird Sarah Zanders Amanda Larracuenta Daven Presgraves Hanna Johannessen Anna Lindholm Polly Campbell Jenn Coughlan Kelly Dawe Omar Akbari Carl Veller Mia Levine

Islandwood is a non-profit environmental education organization that provides a welcoming space for conferences and special events at its 250-acre campus. There are meadows and forests, delicious and plentiful shared meals, and spacious light-filled meeting rooms and sleeping lodges. We will have the whole campus to enjoy for our symposium registrants and their guests.

Visit the website <https://www.theaga.org/agatwentytwentytwo> or contact Lila Fishman [lila.fishman@umontana.edu](mailto:lila.fishman@umontana.edu) for more details.

Anjanette Baker <[theaga@theaga.org](mailto:theaga@theaga.org)>

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## Bainbridge Washington SelfishEvolution Jul25-28

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Early-bird registration until June 1st! <https://www.theaga.org/agatwentytwentytwo> President Lila Fishman will hold the 2022 Symposium July 25-28, 2022, at the beautiful IslandWood < <https://islandwood.org/outdoor-meeting-and-retreat-venue/> > campus on Bainbridge Island near Seattle, Washington (with virtual options for speakers and attendees). The Symposium will open Monday evening with a reception and the AGA Key Distinguished Lecture by David Haig, followed by two days of invited talks, panels, and poster sessions on topics spanning the field of genetic conflict and selfish evolution.

Featured topics include:

- Chromosomal drive
- Spore and gamete killers
- Cyto-nuclear conflict
- Genetic conflicts over offspring
- Gene drive and its applications

AGA Symposia are small meetings that provide excellent opportunities for cross-stage interaction, and the American Genetic Association is committed to supporting early-stage attendees. Students and postdocs who register and submit an abstract before June 1st will receive \*free\* registration.

Invited speakers include:

David Haig, AGA Key Distinguished Lecturer

Yaniv Brandvain

Justin Havird

SaraH Zanders

Amanda Larracuent

Daven Presgraves

Hanna Johannessen

Anna Lindholm

Polly Campbell

Jenn Coughlan (postdoc)

Kelly Dawe

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Visit the website <https://www.theaga.org/agatwentytwentytwo> or contact Lila Fishman [lila.fishman@umontana.edu](mailto:lila.fishman@umontana.edu) for more details.

Anjanette Baker <[theaga@theaga.org](mailto:theaga@theaga.org)>

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## Cleveland Evolution2022 Jun21-28

EVOLUTION 2022 Annual conference of the ASN/SSB/SSE

May 15 is the deadline for: \*virtual talk submission \*in-person talk submission \*early-bird discount on in-person registration

Meeting information: <http://www.evolutionmeetings.org> Conference registration: <https://www.xcdsystem.com/evolution/attendee/-index.cfm?ID=4LdX6xZ> Evolution 2022 is hybrid; join us in-person and/or online: June 21 & 22: virtual conference (talks by virtual attendees; virtual and in-person registrants can view) June 24-28: in-person conference in Cleveland, OH (some content live-streamed for virtual participants)

For everyone's safety, we have strict vaccine and mask requirements. Event staff will also be masked.

Highlights \* Many events and programs in support of diversity, equity and inclusion \* Talk & poster submission are available once main registration is completed \* All talks (virtual and in-person) accepted until May 15. \* All posters are accepted until June 1. \* Virtual participants can present a virtual (faux-live) talk during the virtual meeting; in-person participants can present an in-person (i.e. live) talk and/or in-person poster \* All participants (virtual and in-person) get access to the Virtual platform that will host virtual (faux-live) talks

June 21 & 22, and which will host live streams of all 5 plenaries (Gould Prize, 3 Presidential addresses, IDEA award) and all symposia during the in-person meeting, as well as recordings of these for on-demand viewing for 6 months afterward \* Those giving in-person talks will be encouraged to upload a pre-recording which will also be available for on-demand viewing for 6 months on the virtual platform, accessible to all participants (virtual and in-person) \* Conference-ending Super Social is a private event at the incredible Rock & Roll Hall of Fame! \* Free on-site childcare \* Cleveland has a vibrant and attractive downtown with ample options for food and drinks near the convention center

Howard Rundle <hrundle@uottawa.ca>

## Cleveland Evolution Jun24-28

The early registration discount for in-person participation in EVOLUTION 2022 has been extended until May 15 to accommodate those who are monitoring covid and holding off on their decision. The deadline for the ASN Best Student Poster Award has also been extended to May 15 (<https://www.evolutionmeetings.org/student-awards.html>)

Conference registration: <https://www.xcdsystem.com/evolution/attendee/index.cfm?ID=4LdX6xZ> Meeting information: <http://www.evolutionmeetings.org> Evolution 2022 is hybrid; join us in-person and/or online: June 21 & 22: virtual conference June 24-28: in-person conference in Cleveland, OH

For everyone's safety, we have strict vaccine and mask requirements. Event staff will also be masked.

Highlights \* Many events and programs in support of diversity, equity and inclusion \* Talk & poster submission are available once main registration is completed. \* Talk sign-up is first-come, first-served, with all submissions accepted until capacity is reached or until May 15, WHICHEVER IS EARLIER. \* All posters are accepted until June 1. \* Virtual participants can present a virtual (faux-live) talk during the virtual meeting; in-person participants can present an in-person (i.e. live) talk and/or in-person poster \* All participants (virtual and in-person) get access to our Virtual platform that will host virtual (faux-live) talks June 21 & 22, and which will host live streams of all 5 plenaries (Gould Prize, 3 Presidential addresses, IDEA award) and all symposia during the in-person meeting, as well as recordings of these for on-demand viewing for 6 months afterward

\* Those giving in-person talks will be encouraged to upload a pre-recording which will also be available for on-demand viewing for 6 months on the virtual platform, accessible to all participants (virtual and in-person) \* Hotel and dorm accommodations are still available \* Conference-ending Super Social is a private event at the incredible Rock & Roll Hall of Fame! \* Free on-site childcare \* Cleveland has a vibrant and attractive downtown with ample options for food and drinks near the convention center

hrundle@uottawa.ca

## Edinburgh Conservation Genetics Aug30-Sep1

5th European Conservation Genetics Meeting - ConsGen22

August 30 - Sept 1, 2022 Edinburgh, UK

Abstract submission is open until May 31st.

Organised by the University of Edinburgh, the Royal Zoological Society of Scotland and the Royal Botanic Garden Edinburgh, we will meet in the historic capital of Scotland to share recent developments in conservation genetics from around Europe and beyond.

This year the scientific programme will be divided into four themes focused on the development and application of genetic and genomic methods to conservation management. We have an exciting line-up of key note speakers, as well as opportunities for delegates to contribute through oral presentations and posters. In keeping with previous ConsGen meetings, there will be an emphasis on promoting the involvement of Early Career Researchers.

In-person registration closes on June 30th. Attendees can also register to join online-only.

Find out more at [consngen.org](http://consngen.org) or on twitter @consngen22 #ConsGen22 Any questions, please contact Edinburgh22@consngen.org

RZSS - ConsGen22 <[consngen22@rzss.org.uk](mailto:consngen22@rzss.org.uk)>

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## Edinburgh Conservation Genetics Aug30-Sept1

5th European Conservation Genetics Meeting - ConsGen22

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This year the scientific programme will be divided into four themes focused on the development and application of genetic and genomic methods to conservation management. We have an exciting line-up of key note speakers as well as opportunities for delegates to contribute through oral presentations and posters. In keeping with previous ConsGen meetings, there will be an emphasis on promoting the involvement of Early Career Researchers.

Abstract submission is open until May 31st.

Early bird in-person registration is open until May 16th, with full price in-person registration closing on June 30th. Attendees can also register to join online-only.

Find out more at [consgen.org](http://consgen.org) or on twitter @consgen22 #ConsGen22 Any questions, please contact Edinburgh22@consgen.org

RZSS - ConsGen22 <[consgen22@rzss.org.uk](mailto:consgen22@rzss.org.uk)>

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## Kiel SMBESatelliteEvolutionaryRescue Sep11-14

SMBE Satellite Meeting on Evolutionary Rescue Kiel University, Germany, 11-14 September 2022

Conference website: <https://workshops.evolbio.mpg.de/event/57/> We are currently living in the Anthropocene and thus an era shaped by human impact. The environmental conditions imposed by these human-driven rapid environmental changes

exert selective pressure on natural systems and can result in an evolutionary mismatch between slowly evolving organisms and their new environment, and rapid adaptation of many short-lived species. Evolutionary rescue, which occurs when populations subjected to stress avoid extinction by adaptation through natural selection, is relevant to both consequences: it can help to overcome the evolutionary mismatch and is at the basis of rapid evolution of pathogens.

In this SMBE Satellite meeting we aim to focus on evolutionary rescue in three main fields: species conservation, agriculture, and medicine. These three main fields currently face unforetold challenges due to evolutionary processes invoked by the dramatic human-mediated changes of the Anthropocene, including:

- Risk of species extinction and thus dramatic reductions in biodiversity due to an evolutionary mismatch caused by climate change, globalization, and pathogen evolution
- Risk of dramatic yield reductions in food production due to an evolutionary mismatch caused by climate change, globalization, and pathogen evolution
- Major threats to human health because of rapid pathogen evolution and increased pathogen spread due to globalization
- Rapid evolution of pathogens, parasites, and pest species and especially fast evolution of resistance to chemotherapy and pesticides

By incorporating diverse perspective from multiple fields, we hope to identify knowledge gaps and putative novel research directions in the context of evolutionary rescue in the Anthropocene.

FIRST CALL  $\ddot{u}$ <sub>1/2</sub>“ ABSTRACTS AND REGISTRATION

Early bird registration and abstract submission deadline: 20 June 2022 Registration deadline: July 4 Registration for virtual attendance: August 29

Contributed talks will be selected from among the submitted abstracts. Travel fellowships are available upon application.

CONFIRMED SPEAKERS: Richard Gomulkiewicz, Washington state University Helen Alexander, University of Edinburgh Matt Osmond, University of Toronto Moi Expósito-Alonso, Stanford University Rachel Morgan, Bergen University Hildegard Uecker, MPI Evolutionary Biology Plön Reid Brennan, Geomar Institute Hinrich Schulenburg, Kiel University Brendan Bohannan, Oregon University Yaara Oren, Broad Institute

Looking forward to welcome you in Kiel,  
Tal Dagan Reid Brennan Hildegard Uecker  
Prof. Dr. Tal Dagan

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### La Rochelle France Evolution Marine Parasites Nov15-18

Dear colleagues, We are pleased to send you the announcement for the “International symposium on ecology and evolution of marine parasites and diseases”. If you are interested, do not hesitate to visit the website <https://marineparasites.sciencesconf.org/> and to pre-register in order to stay informed with the latest news from the symposium. Abstract submission is now open and will be closed on the 30th of June. Do not hesitate to share this message with your own contacts. Kind regards

Isabelle Arzul and Lydie Canier

\*International symposium of ecology and evolution of marine parasites and diseases, La Rochelle, France, 15-18<sup>th</sup> of November 2022\*

Is your research related to aquatic parasitology? Then do not miss the “International symposium of ecology and evolution of marine parasites and diseases”!

This event will be held in \*La Rochelle, France\* between the \*15th and 18th of November 2022\*. By trying to integrate aquatic parasitology into ecosystem analyses and global change scenarios, the “International symposium of Ecology and evolution of marine parasites and diseases” will provide a great opportunity to present the latest research findings on marine parasites, to gather international experts from various disciplines and to identify next research priorities in this area, both at the European and international level.

The symposium will combine several thematic sessions spread over 3.5 days including: parasite adaptation and evolution, biogeography and macroecology, parasite detection, disease impact and management, epidemiology, environmental parasitology...

Presentations regarding parasites in freshwater organisms are also very welcome.

\*Keeping updated on the symposium is easy!\* Visit the website <https://marineparasites.sciencesconf.org/> and will be closed on the 30th of June. To submit your abstract, you need to create an account and then to go on the “Abstract submission” section

–  
\*Maude JACQUOT\*

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### Lisbon EvolMedicine

The ISEMPH 2022 program is now final and online, thanks to Program Chairs Michael Hochberg and Alejandra Nuñez De La Mora and the Program Committee. <https://isemph.org/ISEMPH-2022-Program> Discounted early registration expires on Sunday May 15, but the discount will still be available on May 16 to avoid confusion from time zone vagaries.

With 80 talks, including 8 distinguished plenary speakers, 60 posters, and a variety of social events, this will be the best evolutionary medicine meeting yet. Please also note events on July 5, including the welcome reception at 17:30. All are welcome, from students to advanced researchers.

VENUE <https://isemph.org/ISEMPH2022-Travel-and-Lodging> The conference will be held at the Fundação Calouste Gulbenkian (FCG, in the Portuguese acronym) in Lisbon. FCG is a pleasant, iconic, and easily accessible place in the center of Lisbon, with ample indoor and outdoor spaces. Around the FCG, there are many options for accommodation and food, covering a wide range of prices and styles, suitable for all.

KEYNOTE SPEAKERS <https://isemph.org/Plenaries-2022> Sebastian Bonhoeffer, ETH, Switzerland, Combination therapy and the evolution of drug resistance

Mhairi Gibson, University of Bristol, UK, The social and evolutionary dynamics of female genital mutilation/cutting (FGM/C) abandonment

Isabel Gordo, Instituto Gulbenkian de Ciência, Portugal, Eco-evolutionary dynamics of *Escherichia coli* when it colonizes the intestinal tract

Joseph L. Graves, North Carolina A&T State University, USA, Racial health inequality is a solved problem: Now what do we do about it?

Gunther Janssen, Pharma PHC Centre of Excellence, Hoffman-La Roche / Genentech, Switzerland, Afternoon Discussion and Q&A on Pharma in and Evolutionary World C.

Jessica Metcalf, Princeton University, USA, What we can and cant predict about the evolutionary trajectory of SARS-CoV-2

Luca Ermini, Winner of the George. C. Williams Prize for work on Evolutionary selection of alleles in the melanophilin gene that impacts on prostate organ function and cancer risk

Haley Randolph, Winner of the \$5,000 Omenn Prize, Genetic ancestry effects on the response to viral infection are pervasive but cell type specific <https://isemph.org/Omenn-Prize> Questions welcome. Manager@isemph.org or HostingCommittee@ISEMPH.org or ProgramCommittee@ISEMPH.org

Randolph Nesse <nesse@umich.edu>

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## Metz EcologyEvolution Nov22

SFE $\frac{1}{2}$  Gfi $\frac{1}{2}$  EEF Joint meeting, International Conference on Ecological Sciences "Ecology and Evolution: New perspectives and societal challenges"

21-25 November, 2022 Metz, France

Organized by the LIEC (University of Lorraine, CNRS) and other labs in northeastern France working in the fields of ecology and evolution and with the support of three societies (French Ecology & Evolution Society, The Ecological Society of Germany, Austria and Switzerland, European Ecological Federation), we will meet in Metz in November to share recent developments in Ecology and Evolution.

Abstract submission is open until June 20th.

Early bird in-person registration is open until July 31st. Attendees can also register to join online-only.

Find out more at: <https://sfe2gfomeeting.sciencesconf.org/> The organizing committee

Josefa Bleu <josefa.bleu@iphc.cnrs.fr>

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## Napoli EuroEvoDevo May31-Jun3 Registration

Dear Evo-Devo scientists, join us at

EURO EVO DEVO 2022 Napoli 31 May - 3 June

REGISTRATION AND POSTER SUBMISSION STILL OPEN!

For more information visit: <https://www.evodevonapoli.eu/> - More than 400 participants - More than 200 talks - 28 symposia - In beautiful Naples - Chance to visit one of the cradles of EvoDevo: Stazione Zoologica Anton Dohrn

Plenary speakers:

- Paola Oliveri - Robert Cerny - Stephanie Hoehn - Chelsea Specht

For the time table see: <https://www.evodevonapoli.eu/timetable/> Covid regulations: We take covid-19 very seriously and strictly follow the prescribed rules:

<https://www.evodevonapoli.eu/covid-19-measures/>

The local organizing committee The executive committee of the European Society for Evolutionary Developmental Biology

EED Society <eed.soc@gmail.com>

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## Online AgavoideaeGenomics Jun13

Dear Colleagues:

Instituto de Ecología at Universidad Nacional Autónoma de México (UNAM) is happy to announce the Agavoideae Conference and Bioinformatics Workshop. On June 13, 2022 researchers from throughout the Amer-



icas will present their research describing the ecology, evolution, and physiology of plants in the Agavoideae, and how genomic approaches are being harnessed to address research questions in this group. The workshop was made possible through generous support from the American Genetic Association.

To register to attend by zoom, please complete the following Google Form:

<https://forms.gle/wDJG5iakpDaa1Ucv9> Time Title Speaker 10:00 - 10:25 AM Evolutionary biology, diversity, pollination and genomics of agave, yucca and their relatives. Luis Eguiarte (UNAM) 10:30 - 10:55 AM Genomic studies of the Asparagaceae Jim Leebens Mack (University of Georgia) 11:00 - 11:25 AM Phylogenomics of the Agavoideae Michael McKain (University of Alabama) 11:25 - 11:40 AM Break 11:40 - 11:55 AM Phylogeny and morphological evolution of Yucca (Agavoideae, Asparagaceae) Maria Magdalena Ayala (FES Zaragoza, UNAM) Co-authors: Marie-Stephanie Samain, Shannon D. Fehlberg, R. García-Sandoval and Abisai García-Mendoza 12:00 - 12:15 PM Hibridación entre Yuccas endémicas de la península de Baja California Maria Clara Arteaga (Centro de Investigación Científica y de Educación Superior de Ensenada, Baja California) 12:20 - 12:35 PM Evolución de señales volátiles en el género Yucca Evolution of volatile signals in the genus Yucca Rob Raguso (Cornell University) 12:35 - 1:45 PM Lunch 1:45 - 2:00 PM Abiotic and biological defense mechanisms in Agave Jorge Nieto Sotelo (UNAM) 2:05 - 2:20 PM Evolution of CAM photosynthesis in the Agavoideae Karolina Heyduk (University of Hawai'i) 2:25 - 2:50 PM Genomics of the Agave's Pollinator Lucifer Hummingbird / Genómica evolutiva de Calothorax lucifer: un colibrí polinizador de Agaves. Yuyini Licon-Vera (UNAM) 2:50 - 3:05 PM Break 3:05 - 3:20 PM Insights from Chloroplast Phylogenomics on the Origin of Relictual Agave Domesticates in Arizona, U.S.A. Andrew Salywon (Desert Botanical Garden) 3:25 - 3:40 PM Natural History and Conservation of Yucca queretaroensis Fabiola Magallán Hernández (Universidad Autónoma de Querétaro) 3:40 - 3:55 PM Age of Yucca and The Yucca queretaroensis problem Christopher Irwin Smith (Willamette University) 4:30 - 6:00 PM Student Lightning Talks

\*Christopher Irwin Smith\* \*He/His/Him (Or any respectful pronouns)\* Professor of Biology Willamette University Salem, OR 97301 ph: 503-370-6181 fax: 503-375-5425 Make an appointment: Google Calendar < <https://tinyurl.com/rfekcabc> >

\*Joshua Tree Genome Project:\* JoshuaTreeGenome.org Watch the Joshua Tree Genome Project Documentary on Great Big Story < <https://www.youtube.com/>-

[watch?v=REPABdXQHc0&feature=youtu.be&t=35m15s](https://www.youtube.com/watch?v=REPABdXQHc0&feature=youtu.be&t=35m15s) >

Christopher Smith <csmith@willamette.edu>

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## Online eQTLs Jun1

Dear All,

Hi, I'd like to introduce our next guest at the CIGENE seminar.

Next speaker: Wednesday, June 1st, 12-13 CET Kaur Alasoo, Lecturer of Bioinformatics, University of Tartu  
Title: A compendium of uniformly processed human gene expression and splicing quantitative trait loci

Abstract: Many gene expression quantitative trait locus (eQTL) studies have published their summary statistics, which can be used to gain insight into complex human traits by downstream analyses, such as fine mapping and co-localization. However, technical differences between these datasets are a barrier to their widespread use. Consequently, target genes for most genome-wide association study (GWAS) signals have still not been identified. In the present study, we present the eQTL Catalogue (<https://www.ebi.ac.uk/eql>), a resource of quality-controlled, uniformly re-computed gene expression and splicing QTLs from 21 studies. We find that, for matching cell types and tissues, the eQTL effect sizes are highly reproducible between studies. Although most QTLs were shared between most bulk tissues, we identified a greater diversity of cell-type-specific QTLs from purified cell types, a subset of which also manifested as new disease co-localizations. Our summary statistics are freely available to enable the systematic interpretation of human GWAS associations across many cell types and tissues.

This will be an online event. Contact us to receive the meeting link. <https://cigene.no/contact/> Best, Marie

Marie SAITOU, Ph.D. Tenure-Track Principal Investigator, Centre of Integrative Genetics (CIGENE), Faculty of Biosciences, Norwegian University of Life Sciences <https://sites.google.com/view/saitou-lab> Marie Saito <marie.saitou@nmbu.no>

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## Online FrontiersOfPopGenetics May11

Dear colleagues,

you are cordially invited to tune in to a hybrid Mini-Symposium organised by the Vienna Graduate School of Population Genetics:

\*Frontiers of Population Genetics V\* \*May 11, 2022\*  
\*14:00 - 17:30 CEST\*

\*Sign up for zoom link: \*<https://forms.gle/rXDBjkWsvJg5oLNG9> 14:00 Opening remarks

\*14:05-14:50 John Parsch ' LMU M<sub>1/2</sub>nchen\* "The maintenance of gene regulatory polymorphism in Drosophila."

\*14:50-15:35 Virginie Courtier-Orgogozo ' Univ. Paris Diderot, FR\* "Evolution of Drosophila glue"

15:35-16:00 break

\*16:00-16:45 Nick Barton ' IST Austria\* "Understanding haplotypes"

\*16:45-17:30 Andrew Clark ' Cornell Univ.\* "Multi-generation genome-wide allele frequency dynamics in a wild, collapsing population"

– Dr. Julia Hosp

Vienna Graduate School of Population Genetics Coordinator

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

T +43 1 25077 4302

Julia Hosp <[Julia.Hosp@vetmeduni.ac.at](mailto:Julia.Hosp@vetmeduni.ac.at)>

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## Online GutMicrobiota May4

Dear all,

Next speaker: Wednesday, May 4th, 12-13 CET, Lindsay Hall, Professor, Quadram Institute will be present

"Exploring the delicate balance of the early life gut microbiota"

This will be an online event. Contact us < <https://cigene.no/contact/> > to receive the meeting link.

Abstract: Initial colonisation of the gut by pioneer bacterial species is the first key step for host well-being. The process of initial gut microbiota colonisation in preterm babies is radically interrupted due to a variety of factors including mode of delivery and antibiotics. This aberrant colonisation of premature infants appears pivotal to the development of a number of diseases, including necrotising enterocolitis (NEC). I will discuss how the microbiota 'balance' in the preterm gut impacts NEC outcomes - exploring the role of both beneficial and pathogenic microbiota members.

Sincerely,

Marie SAITOU, Ph.D. Tenure-Track Principal Investigator, Centre of Integrative Genetics (CIGENE), Faculty of Biosciences, Norwegian University of Life Sciences <https://sites.google.com/view/saitou-lab> Marie Saito <[marie.saitou@nmbu.no](mailto:marie.saitou@nmbu.no)>

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## Online Phylogenetics May24

Dear Colleagues,

we would like to invite you to our ongoing virtual seminar

series: "Horizontal evolutionary processes in phylogenetics"

(<https://www.shh.mpg.de/2022486/tide-seminar-series>).

We are excited to announce our next speaker in the series: Outi Vesakoski (University of Turku).

The event will take place on Tuesday 24 May 2022 at 2pm (CET).

-

Title: Divergence and convergence of Uralic languages and Finnish dialects

Abstract:

Both in biological species and languages, the process of divergence is counteracted by population convergences. In biology, the degree of convergence can be measured as gene flow indicating direction and intensity of genetic contact between populations. Adapting the population

genetic admixture model BAPS for language data, we calculated 'language flow' values for Finnish dialects to measure linguistic contacts. The 'language flow' values were further used to study the drivers of linguistic contacts. I will discuss the potential of population genetic admixture models to measure independently language divergence and convergence.

To attend the seminar, please subscribe to our mailing list onto which a zoom link will be sent prior to the event. Use the form at the bottom of this page: <https://www.shh.mpg.de/2022486/tide-seminar-series>  
Feel free to circulate to anyone who might be interested.

Looking forward to seeing you there!

The tide research group

<https://www.shh.mpg.de/tide> Max Planck Institute for the Science of Human History

Tide Seminars <[tide-seminars@shh.mpg.de](mailto:tide-seminars@shh.mpg.de)>

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## Online SMBEverywhere Mutational Biases Adaptation Aug2

Dear colleagues,

We are happy to invite your submission to the Mutational Biases and Adaptation Symposium that is part of the SMBE Symposia series for 2022-23, SMBEEverywhere. The symposium will be held on 2nd August 2022 and all details are given below. For any questions please contact James Horton ([jsh51@bath.ac.uk](mailto:jsh51@bath.ac.uk)) or David McCandlish ([mccandlish@cshl.edu](mailto:mccandlish@cshl.edu)). Submit your abstract at <http://www.smbe.org/smbe/MEETINGS/-SMBEeverywhere.aspx> GS3: Mutational Biases and Adaptation : August 2, 2022 : 12:00 - 20:00 UTC

Invited Speakers: Deepa Agashe (National Centre for Biological Sciences/Tata Institute of Fundamental Research), Alejandro Couce (Polytechnic University of Madrid)

Lead Organizers: James Horton (University of Bath) and David McCandlish (Cold Spring Harbor Laboratory)

Abstract submission deadline: June 28, 2022

Registration deadline: July 5, 2022

Abstract: Different types of mutations vary in their rate of occurrence, a phenomenon known as mutation

bias. Such biases are well understood to exert directional influences on patterns of neutral genetic variation. However, mounting evidence also supports a role for mutation bias in guiding the direction of adaptive evolution. Theoretical modeling has shown that adaptive evolution can enrich for mutationally-favored but selectively sub-optimal alleles, and recent empirical studies have found biases among documented adaptive substitutions consistent with these theoretical predictions. In particular, these studies have shown that mutation types favored by a handful of specific biases, such as transition-transversion bias and CpG hotspots, are also statistically overrepresented among adaptive amino acid substitutions. However, a number of key questions remain unanswered regarding how mutation and selection interact during adaptive evolution. For instance, the roles of different types of mutation bias in adaptation are not well understood. These include context-dependent biases involving flanking nucleotides, spatial heterogeneity in mutation rates across the genome, idiosyncratic mutation signatures driven by either endogenous processes or external environmental exposures, and heritable variation in mutation biases as often observed in mutator strains or even in different human populations. This symposium will showcase recent advances in understanding the complex interplay between mutation and selection in shaping molecular adaptation, and will include contributions from a wide array of systems including experimental evolution, protein evolution, parallel adaptation and evolutionary prediction, evolution of drug and pesticide resistance, and cancer.

Tiffany Taylor <[tt515@bath.ac.uk](mailto:tt515@bath.ac.uk)>

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## Oxford Statistical Genomics Jun19-24

Apply by Monday May 9th to join us for an immersive week-long residential post-graduate summer school on Statistical Genomics < <https://www.conted.ox.ac.uk/courses/oxford-statistical-genomics-summer-school?code=O22I410SGS> > at St Hilda's College Oxford, overlooking the River Cherwell and Christ Church Meadow, on 19th-24th June 2022.

This course aims to connect post-graduate and post-doctoral researchers from academia and industry with experts at Oxford's Big Data Institute, Wellcome Centre for Human Genetics, and Department of Statistics.

Our friendly tutors, internationally recognised for their

scientific expertise, will offer specialist instruction and hands-on computer practicals across five broad areas of Statistical Genomics: Next-generation Sequence Data Analysis, Gene and Variant Association Testing, Genomics of Infectious Diseases, Genealogical Inference and Analysis, and Medical Genomics.

The course is aimed at trainee scientists actively engaged in statistical genomics research, who wish to expand their knowledge of concepts and techniques.

For more information including how to apply please visit: <https://www.conted.ox.ac.uk/courses/-oxford-statistical-genomics-summer-school?code=-O22I410SGS> – Associate Professor Daniel Wilson Big Data Institute Robertson Fellow, Nuffield Dept. Population Health Director of Studies in Data Science, Dept. for Continuing Education University of Oxford Web: [www.danielwilson.me.uk](http://www.danielwilson.me.uk) Daniel Wilson <daniel.wilson@bdi.ox.ac.uk>

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## Paris EvolSexChromosomes Jun9-10

Dear all, We are pleased to share the program for the conference in Paris, June 9-10 th

Evolution of sex chromosomes and supergenes

College de France (11 Pl. Marcelin Berthelot Paris, France)

[https://www.college-de-france.fr/site/tatiana-giraud/-p109830952499656\\_content.htm](https://www.college-de-france.fr/site/tatiana-giraud/-p109830952499656_content.htm) Attendance is free and without registration but within room limits; talks will be available online afterwards

The scientific comitee, Tatiana Giraud, Paul Jay, Ricardo Rodriguez de la Vega

Tatiana Giraud

Directrice de recherches CNRS Professeur au Collège de France Membre de l'académie des sciences Institut Diversité Ecologie et Evolution du Vivant (IDEEV) Laboratoire Ecologie, Systématique et Evolution (ESE) Université Paris-Saclay Bureau 2314 12 Route 128 91190 Gif-sur-Yvette

phone: +33 1 69 15 56 69 + 33 6 34 64 45 14 fax: +33 1 69 15 46 97

Avoid 1 e-mail 1 Mo sent to 10 persons = 190 g CO2 (1 km by car) , 33 emails per day (daily average number of emails sent per pers.) = 33 km (source ADEME)

English: <https://www.esu-psud.fr/en/team-members/tatiana-giraud/> Francais: <https://www.esu-psud.fr/personnel/tatiana-giraud/> @GenEcoEvo <http://www.esu-psud.fr/> Tatiana Giraud <tatiana.giraud@u-psud.fr> Tatiana Giraud <tatiana.giraud@u-psud.fr>

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## Paris EvolutionSexChromosomes

Dear all

For our Conference in Paris, France, on June 9th-10th, here is the program:

<https://www.college-de-france.fr/site/tatiana-giraud/-symposium-2021-2022.htm> All talks but two will be in-person; no registration is needed, attendance is free and the room can host 168 persons

Below is a link for a poster of the conference program:

<https://filesender.renater.fr/?s=download&token=-b7a41941-0eb2-4e62-ba15-119d9cef2f57> Best regards

Tatiana Giraud, Paul Jay and Ricardo Rodriguez de la Vega

Tatiana Giraud

Directrice de recherches CNRS Professeur au Collège de France Membre de l'académie des sciences Institut Diversité Ecologie et Evolution du Vivant (IDEEV) Laboratoire Ecologie, Systématique et Evolution (ESE) Université Paris-Saclay Bureau 2314 12 Route 128 91190 Gif-sur-Yvette

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English: <https://www.esu-psud.fr/en/team-members/tatiana-giraud/> Francais: <https://www.esu-psud.fr/personnel/tatiana-giraud/> @GenEcoEvo <http://www.esu-psud.fr/> Tatiana Giraud <tatiana.giraud@u-psud.fr>

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## Prague ESEB Aug14-19 RegisterJun15

ESEB Congress 2022 - EARLY BIRD REGISTRATION POSSIBLE UNTIL JUNE 15, 2022!

The next ESEB congress will take place from 14-19 August 2022 in Prague, Czech Republic.

Please register early by June 15 and make sure your ESEB membership is valid for the membership discount.

Note that abstract submissions for posters in the open symposium are also possible until June 15th!

Further details are available at <https://www.eseb2022.cz>  
 ... Dr. Ute Friedrich | Email: [office@eseb.org](mailto:office@eseb.org) European Society for Evolutionary Biology | [www.eseb.org](http://www.eseb.org) "office@eseb.org" <[office@eseb.org](mailto:office@eseb.org)>

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### QueenMaryU PopulationGeneticsGroup Jan4-6

Next year's Population Genetics Group conference will be at Queen Mary's University London, Jan 4th-6th 2023, with arrival on Jan 3rd. This is a small conference of ~250 delegates run over 2.5 days. The conference covers the full range of evolutionary biology and population genetics. Further details, including how to register will be published later in the year.

Adam Eyre-Walker

Adam Eyre-Walker <[a.c.eyre-walker@sussex.ac.uk](mailto:a.c.eyre-walker@sussex.ac.uk)>

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### SpeciesDistributions Aug1-10 CallAbstracts

Biological dispersal: connections at continental and intercontinental scales.

For a long time, scientists have been fascinated by the idea that species might disperse long distances, and how dispersal might underpin distributions; the "grand game of chess with the world for a board" as Charles Darwin wrote in one of his letters. We now have a wealth of powerful methods to investigate where, when and how biological dispersal occurs. Understanding the processes and patterns of species distribution and ecological and genetic connectivity of populations is particularly relevant in the geographically isolated and rapidly warming Antarctic and sub-Antarctic regions. How will species in these regions respond to environmental changes? Which can or can't shift their distributions through dispersal?

Where are the biogeographic barriers, and where are the primary dispersal pathways? What mechanisms do different species use to disperse? This session will bring together recent research on active and passive dispersal of Antarctic organisms at regional, continental and intercontinental scales. We particularly welcome talks that bring together different sources of evidence to investigate dispersal and the processes that drive it, and / or that shed light on species distributions and population connectivity, in and around the Antarctic and sub-Antarctic.

Session Convenors: Chiara Papetti and Jamie Maxwell

Abstract submission: <https://scar2022.org/588-2/> Deadline: 1 June 2022

"MAXWELL, JAMIE" <[J.MAXWELL4@nuigalway.ie](mailto:J.MAXWELL4@nuigalway.ie)>

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### UKonstanz Convergence Jun1-5

Symposium on the "Genomics of Convergence" from June 1. - 5. 2022 in Konstanz, Germany.

See conference page

<http://www.convergencesymposium.com/> The topic of the conference: convergence and parallelism will be addressed at all levels of biological organization (from genomes to phenotypes) and we are inviting interested participants (particularly, but not limited to, junior scientists such as PhD students and postdocs) to submit their titles and abstracts:

<http://www.convergencesymposium.com/submit-your-abstract/> Please do so before the deadline on MAY 11th.

>From the submitted abstracts we'll select those who fit to the topic of the conference most closely for presentations (for space reasons we're limited to only a few dozen participants).

We have reserved a number (~40) of hotel rooms in the conference venue overlooking lovely Lake Constance.

<http://www.convergencesymposium.com/venue/> We can offer (to a limited number of participants) hotel accommodation for free, others will be invited to participate, but need to secure their own accommodation in the same hotel or elsewhere).

We're planing to give out prizes (1500€in total, thanks to the Hector Fellow Academy) for the best presentations by ECRs.

We'll have a number of keynote addresses including:

Catherine Peichel - University of Bern, Switzerland  
 Scott Edwards, Harvard University, USA  
 RoÉie Gillespie, UC-Berkeley, USA  
 Jonathan Losos, Washington University, USA  
 Wen-Hsiung Li, Academia Sinica, Taiwan

We are looking forward to a highly interactive and social meeting during three days of talks. Some talks will be by Zoom and we are planing to conduct the meeting as a hybrid presence/Zoom meeting.

The arrival of participants is planed for June 1st in the afternoon and the departure is on June 5th in the morning. Talks will be on June 2nd, 3rd and 4th.

Please contact [axel.meyer@uni-konstanz.de](mailto:axel.meyer@uni-konstanz.de) for more information if you cannot find what you're looking for on the conference [www](http://www) page.

Axel Meyer <[a.meyer@uni-konstanz.de](mailto:a.meyer@uni-konstanz.de)>

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## UPadova and Online MateChoice May27

We are excited to share our upcoming mini-symposium on "Aesthetics, Mate Choice, and Sexual Selection", featuring Profs. Gasparini, Mendelson, Pilastro, Renoult, and Shuker - details below. For planning purposes and logistical assistance, please email [gil.rosenthal@unipd.it](mailto:gil.rosenthal@unipd.it) if you're visiting Padova in person.

A presto,

Gil

27 May 0930-1300 CET

Aula Africa, ground floor, Palazzo Wollemborg - Via del Santo, 26, Padova

or via ZOOM at the following link <https://unipd.zoom.us/j/82242984785> 9.30-10.00 Introduction: Prof. Gil Rosenthal

10.00-10.30 Prof. Andrea Pilastro, University of Padova  
 Total sexual selection.

10.30-11.00 Prof. David Shuker, University of St. Andrews, Scotland

What is sexual selection?

11.00-11.30 Break

11.30-12.00 Prof. Tamra Mendelson, University of Maryland, U.S.A.

Beauty and speciation in North American freshwater fishes.

12.00-12.30 Prof. Julien Renoult, University of Montpellier, France

The evolution of beauty: insights from the fluency theory of aesthetics.

12.30-13.00 Prof. Clelia Gasparini, University of Padova

Mating biases after mating.

[gil.rosenthal@unipd.it](mailto:gil.rosenthal@unipd.it)

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## GradStudentPositions

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## AMUPoznan BehavioralEcology

Graduate position: AMUPoznan\_BehavioralEcology

PhD position in the project “Linking immunogenetic variation, microbiome and personality” is available for three years starting from 1st October 2022. The project is led by Magdalena Herdegen-Radwan (Adam Mickiewicz University, Poznan), and is funded by Polish Science Centre (NCN). The student will receive a stipend of 5000 PLN/month for three years. In addition to carrying out research, the student will have opportunity to attend specialized courses for PhD students in English. The candidate should hold MSc degree in biological sciences. Interested candidates should send their CV and a motivation letter (via email) to the project leader, who will provide further information about the project and application procedure (email: magher@amu.edu.pl).

Project summary:

During the last decades, the field of animal personalities flourished bringing significant advances in our knowledge of their importance for individual fitness, but the mechanisms maintaining variation in those traits are still not clear. In parallel, research on animal microbiome advanced bringing strong evidence for complex interactions between microbial communities harboured by animals and host behaviour, including personality, and resulted in revealing links between host gut microbiome and various behaviourally expressed deficits in humans and animal models of human behaviours. However, studies on undisturbed populations of non-model species are rare, leaving open the question of the importance of microbial variation in such populations. Even more scarce are studies testing microbiome effects on fitness, and those few that do measure some fitness-related traits did not incorporate the personality dimension, leaving open an important question of whether microbiomes can affect fitness via their effects on personality. The first aim of this project is to fill this gap of knowledge by testing (hypothesis I) that gut microbiome affects a personality trait with documented effect on fitness, using both correlational and manipulative approach. Additionally, I will test another intriguing hypothesis (II), that it is the sperm microbiota that affects the

fitness-related personality trait. A tempting indication for such an effect is the correlation between male boldness and sperm number reported in guppy - the species and personality trait I plan to use here.

An important reason for variation in microbiome composition is immunogenetic variation. One of the hypotheses links the genetic variation at MHC, a complex of immune molecules of the adaptive immune system responsible for antigen presentation, to microbiome variation. While there are some hints as to the links of MHC separately with either microbiome or personalities, the integration of those MHC-related processes in microbiome-personality framework is missing. Therefore, the other aim of the project will be to investigate the effect of MHC genotype on personality via microbiome (hypothesis III).

I will use a large, outbred guppy population in which I previously showed that male boldness is a highly repeatable personality trait and positively associated with reproductive success 1. In the correlational approach, I will correlate the boldness level in untreated males from the general population with the microbiome found in their gastro-intestinal tract (hypothesis I) or on their sperm (hypothesis II). These correlational analyses, unlike the manipulation-based studies of microbiome effects, will allow to conclude if the putative association is strong enough to have ecological meaning in non-manipulated, healthy populations, which is one of the strengths of the present project. Incorporating individual MHC profiles into these analyses will allow to assess its association with both the microbiome and the personality (hypothesis III).

In the test of hypothesis I using experimental manipulation I will check if transfer of bold- and shy-guppy derived gut microbiome into the gut of guppies from two respective treatments will affect their boldness. While performing microbiome transplantation, I will choose individuals so as to obtain groups of MHC-similar and -dissimilar individuals, which will allow me to test if immunogenetic profile determines boldness level via its effect of host microbiome (hypothesis III). The integration of the three dimensions of animal phenotype mostly studied in tandems, i.e. the microbiome, personality and immunogenetics, in relation to their effect on fitness, will constitute the innovative value of the present project.

dr Magdalena Herdegen-Radwan Department of Behavioural Ecology Collegium Biologicum Adam Mickiewicz University Uniwersytetu Poznańskiego 6 61-614 Poznań <http://behaecol.home.amu.edu.pl/> [<http://behaecol.home.amu.edu.pl/resources/DSCF3495.JPG>] Home [[behaecol.home.amu.edu.pl](http://behaecol.home.amu.edu.pl)]

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Avignon, France ([https://www6.paca.inrae.fr/ecologie\\_des\\_forets\\_mediterranneennes](https://www6.paca.inrae.fr/ecologie_des_forets_mediterranneennes)).

Thesis supervisors : Hendrik Davi ([hendrik.davi@inrae.fr](mailto:hendrik.davi@inrae.fr)), Caroline Scotti-Saintagne ([caroline.scotti-saintagne@inrae.fr](mailto:caroline.scotti-saintagne@inrae.fr)),

Socio-economic partnership: Office National des Forêts (ONF) Budget contributors: INRAE, SUD PACA Region, ONF Duration: 3 years (end 2022 - end 2025)

Bruno Fady <[bruno.fady@inrae.fr](mailto:bruno.fady@inrae.fr)>

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## Avignon France Forest Adaptation

PhD position: Predicting the effects of hybridization on forest adaptation in the context of global climate disruption

Summary: Climate change threatens our forests and the multiple services they provide. Hybridization is one of the possible genetic mechanisms for resilience and adaptation of natural and plantation-based forest stands to this threat. We propose to model the adaptive impacts of hybridization of the native silver fir (*Abies alba* Mill.) in mainland France, a species vulnerable to climate change, by more drought-resistant species of the genus *Abies*. To this end, we will modify a physio-demographic model (PDG) developed at INRAE, simulating tree growth, survival, reproduction, migration and genetic evolution at the population level, to integrate gene flow between “sister” species of different adaptive potentials.

We will focus on tree traits related leaf phenology (bud break date) and response to water stress (stomatal closure and xylem vulnerability to cavitation). These traits determine drought and late frost susceptibility, which are the two main climatic risks affecting Mediterranean fir trees.

The thesis will contribute to the development of a generic modeling tool, allowing to evaluate the evolutionary consequences of hybridization between sister species. The thesis will also address the possible positive consequences of hybridization (genetic enrichment, mitigation of the risk of decline), but also its potential negative consequences (risk of maladaptation, of loss of local genetic diversity) associated with climate change.

Location: INRAE, URFM, Campus St Paul,

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## Avignon Hybridization Forest Adaptation

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Location: INRAE, URFM, Campus St Paul, Avignon, France (<https://www6.paca.inrae.fr/>)



[ecologie\\_des\\_forets\\_mediterraneennes](#)). Thesis supervisors : Hendrik Davi ([hendrik.davi@inrae.fr](mailto:hendrik.davi@inrae.fr)), Caroline Scotti-Saintagne ([caroline.scotti-saintagne@inrae.fr](mailto:caroline.scotti-saintagne@inrae.fr)), Socio-economic partnership: Office National des Forêts (ONF) Budget contributors: INRAE, SUD PACA Region, ONF Duration: 3 years (end 2022 - end 2025)

Bruno Fady <[bruno.fady@inrae.fr](mailto:bruno.fady@inrae.fr)>

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## Brno Czechia FishEvolution

Brno\_Czechia.FishBiology

Ph.D. position on Fish Biology

\*\*applications until 20 June 2022

REICHARD LAB ([www.reichardlab.eu](http://www.reichardlab.eu))

Institute of Vertebrate Biology, Czech Academy of Sciences, Brno

Fully-funded PhD student position is available at the Institute of Vertebrate Biology, Czech Academy of Sciences, located in Brno, Czech Republic. Formal start of PhD. study is expected in October 2022, but potential later start is possible.

\*\*The successful candidate will work on brood parasitism, primarily on the cuckoo catfish and their cichlids hosts and/or bitterling fishes and their mussel hosts using field and experimental approaches. There is flexibility in the specific topic within the large research project.

\*\*RESEARCH PROJECT:

The Expro-funded project uses brood parasitic fishes to study how co-evolutionary processes and ecological interactions shape biodiversity at local and global scales. Using two fish systems that are highly amenable to laboratory and field studies (cuckoo catfish and bitterling), we employ comparative and experimental approaches to understand how coevolution drives and constrains diversification. In particular, we aim to identify the origin and early evolution of host specificity, quantify large-scale patterns of host specificity and their association with parasite traits and diversification, and measure the constraints and benefits of host specificity. Field and lab studies are combined with population genetics, phylogenetics and mathematical modelling.

For experimental work, access to well-equipped fish breeding facility and an outdoor mesocosm system is granted.

Selected candidate will have some flexibility in the specific focus within the broad terms of the project, although we would particularly welcome a candidate with expertise/interest in fish morphology (dentition, gill rakers, osteology). There are 3 postdocs and 2 PhD students working on the project, along with a set of more senior researchers.

QUALIFICATIONS - MSc. in Biology or a related discipline. Experience with experimental work using fish, molecular laboratory work and/or mathematical modelling of evolutionary processes is welcome.

INCOME

No tuition fees, decent SALARY from the research project and STIPEND from the Masaryk Universit in Brno ensure an income for very good standard of living.

Full coverage of social and health insurance.

Net income of at least 1200 EUR per month, which can significantly increase on a merit-based system for stipends. Selected candidate will have some flexibility in the specific focus within the broad terms of the project, although we would particularly welcome a candidate with expertise in fish morphology (dentition, gill rakers, osteology).

APPLICATION PROCEDURE

For applications, please submit a CV and explain your motivation to apply for this position in your Cover Letter (single page is sufficient).

Email your application to [reichard@ivb.cz](mailto:reichard@ivb.cz).

All applications submitted until 20 June 2022 will be fully considered.

Selected candidates will be interviewed online.

For informal enquires and more details, feel free to email [reichard@ivb.cz](mailto:reichard@ivb.cz)

Martin Reichard <[reichard@ivb.cz](mailto:reichard@ivb.cz)>

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## DanishTechU BioinformaticsAncientDNA

DTU Health Tech is looking for a qualified candidate for a PhD position in Bioinformatics.

In this position, you will develop algorithms and computational methods to deal with the analysis of large datasets from modern and ancient sources. More specifically, these algorithms will be aimed at analyzing human

genomes from sedimentary DNA. The bioinformatics section of DTU Health Tech performs research in the areas of different metagenomics, machine learning, cancer genomics and population genomics.

Current bioinformatics algorithms and software are often ill-equipped to deal with DNA extracted from ancient soil samples. This ancient DNA shows high levels of fragmentation and accumulated chemical damage. Furthermore, ancient sediments often contain DNA from multiple species and often multiple individuals. Fortunately, several problems pertaining to ancient DNA can be described in a maximum-likelihood framework and computer science techniques can help us to solve such numerical problems efficiently via numerical algorithms and data structures. You will work in collaboration with other partners including the University of Copenhagen and McMaster University in order to develop the next generation of algorithms and software applied to DNA extract from fossils, ancient soils and sediments.

**Qualifications** You must have a two-year master's degree (120 ECTS points) or a similar degree with an academic level equivalent to a two-year master's degree. Ideally, your degree should be in computer science, mathematics or biological science with a focus on quantitative and mathematical aspects.

More specifically you should ideally have the following qualifications: \* Knowledge of a programming language like Python, Perl, C++ and/or Java (C/C++ is preferred) \* Ability to work in a UNIX environment, ideally in a high-performance computing environment \* Thorough understanding of basic algorithms and data structures used in computer science \* Knowledge of probabilities and statistics \* Firm grasp of first-year university mathematics (differential calculus/linear algebra) \* Experience in bioinformatics and knowledge of metagenomics are a plus \* Expertise in next-generation sequencing data generation and processing are also a plus

The language of communication at DTU is English.

**Application procedure** Your complete online application must be submitted no later than 14 June 2022 (Danish time). Applications must be submitted as one PDF file containing all materials to be given consideration. To apply, please open the link "Apply online", fill out the online application form, and attach all your materials in English in one PDF file. The file must include:

A letter motivating the application (cover letter) \* Curriculum vitae \* Grade transcripts and BSc/MSc diploma (in English) including official description of grading scale \* Link to a code portfolio stored in repositories like GitHub/bitbucket is not required but helpful

You may apply prior to obtaining your master's degree but cannot begin before having received it.

All interested candidates irrespective of age, gender, race, disability, religion or ethnic background are encouraged to apply.

Applications received after the deadline will not be considered.

Deadline: June 14th 2022

Apply at <https://www.dtu.dk/english/about/-job-and-career/vacant-positions/job?id=09a1546e-7501-47c5-bca9-ee43605153f7>  
 Gabriel Renaud  
 <gabriel.reno@gmail.com> Gabriel Renaud  
 <gabriel.reno@gmail.com>

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## George Washington U Onychophoran Systematics

PhD student position in systematics available at The George Washington University <https://biology.columbian.gwu.edu/gustavo-hormiga> I am seeking a PhD student to carry out research in the systematics and evolution of onychophorans (velvet worms). The PhD student will contribute to an NSF-funded project in the laboratories of Gustavo Hormiga (The George Washington University) and Gonzalo Giribet (Harvard University). This research project will focus on the least-understood group of Onychophora, the Neotropical Peripatidae, and their radiation around the Caribbean region. We will describe new species, assess their conservation status, with the goal of understanding how this group of placental invertebrates has been able to colonize the Caribbean region through geological time. The research team and several trainees will combine cutting-edge molecular phylogenetic approaches with modern anatomical methods to advance our knowledge of the diversity and evolutionary history of this understudied group. The PhD student will develop their own projects in alignment with the goals of the NSF-funded project.

Applicants can come from a variety of backgrounds, but we are particularly interested in those with a strong interest in phylogenetics, evolution, and invertebrate zoology. The doctoral degree and coursework will be based at the Department of Biology of The George Washington University (Washington, DC). Financial support will be provided through research and teaching assistantships at GW.

To be considered, send an email to Gustavo Hormiga (hormiga@gwu.edu) that includes the following attachments: 1) a cover letter expressing your interest, your qualifications for the position, and your future career goals, 2) your curriculum vitae, 3) an unofficial copy of your college transcripts, and 4) names and contact information of 2-3 professional references. We will consider candidates until the position is filled. Please note that the selected candidate will need to apply and be accepted to the doctoral program in Biology at GW (<https://biology.columbian.gwu.edu/phd-biology>). Applications are due on Dec. 1, 2022 for a start date of Fall 2023). If needed, the student may begin as early as January 2023. Please email Gustavo Hormiga (hormiga@gwu.edu) with any questions or concerns about this position.

Gustavo Hormiga <hormiga@gwu.edu>

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## GreifswaldU DispersalColonizationGenomics

Job Advertisement 22/Wi07

At the University of Greifswald's DFG-funded Research Training Group RTG 2010 - "Biological responses to novel and changing environments - RESPONSE", sub-project 4, there is a job vacancy expected to be available from 1 July 2022, subject to the allocation of funds, for a part-time (65 %)

Doctoral researcher The employment is limited until 31 March 2024. We will try to secure a follow-up financing. Payment will be made according to pay group 13 TV-L Wissenschaft.

The ability to respond to novel and changing environmental conditions, either by phenotypic plasticity, genetic adaptation, or range shifts, is pivotal to the longer-term survival of all organisms. Owing to increasing concerns about the consequences of human-induced global change, such responses have attracted increasing interest in recent years. RESPONSE focuses on the plastic and genetic capacities for in situ responses (cluster A) and on the factors limiting or facilitating dispersal to new habitats (cluster B). The RTG aims at deepening our understanding of the limits to population persistence, enabling more accurate predictions regarding the fate of populations under changing conditions. Our research programme spans different levels of biological organisation, ranging from molecular and physiological mechanisms to ecological population-level responses, and a wide vari-

ety of organisms including lichens, myxomycetes, plants (trees), and animals (snails, crustaceans, insects, spiders, bats). The proposed project adds to the overall aims of RESPONSE by investigating the factors underlying the dispersal and colonization pattern of the butterfly *Pieris mannii* - a species showing a rapid range expansion across Central Europe.

Work tasks: In the proposed project B4, the dispersal and colonization patterns of the Southern Small White (*Pieris mannii*) will be investigated. This butterfly species is currently undergoing a rapid northward expansion and is therefore ideally suited for RESPONSE's research program. The candidate will not only focus on the genetic and morphological analysis of the expanding populations, but also investigate their physiological potential in comparison to their original ranges. A teaching programme accompanies the interdisciplinary research strategy. It covers different scientific topics and techniques relevant to the RTG as well as soft skills relevant to career development, and includes summer schools, journal clubs, practical courses, lectures, as well as individualised education and mentoring programmes. Each doctoral project involves research stays at different laboratories, partly abroad. The participation in the teaching programme is mandatory. Tasks will be transferred that are conducive to the preparation of a doctorate.

Requirements: We invite applications from highly motivated candidates with above-average qualifications, a passion for and experience in research, and the willingness to make active contributions to the RTG. Successful applicants must 1) hold a M.Sc. degree (or equivalent) in Biology or another relevant discipline, 2) have a solid background in ecology and evolutionary biology, 3) experience with methods and/or organisms relevant to the RTG, 4) have an excellent command of English, which is the official language of the RTG, and 5) be motivated to join an interdisciplinary research training environment. The position is open to all persons, irrespective of gender. The University would like to increase the proportion of women in areas in which they are underrepresented and thus applications from women are particularly welcome and will be treated with priority if they have the same qualifications and as long as there are no clear reasons which make a fellow applicant more suitable. Severely disabled applicants with the same qualifications will be considered with preference. According to § 68(3) PersVG M-V, the Staff Council will only be involved in staff matters of the academic or artistic staff on request.

Please only submit copies of your application documents as they cannot be returned. Unfortunately, application costs (e.g. travel expenses for interviews) will not be reimbursed by the State of Mecklenburg-Vorpommern.

Please note that by submitting your application, you provide your consent pursuant to data protection law for our processing of your application data. Further information about the legal bases and the use of your data can be found here.

Applications comprising all usual documents (curriculum vitae, copies of academic certificates) must be sent, preferably via email (one file in PDF-format), with reference to the job advertisement number 22/Wi07 by 07 June 2022 to:

Universität Greifswald Zoologisches Institut und Museum Koordination des Graduiertenkollegs 2010 RESPONSE Dr. Susann R ath Loitzer Str. 26 17489 Greifswald email: susann.raeth@uni-greifswald.de

Dr. Martin Wiemers Head of Ecology

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## INRAE BordeauxU OakPangenomicAdaptation

We are looking for a highly motivated student for a PhD position within the project “Pan-genome evolutionary dynamics and role of structural variants in local adaptation within the European white oak species complex”.

PhD STUDENT POSITION - Pangenomic and role of structural variants in oak adaptation - Based at UMR Biogeco INRAE - University of Bordeaux - Subject area: Population genetics and genomics - Application deadline: 20 May 2022.

PROJECT DESCRIPTION This PhD project will focus in understanding the evolutionary dynamics of genomes in perennial species and construct a pan-genome to investigate the role of structural variants (SVs) in key adaptive traits such as drought resistance and bud burst. The PhD candidate will be in charge of the bioinformatics, comparative and population genomics analyses of the data already available at UMR Biogeco for the white oak species (high quality genome assemblies, long and short read sequencing, pool-seq...). More information at [https://www.adum.fr/as/ed/propositionFD.pl?site=ed\\_se](https://www.adum.fr/as/ed/propositionFD.pl?site=ed_se) (see below for more instructions).

PROFILE We expect candidate profiles with skills in evolutionary ecology/population genomics and strong will to deepen his/her bioinformatics skills or alternatively candidates with skills in bioinformatics/computing science and strong interest in evolutionary processes. The work involves mostly computer work and programming with opportunities for field work.

SUPERVISION The PhD student will be supervised by Dr. Ludovic Duvaux and Dr. Christophe Plomion (INRAE - Biogeco) and will be registered at the “Sciences et environnements” Doctoral School (<https://ed-environnements.u-bordeaux.fr/en>) of the University of Bordeaux.

Contacts: - Ludovic Duvaux: ludovic.duvaux@inrae.fr - Christophe Plomion: christophe.plomion@inrae.fr

HOW TO APPLY Interested applicants should contact the supervisors to get more details (ludovic.duvaux@inrae.fr and christophe.plomion@inrae.fr) then apply by May 20, 2022.

- Go to [https://www.adum.fr/as/ed/propositionFD.pl?site=ed\\_se](https://www.adum.fr/as/ed/propositionFD.pl?site=ed_se) - click the tab “Sp cialit  Acologie  volutive, fonctionnelle et des communaut s” - click the the link “Dynamique  volutive du pan-g nome et r le des variants structuraux dans l’adaptation locale au sein du complexe d’esp ces des ch nes blancs europ ens” - click the button “candidater” - choose the language on the top left “EN” or “FR” - then Create an account if needed

COLLABORATIONS AND NETWORKING The PhD student will be able to interact with our network of collaborators. Locally, strong interactions already exist with Veronique Decrooq & Quynh-Trang Bui (BFP, INRAE Bordeaux). They work on the genomic bases of adaptation and domestication in apricot trees and share the same interest in SV and tree pan-genome dynamics. Thus, a long term collaboration is ongoing. The candidate will also collaborate with national experts in genome assemblies and annotations (Jean-Marc Aury from G noscope, William Marande from CNRGV, INRAE URGI staff members), structural variation analyses (Olivier Panaud, from Perpignan University), comparative genomics and population genetics (within the BIOGECO and BFP).

FULL SUMMARY WITH OBJECTIVES: Structural variation (SV) - i.e. pieces of DNA being deleted, inserted, or rearranged among chromosomes - strongly influences gene content and genome structure within and between closely related species. SV may have strong impacts on phenotypes of ecological and agronomical interest but are poorly captured when genotypes are produced in comparison to one single reference genome.

Consequently, the evolutionary dynamics of SV in natural populations (mutation rate, role of selection in shaping genetic variation) and their role in local adaptation remain poorly documented compared to that of single nucleotide polymorphisms (SNPs), especially in forest tree species. Hence, in order to capture variation of SV and its impact on phenotypic variation, comparative and evolutionary genomics areas are now turning to pan-genome based analyses of genetic variation. White Oaks are species of ecological, economic and cultural importance in Europe, accounting for a third of the metropolitan French forests (i.e. 5M ha). These populations display signs of stress or even decline related to biotic and abiotic stresses and their adaptive potential in the context of climate changes is uncertain. The genome of the pedunculate oak was sequenced recently, providing the blueprints to discover genes underlying adaptive variation in these keystone species. However, given the complicated speciation history of white oaks (with a recent secondary contact between species), it is highly likely that

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## JagiellonianU Poland InsectSymbiosisEvolution

Ph.D. Student position: The diversity and evolution of insect microbial symbionts

We are looking for a motivated and enthusiastic candidate for a Ph.D. Student position in Biology at Jagiellonian University in Krakow, Poland. The Student will be involved in the NCN Opus project “The patterns, factors, and drivers of insect microbiome variability”. The project is a collaboration between dr Anna Michalik (Institute of Zoology and Biomedical Research) and dr hab. Piotr ukasik (Institute of Environmental Sciences; symbio.eko.uj.edu.pl).

The Student will address a series of questions about the diversity, specificity, transmission, and roles of insect microbial symbionts. The research will focus on hoppers (Auchenorrhyncha), a diverse and ecologically and economically significant clade of hemipterans (true bugs) that includes planthoppers, leafhoppers, treehoppers,

spittlebugs, and cicadas. Their nutrient-limited diet of plant sap is supplemented by specialized heritable bacterial symbionts that produce amino acids and vitamins. These symbionts co-diversify with hosts - but in many insect lineages, they were joined or replaced by other microbes that contribute nutritional functions. Many of them also host heritable facultative endosymbionts such as Wolbachia and Rickettsia that may affect insect reproduction, resistance to natural enemies, or abilities to vector plant pathogens. All these microbes can play critical importance in insect biology, but there is rapidly accumulating evidence that the infections may vary among insect clades, species, populations, and even individuals sampled at the same time, at the same site. Unfortunately, we know very little about these diversity patterns or their biological importance.

The Student will address these questions using a combination of field collections across Central Europe and Baltic countries, high-throughput sequencing and bioinformatic analysis of host and symbiont marker genes and metagenomes, and microscopy (light microscopy, transmission electron microscopy [TEM], fluorescence in-situ hybridization [FISH]).

The Student will be encouraged to work closely with other team members and project collaborators in Poland and abroad, and supported in pursuing their related ideas. The Student will be based at one of the top research institutes in the fields of Ecology and Evolution in Central Europe, in a medieval city known as the cultural capital of Poland, with good access to outdoor recreation opportunities and well-connected to the rest of Europe. A competitive stipend is available for the suitable candidate. We have generous funding for research and research travel.

The successful candidate will have an M.Sc. degree in a relevant field by September 2022; a demonstrated interest in Evolution, Entomology, Microbiology, and/or Genomics; experience with, or a keen interest in learning, Bioinformatics, Computational Biology, and Microscopy techniques; and strong English language, communication, and organizational skills. Previous experience with insect diversity, ecology, evolution, and especially symbioses, molecular biology, microbiome surveys, phylogenomics and/or comparative genomics, as well as willingness to travel are advantageous.

The candidates are asked to e-mail a cover letter explaining their background, skills, and interest in the project, a CV, and contact details of two academics who can provide a confidential reference, to Dr. Anna Michalik (a.michalik@uj.edu.pl). Informal inquiries are welcome. The review of applications is ongoing; please apply by 15th June 2022 to ensure full consideration. The se-

lected candidate or candidates will be assisted with a formal application for the Ph.D. Program in Biology at Jagiellonian University.

Anna Michalik, PhD Department of Developmental Biology and Morphology of Invertebrates Institute of Zoology and Biomedical Research Jagiellonian University, Gronostajowa 9, 30-387 Krakow, Poland

Anna Michalik <a.michalik@uj.edu.pl>

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## JamesCookU FairyWrenEvolution

Expression of interest: PhD scholarship behavioural adaptation to climate change in fairy-wrens

I'm looking for outstanding candidates who wish to apply for a competitive PhD scholarship at James Cook University (Townsville, Australia) to study topics related to behavioural adaptation to climate change using fairy-wrens as a study system. The project involves a combination of fieldwork in south-west Australia with analyses of long-term datasets.

Summary: It has been suggested that social species have evolved in harsh environmental conditions, allowing for successful reproduction and survival in environments where pairs alone cannot succeed. This implies that social behaviour may buffer against adverse weather conditions. However, an overlooked issue is that social behaviour itself will also be affected by adverse weather. This project will study the dynamic interplay between ecological conditions and social behaviour through new experiments and detailed behavioural observations using an iconic Australian bird as a model system.

You need to be eligible to apply for an (International) Research Training Program Scholarship (<https://www.jcu.edu.au/graduate-research-school/hdr-candidates/postgraduate-research-scholarships>). Requirements typically include at least one first-authored peer reviewed publication and a MSc/ first class Honours, or equivalent (<https://www.jcu.edu.au/graduate-research-school/forms-and-policies/scholarship-scoring-procedure>)

Please send me a letter with your interests, including a current CV to Dr Lyanne Brouwer: Lyanne.Brouwer@jcu.edu.au

See my website for more information about my research: <https://myscience.eu/lyanne/> Lyanne Brouwer Lecturer

College of Science & Engineering James Cook University, Australia

JCU Researcher Profile I Personal Website I Google Scholar

T 07 4781 5389 I T (INT'L) +61 7 4781 5389

E Lyanne.brouwer@jcu.edu.au

JCU Townsville I Bebegu Yumba campus I Douglas I Building 142 I Room 208

1 James Cook Drive Townsville QLD 4811 AUSTRALIA  
jcu.edu.au

We acknowledge the Australian Aboriginal and Torres Strait Islander peoples as the traditional owners of the lands and waters where we live and work.

Your feedback is appreciated and can be submitted to: [feedback@jcu.edu.au](mailto:feedback@jcu.edu.au)

Lyanne.brouwer@jcu.edu.au

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## KU Leuven HumanEvolutionaryGenetics

Doctoral research on evolutionary genetics of human cold adaptation

Human Evolutionary Genetics lab at KU Leuven is a dynamic team of driven, enthusiastic and inclusive scientists. We use genomic information from human populations to address questions about demographic history and selection. In this position, you will play a key role in the FWO-funded research on cold adaptation that strives to expand our knowledge of the regions of the genome that have been targets of selection and to functionally study the role of such genes in *Drosophila* model.

Project Genetic adaptations are important in determining long-term survival and distribution of species across a range of different environments. Humans are a tropically adapted species that expanded only recently to high latitudes. The genetic basis and the molecular mechanisms that govern human adaptation to high latitude environments, including adaptations to diet and cold, remain incompletely understood. We previously identified genomic regions with evidence of positive selection in human populations living in the extreme cold conditions in Central and Northeast Siberia. Many of these genomic regions include genes of unknown function

while showing a significant enrichment of liver-expression consistent with the proposed role of the liver as an important metabolic hub. Your role in this project will be to consolidate the list of human cold adaptation candidate genes by further selection scans on human genomic data. In parallel to the work on human genes, and in collaboration with Prof. Patrick Callaert's team in the same department, we will use *Drosophila melanogaster* as a genetic model for the functional annotation of poorly annotated genes associated with cold adaptation in humans to gain a better understanding of the genetic basis and the molecular mechanisms behind human cold adaptation.

Profile You ideally have:

— a keen interest and motivation to work on ambitious projects in a dynamic, driven team. — the ability to meet timelines and work accurately. — a passion for analyzing large genomic data. — a Master's degree in bioinformatics, population genetics, biomedical sciences, or equivalent qualifications. — experience in human genome or population genetic data analyses, statistics, or programming (desirable, not a prerequisite).

You will:

—work with and responsibly manage large genomic data sets on the VSC computing environment. —develop pipelines for selection scanning and population genetics, and statistical analyses. —communicate results in a professional manner in spoken and written English through papers, presentations and discussions with consortium members. —coordinate with other team members on cfDNA analyses.

Offer Working with us: We have onsite access to state-of-the-art facilities, including high-throughput sequencing, bioinformatics, imaging, high-capacity computing, single cell analysis platforms, flow cytometry and others. We are committed to inclusivity and diversity in the workplace, and value a positive, empowering and actively engaging attitude in every team member. Located in Leuven, a small but vibrant and international town by the river Dijle where centuries of history meet cutting-edge science, we are only a stone's throw away from the cosmopolitan city of Brussels, the heart of Europe. We are part of the University of Leuven, one of the oldest and most prestigious universities of Europe. Founded in 1425, it is Belgium's largest university, currently featuring among the best universities in the world according to the Times Higher Education and recently ranked as Europe's most innovative for the third year in a row.

Applicants must hold a Master's degree when commencing the post. The earliest start date of the position is

October 1st, 2022, but we are very happy to cater this for the ideal candidate. We offer a 4-year contract on a competitive salary, pending positive evaluation by our doctoral school after 1 year.

Interested? For more information please contact Prof. dr. Toomas Kivisild, mail: [toomas.kivisild@kuleuven.be](mailto:toomas.kivisild@kuleuven.be). You can apply for this job no later than June 15, 2022 via the online application tool <https://www.kuleuven.be/-personeel/jobsite/jobs/60111750?hl=en&lang=en> KU Leuven seeks to foster an environment where all talents can flourish, regardless of gender, age, cultural background, nationality or impairments. If you have any questions relating to accessibility or support, please contact us at [diversiteit.HR@kuleuven.be](mailto:diversiteit.HR@kuleuven.be).

Toomas Kivisild <[toomas.kivisild@kuleuven.be](mailto:toomas.kivisild@kuleuven.be)>

## LundU EvolutionGeneExpression

LundUniversity\_EvolutionaryHybridizationGenomics

Attractive 4-year fully funded PhD-position within the ERC projectHybridExpressat Lund University, Sweden.

We have an opening for a PhD-student within the project "Hybridization derived novel patterns of gene expression". This project addresses the role of gene expression in evolutionary novelty from hybridization. Specifically, it will investigate if new, transgressive gene expression profiles can evolve in hybrid lineages, using four independently evolvedisland lineages of thehybrid Italian sparrow *Passer italiae* as a model system.This is an excellent opportunity for an ambitious student with strong skills in bioinformaticsto address the role of regulation ofgene expression in hybridization derived novelty.

Contact person: Anna Runemark  
[anna.runemark@biol.lu.se](mailto:anna.runemark@biol.lu.se)

Please find more information and apply here:

<https://lu.varbi.com/en/what:job/jobID:508485/-type:job/where:4/apply:1> Anna Runemark  
<[anna.runemark@biol.lu.se](mailto:anna.runemark@biol.lu.se)>

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## MartinLutherU BeePopulationGenomics

PhD position: “A comparative population genomic approach to address the effects of habitat loss and fragmentation on South American *Centris* oil-bees”

At the Martin Luther University Halle-Wittenberg, Natural Sciences Faculty I, Institute of Biology, the General Zoology group offers a 3 years position (65%) starting on the 01.09.2022 for a Doctoral Researcher (m-f-d). The salary is according to national norms, i.e. 65% of 13 TV-L, which translates to approximately 27K-32K euros per annum (depending on experience).

The project: Landscape fragmentation and habitat loss are among the major threats to global bee diversity. However, it is still not well understood if certain functional traits render some bee species more vulnerable to environmental change than others. We seek a highly motivated PhD student to investigate whether South American oil bees of the genus *Centris* that vary in functional traits also differ in their population genomic response to fragmentation and habitat loss. Moreover, the PhD student will study the effects of such habitat disturbances on *Centris* bee- oil plant-interactions as well as on the ecosystem service of pollination. This will allow to link habitat disturbance, population genomics, ecologically relevant traits, species interactions and ecosystem services (pollination). The research work includes large scale sampling of bees in Brazil (3-4 months), whole genome sequencing to generate single nucleotide polymorphism (SNP) data, landscape genomics, building plant-pollinator networks and conducting pollination experiments. The selected PhD candidate will work in an ambitious international research team with modern lab facilities.

Requirements: - MSc/Diploma in Biology or related subject - Knowledge on population genetics/genomics and SNP data - Field work experience (especially in collecting insects) - Knowledge on wild bee biology, using GIS, R and Linux is an advantage but not mandatory - Experience in speaking and writing in English - Knowledge of German and Portuguese is an advantage but not mandatory - Driving license (class B) - Willingness to work under potentially uncomfortable field conditions - Team-oriented and strong organizational skills

The Martin Luther University Halle-Wittenberg gives

priority to applications from severely disabled candidates with equivalent qualifications. Women are particularly encouraged to apply.

All applications should include the following: - Cover letter in English or German describing your motivation, research interests and relevant experience - Curriculum vitae including names and contact details of two scientific references - Digital copy of MSc/Diploma certificates and transcript of records

Kindly send your application in electronic form as a single PDF file, quoting the reference number 5-5672/22-D to Dr. B. Kahnt (E-Mail: [belinda.kahnt@zoologie.uni-halle.de](mailto:belinda.kahnt@zoologie.uni-halle.de)).

Submission deadline is 27/06/2022.

[belinda.kahnt@zoologie.uni-halle.de](mailto:belinda.kahnt@zoologie.uni-halle.de)

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## MemorialU SalmonClimateAdaptation

Graduate Student Position (Ph.D.): Characterizing mechanisms of rapid adaptation to predict responses to climate change in Atlantic salmon

We are seeking a graduate student (PhD funded for 4 years) to work on thermal tolerance and climate adaptation in wild Atlantic salmon (*Salmo salar*) in Newfoundland, Canada. The position will be held at Memorial University of Newfoundland and Labrador (MUNL) in St. John's and will be co-supervised by Dr. Sarah Lehnert of Fisheries and Oceans Canada (DFO) and Dr. Ian Fleming of MUNL's Department of Ocean Sciences. The position is fully funded through NSERC and DFO. Major scholarship holders will receive generous top-ups to their awards.

Atlantic salmon is a culturally, economically, and ecologically important species, and many populations range-wide are experiencing declines in abundance with climate change being identified as one potential contributing factor. In Atlantic Canada, warming river temperatures continue to result in fisheries closures and mortality events for Atlantic salmon. These events are expected to become more frequent under future climate scenarios. Currently, there is limited knowledge on how Atlantic salmon populations will respond to climate change. While evidence suggests that salmon can adapt to warmer temperatures, there are upper limits to this capacity that depend on both environmental and ge-



netic factors. To understand and predict the effects of climate change on salmon in freshwater, this PhD project will use field and tank-based experiments to measure thermal tolerance and stress in Atlantic salmon from populations spanning a thermal gradient. The project will also employ both genomic and transcriptomic approaches to identify key genes and mechanisms underlying thermal adaptation and will build on current forecasting methods to understand and predict the effects of climate change on salmon populations.

Prospective students should be prepared to share their enthusiasm for research and associated skills openly within and among the research groups, and by doing so, contribute to a dynamic research environment. While they will be based in the respective laboratories in St. John's at MUNL and DFO, students should be prepared to travel to rivers around Newfoundland for fieldwork.

Qualifications: The ideal candidate will possess an MSc; have research interests and training in the areas of fish ecology or physiology and molecular biology; be capable of designing and undertaking both field and laboratory research; and have reasonable facility with the analysis of large data sets.

Start date: The ideal start date is on or before September 2022, although later dates are possible.

How to apply: Prospective candidates should email a cover letter, CV, unofficial transcripts, and contact information for three people who can serve as references. Review of applicants will begin June 1 2022 and continue until the position is filled. An email can be sent to both Drs. Sarah Lehnert and Ian Fleming.

We are committed to promoting equity, diversity, and inclusivity in fisheries research. We encourage people from historically underrepresented groups to apply for this position, including women, Indigenous peoples, persons with disabilities, members of visible/racialized minorities, and diverse sexual orientation and gender identities.

Dr. Sarah Lehnert Fisheries and Oceans Canada Salmonid Section, Northwest Atlantic Fisheries Center Sarah.Lehnert@dfo-mpo.gc.ca

Dr. Ian Fleming Department of Ocean Sciences, Memorial University of Newfoundland and Labrador ifleming@mun.ca

“Lehnert, Sarah” <Sarah.Lehnert@dfo-mpo.gc.ca>

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## MontpellierU HumanVirusGenomes

Fully funded PhD position in genetic epidemiology at Montpellier university, France

Title: Interactions between the human and dengue virus genomes

Supervisor: Vincent Pedergrana, CRCN, vincent.pedergrana@cnrs.fr Co-supervisor: Stéphane Guindon, CRHC, stephane.guindon@lirimm.fr

Host Units: MIVEGEC, UMR5290 & LIRMM, UMR 5506 Institution: University of Montpellier, France

Subject description:

Our main objective is to identify new genes in the host and virus genomes that explain the pathogenicity of the dengue virus. We will also aim at identifying new targets to potentially develop a new therapy and a vaccine against dengue. Indeed, the targets identified over the last 15 years have not been able to control the epidemic. Drug development needs the support of genomics to identify promising new targets, as these have been shown to be more likely to lead to effective therapeutics. However, to date, only two human targets have been identified for dengue.

We propose to apply the new genetic analysis techniques that Dr. Pedergrana and colleagues have recently developed to identify more targets and more important interaction points between the viral and human genomes at the same time. This approach represents a significant improvement over current solutions by integrating the genomes of both interacting organisms in the same analysis.

In addition, we will explore, through phylogenetic reconstruction, inter- and intra-host viral diversity during acute infection, which will allow us to better understand the revealed genomic interactions.

PhD student role: Dr. Pedergrana and Dr. Guindon will co-supervise the PhD student. Their laboratories are both located in Montpellier, which will be an asset for this double supervision, allowing frequent interactions with both supervisors for the PhD student as well as providing a stimulating and complementary environment and scientific communities. Thus, the doctoral student will share his/her time between the two sites, depending on the specific objectives of his/her thesis.

The PhD student will have a strong background in math-

emetics, population genomics and statistical genetics, and be able to code and work on a cluster. He/she will be primarily responsible for the genetic analysis and the development of statistical methods under the supervision of Drs Pedergrana and Guindon. He/she will first reconstruct viral genomes from the viral sequences obtained by full genome sequencing. He/she will then construct consensus genomes and call the viral variants. Based on these data, she/he will reconstruct viral phylogenies and estimate intra- and inter-host viral diversity. Dr. Guindon will supervise this first part. She/he will then cut the human genetic data and deduce the missing genotypes and HLA alleles. Finally, he/she will be able to integrate the human clinical and genomic data and perform a genome-to-genome analysis under the supervision of Dr. Pedergrana.

The PhD student will be fully involved in the development of statistical methods. He/she will also participate in national or international conferences to present the results of this project. Finally, he/she will be the first author of any manuscript resulting from this work. He/she will be able to attend any courses that may help in the development of his/her career.

**Expected Profile:** This position is ideal for someone with a combination of interest in theory, real world data, and public health. Curiosity and the ability to learn are more important than specific training. Essential requirements include. - Master's degree in statistical genetics, genetic epidemiology, evolutionary genetics or statistics and strong analytical and quantitative skills. - Proficiency in at least one programming language (e.g., R, Python). - Excellent written and oral communication skills in English.

Applications are due on July 15, 2022 for a start date in October 2022

Publications directly associated with this thesis:

Sigera PC, Amarasekara R, Rodrigo C, Rajapakse S, Weeratunga P, De Silva NL, et al. Risk prediction for severe disease and better diagnostic accuracy in early dengue infection; the Colombo dengue study. *BMC infectious diseases*. 2019;19(1):680.

Ansari, [Â], Pedergrana V; Interferon lambda 4 impacts the genetic diversity of hepatitis C virus; *eLife* 2019

Ansari MA\*, Pedergrana V\* et al.; Genome-to-genome analysis reveals the impact of the human innate and adaptive immune systems on the hepatitis C virus ; *Nature Genetics*, 2017

Accounting for spatial sampling patterns in Bayesian phylogeography. S Guindon, N De Maio. *Proceedings of the National Academy of Sciences* 118 (52). 2021.

Accounting for calibration uncertainty: Bayesian molecular dating as a “doubly intractable” problem. S Guindon. *Systematic Biology*. 67 (4). 2018.

New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. S Guindon et al.. *Systematic Biology* 59 (3). 2010.

Vincent Pedergrana

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## Munich Lichen Adaptations

PhD position: “Genetic adaptations and mechanisms of stress tolerance in green-algal lichen photobionts and their host fungi” We seek applicants to perform thesis research on how green algal lichen photobionts are able to tolerate stressful conditions and to study genetic adaptations of individuals and populations. Applicants must have the ability both to work independently and to integrate in a team environment. They are expected to publish their results in well-respected peer-reviewed journals. Applicants should hold a MSc degree or equivalent in a program providing experience in evolutionary biology, systematics, ecophysiology or similar. Essential are German language skills. Experience with fungi or green algae is desirable, and candidates possessing this experience will rank higher. Advantageous are skills in R and python.

Salary and benefits are in accordance with a public service position in Germany (collective agreement TV-L E13, 50%). The position includes a teaching duty of 2.5 hours per week during the semester. The contract shall start in October (negotiable) and will be limited to 12 months, with a possibility for extension by up to 2 years. Equally qualified handicapped applicants will be given preference.

Our major research areas are population genetics, systematics and ecology of symbiotic fungi and their photosynthetic partners. The core study systems of our research group is the model lichen lungwort (*Lobaria pulmonaria*). Lungwort is an epiphytic lichen which has been well studied regarding its ecology and dispersal biology. Extensive genome sequence datasets are available

for lungwort, including multiple annotated genomes of the mycobiont and of its primary photobiont.

The candidate's workplace will be located near the premises of the beautiful Botanical Gardens of Munich in Nymphenburg. With its picturesque old town, Nymphenburg castle, its vivid green spaces such as the forests along the Isar river, the English Garden, numerous beer gardens and an active night life, Munich is arguably one of the cities with the highest life quality in Germany. Being located proximate to the Alps, Munich moreover provides interesting opportunities as a location both for biological studies and for various recreational activities.

Applications consisting of a CV, publication list, possible starting date, and a statement of research interests (maximum 1 single-spaced page in length), names and contact information for up to three references should be prepared in a single pdf file and sent by email to Silke Werth at werth@bio.lmu.de with subject line "PhD position Genetic adaptations and mechanisms of stress tolerance". Review of applications will start June 20th, 2022, but applications will be accepted until a suitable candidate has been found. The position is available from October 2022.

Information on the research environment at LMU Munich can be found here: [www.en.biologie.uni-muenchen.de](http://www.en.biologie.uni-muenchen.de). Information on relocation to LMU Munich is available here: [www.en.uni-muenchen.de/-about\\_lmu/contact/int\\_office/index.html](http://www.en.uni-muenchen.de/-about_lmu/contact/int_office/index.html) Prof. Dr. Silke WERTH LMU Munich Systematics, Biodiversity and Evolution of Plants Menzingerstraße 67, 80638 Munich, Germany Email: werth@bio.lmu.de

Werth <werth@biologie.uni-muenchen.de>

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## Nebraska Turkey Conservation

Ph.D. Assistantship: Conservation genomics of wild turkeys in Nebraska

We are seeking a candidate for a Doctor of Philosophy assistantship in Applied Ecology at the Nebraska Cooperative Fish and Wildlife Research Unit and the University of Nebraska-Lincoln. The student will develop large multi-locus genomic datasets to conduct analyses to evaluate the influence of social behaviors (social dominance) on reproduction and fitness as well as genomic connectivity in western Nebraska. The project will produce actionable science with the results of this multi-

faceted study informing management actions on the wild turkey in Nebraska as well as contributing to nationwide studies investigating the decline of this important game species. The successful candidate will be involved in intensive field (capture, monitoring of transmitted individuals and nests, and vegetation surveys) and laboratory work (genomic data collection). This a collaborative project with the Nebraska Game and Parks Commission and faculty at University of Nebraska-Lincoln and University of Georgia. As such, the successful candidate will work with a team of students, technicians, private landowners, university faculty, and Nebraska Game and Parks Commission biologists.

Start Date: August 2022 (flexible to Jan 2023)

Salary and Benefits: \$27,000 per year (4.5 years) will be paid through a research assistantship. Tuition and health insurance will be covered by the project. Student is responsible for fees.

Qualifications: Bachelor of Science (exceptional candidates) and Master of Science (preferred) in biology, ecology, evolution, wildlife or other relevant discipline. Experience with molecular biology techniques, avian capture methods, and coding in R or python is desirable. A willingness to learn, attention to detail, and a strong work ethic are essential.

Contact: Please contact Sarah Sonsthagen (ssonsthagen2@unl.edu) for more information about the project. To apply, please send the following to the email address above: 1) One-page cover letter describing your interest in the position, skills, and goals, 2) CV, 3) unofficial transcripts, and 4) contact information for 3 references. If possible, please include a writing sample (published manuscript, official report, etc.). UNL and NECFWRU values equity, diversity, and inclusion.

Review of applications will begin immediately and continue until the position is filled. Preference will be given to applications received by July 10, 2022.

Sarah Sonsthagen <ssonsthagen2@unl.edu>

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## Paris Saclay France Deep Learning Pop Genetics

PhD proposals in Deep Learning for Population Genetics

When/Duration: September 2022, 3 years.

- Supervisors: Flora Jay (CR CNRS), Guillaume Charpiat (CR INRIA), - Direct collaborators: Burak

Yelmen (postdoc U Paris-Saclay), Cyril Furtlehner (CR INRIA), Aurélien Decelle (Complutense University of Madrid)

We are looking for one highly motivated candidate to do a PhD in our lab and suggest two potential projects. They are follow-up research of two of the lab papers: - “Creating artificial human genomes using generative neural networks”, Yelmen et al 2021 - “Deep learning for population size history inference: design, comparison and combination with approximate Bayesian computation”, Sanchez et al 2020

Please note that we would happily talk with candidates that have an alternative project in mind, as long as it falls in the scope of deep learning for population genetics.

In their motivation letter, the candidates should explain which of these topics they are interested in (it could be both).

\* Keywords deep learning, population genetics, generative models, interpretability, inference, evolution

\* Projects  $i_{\frac{1}{2}}$  full description at [\\*https://www.lri.fr/~fjay/archive/phd2022\\_DL\\_popgen.pdf\\*](https://www.lri.fr/~fjay/archive/phd2022_DL_popgen.pdf) - Subject 1: Creating artificial human genomes using generative neural networks

- Subject 2: Inferring the evolutionary past of populations from genomic data and interpreting neural networks.

- Subject 3: Your project Feel free to contact us if you have a strong opinion on the PhD project that you would like to pursue, as long as it remains in the scope of machine learning and population genetics!

\* Requirements The ideal candidate should be good at python scripting and machine learning/statistics concepts. Experience with deep learning is a plus. Familiarity with some of the following topics: genomics, population genetics, generative models, bash scripting and high-performance computing is not mandatory but a clear plus. Being curious and autonomous is highly recommended for any PhD. Being able to communicate, read and write in English (French not required).

\* Salary: regular PhD stipend in academia. The PhD fellowship is fully funded (ANR grant) for 3 years from September 2022.

\* Application: Ideally the candidate should provide a  $i_{\frac{1}{2}}$ CV, motivation letter, past scores/ranks, names and emails of previous mentors that can be contacted. Send your application to: [flora.jay@lri.fr](mailto:flora.jay@lri.fr) ;  $i_{\frac{1}{2}}$  [guillaume.charpiat@inria.fr](mailto:guillaume.charpiat@inria.fr)  $i_{\frac{1}{2}}$  Deadline: a.s.a.p., preferably before May 26th, however we will keep reading applications received after this date until the position

is filled.

\* Lab environment The PhD candidate will interact with two teams with the LISN, a machine learning team and a bioinformatic team. They host many permanent researchers, postdocs and PhD students with whom to interact. There are weekly meetings on population genetics (informal working groups), bioinformatics and machine learning topics.

Location: LISN (Paris-Saclay University) machine learning and bioinformatics groups 1, rue Raimond Castaing 91190 Gif-sur-Yvette, France  $i_{\frac{1}{2}}$  (Paris suburban area)

Flora Jay CR CNRS LISN Laboratoire Interdisciplinaire des Sciences du Numérique, the interdisciplinary computer science laboratory, Paris-Saclay University 1, rue Raimond Castaing 91190 Gif-sur-Yvette more info < <https://flora-jay.blogspot.com/> >

Flora Jay <[flora.jay@lri.fr](mailto:flora.jay@lri.fr)>

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## Sanofi Toronto ComputationalBiology

Sanofi, one of the biggest and most successful pharma companies is making a strategic investment in machine learning for drug discovery. I recently joined Sanofi after almost 20 years as a Professor in the School of Computer Science at Carnegie Mellon University to lead a large team focused on using and developing advanced ML and AI methods for all stages of drug and vaccine discovery. We are now recruiting for several ML focused positions. We have projects spanning the range of activities related R&D including the use of active learning to design automated experiments and molecules, the use of deep learning to analyze and model single cell and spatial transcriptomics and proteomics data and the analysis, modeling and integration of clinical and real world data using NLP and graphical models.

We are building a new global ML / AI hub in Toronto. There you would be working with leading computational and experimental scientists to develop new cures and vaccines for the some of the most challenging diseases. We are building and using advanced computing and cloud platforms. Come join us to develop the next generation of computational methods and to make a difference by improving people lives and health. Please apply at: [https://-sanofi.wd3.myworkdayjobs.com/SanofiCareers/job/-Toronto-ON/Computational-Scientist\\_R2645832](https://-sanofi.wd3.myworkdayjobs.com/SanofiCareers/job/-Toronto-ON/Computational-Scientist_R2645832) Ziv

Bar-Joseph Head, R&D Data and Computational Sciences

“Bar-Joseph, Ziv /US” <Ziv.Bar-Joseph@sanofi.com>

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## SGN Frankfurt MolluscsMethylation

Job Announcement ref. #12-22007

The LOEWE Center for Translational Biodiversity Genomics (LOEWE-TBG, <https://tbg.senckenberg.de/>) aims at making the genomic basis of biological diversity accessible for basic and applied research. Building on genome sequencing and analysis, LOEWE-TBG research topics range from comparative genomics, natural products genomics, and genomic biomonitoring to functional environmental genomics. LOEWE-TBG is based in Frankfurt am Main, Germany, and is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology.

The Senckenberg Gesellschaft für Naturforschung and the LOEWE -TBG invite applications for a PhD Candidate (m/f/d)

Epigenetics and DNA methylation in molluscs

We are seeking highly motivated PhD students with interest in epigenetics and DNA methylation. The project involves functional evaluation of DNA methylation in the sacoglossan sea slug species *Elysia timida* as a model system to understand the fundamental roles of this epigenetic mark in the phylum Mollusca and to identify potential genes important for successful chloroplast incorporation (functional kleptoplasty). Epigenetic mechanisms regulate the interpretation of genetic information and adapt gene expression patterns to changing developmental or environmental conditions. Several epigenetic mechanisms have been identified to date, with DNA cytosine methylation being the best studied and possibly the most important epigenetic mark. The project will be supported by the excellent laboratory and bioinformatics facilities of the center.

Your tasks - Establishment of a culture of the alga *Acetabularia acetabulum* and *E. timida* at LOEWE-TBG - Perform experimental time series (whole genome bisulfite sequencing (WGBS) / RNA-seq) during the life cycle of *E. timida* - Perform subsequent bioinformatic analyses of whole-genome bisulfite sequencing and RNAseq data using existing recipes/scripts - Publication of results in

high-profile international journals

Your profile - Master degree in evolutionary biology, molecular biology, computational biology/bioinformatics or a related subject - Experience with analyzing WGBS and RNA-seq data (scripting in R or python would be beneficial) - Teamwork oriented and excellent communication skills with proficiency in written and oral English - Interest to collaboratively work in an interdisciplinary, international team

What is awaiting you? - An interesting task in a dynamic team of researchers in an international research group and joining the new LOEWE TBG excellence centre with its 20 new research groups - A relevant and timely research topic for a PhD project - The possibility to create a network with scientists in interdisciplinary fields in translational biodiversity genomics - Flexible working hours - dual career service - leave of absence due to family reasons (certified by “auditberufundfamilie”) - parent-child - office - annual special payment - company pension scheme - Senckenberg badge for free entry in museums in Frankfurt - leave of 30 days/year

The Senckenberg Gesellschaft für Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The employer is the Senckenberg Gesellschaft für Naturforschung.

Place of employment: Frankfurt am Main Working hours: part time (65% position) Type of contract: 3 years, starting as soon as possible Salary: according to the German collective agreement TV-H (pay grade E 13) The Senckenberg Gesellschaft für Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The employer is the Senckenberg Gesellschaft für Naturforschung.

How to apply Please send your application, mentioning the reference of this job offer (ref. #12-22007) until 06 June 2022 (deadline), by e-mail (attachment in a single pdf document) including a brief cover letter detailing your research interests and experience (1 page), a CV and copies of your certificates, transcripts and grades to:

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt a.M. E-Mail: [recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)

For scientific information please contact Dr. Carola Greve, E-Mail [carola.greve@senckenberg.de](mailto:carola.greve@senckenberg.de).

Dr. Carola Greve (Lab and Project manage-

ment) Zentrum für translationale Biodiversitätsgenomik (LOEWE-TBG) Tel.: +49 69 7542 1844 Mail: Carola.Greve@senckenberg.de

Senckenberg Gesellschaft für Naturforschung  
Rechtsfähiger Verein gemäß § 22 BGB Senckenberganlage 25 60325 Frankfurt

Direktorium: Prof. Dr. Klement Tockner, Prof. Dr. Andreas Mulch,

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## TrentU CaribouConservationGenomics

Dr. Paul Wilson (Trent) and Dr. Micheline Manseau (ECCC, Trent) through EcoGenomics ([ecogenomicscanada.ca](http://ecogenomicscanada.ca)), a long-term national scale program, are recruiting PhDs and Post-doctoral Fellows (PDFs) focusing on genomic applications to caribou conservation. This national-scale collaborative research program on caribou conservation genomics is supported by whole-genome sequences of caribou representing diverse subspecies, ecotypes and populations, with additional genomes being planned for sequencing, and development of targeted caribou-specific loci for Population Genomic surveys of a long-term (20-year) database of samples (40,000 across Canada). The national network supporting these positions include partnerships with Environment & Climate Change Canada; Canadian Wildlife Service; Parks Canada; the Ontario Ministry of Northern Development, Mines, Natural Resources & Forestry, Ontario Ministry of the Environment, Conservation and Parks and other provincial (e.g. Alberta, British Columbia, Manitoba, Saskatchewan) and territorial jurisdictions (Northwest Territories, Yukon, Nunavut); wildlife management boards and Indigenous communities (e.g. the Sahtu Wildlife Management Board); and industry such as MB Hydro. Positions may be based out of Peterborough, Ontario at Trent University or Ottawa at the National Wildlife Research Centre, Environment & Climate Change Canada.

The following positions/projects are available:

PDF studying Demographic Parameters in caribou ranges across Canada using applications such as spatial

capture-recapture (sCR); density estimation; population modelling; and network analyses. Position requires strong quantitative skills, and experience in software development will be considered an asset.

PDF in establishing metrics for large-scale and long-term Genomic Monitoring of caribou through the implementation of sequencing technologies, e.g. high/low coverage genomes and amplicon sequencing, and development of analytical pipelines. Position requires strong bioinformatic skills, and knowledge of molecular genomic protocols will be considered an asset.

PhDs supporting the above projects will be considered in addition to projects related to caribou ecotype dynamics in Ontario's Ring-of-Fire region; assessment of genomic erosion in isolated caribou populations (natural and captive) and at the southern range margins of boreal caribou; and an assessment of rapidly evolving genomic elements in adaptive genes of caribou subspecies and ecotypes across Canada.

Starting dates flexible for all positions

<https://www.ecogenomicscanada.ca/phd-and-pdf-recruitment-may-2022/> Send a Cover Letter and CV to: [pawilson@trentu.ca](mailto:pawilson@trentu.ca) or [micheline.manseau@ec.gc.ca](mailto:micheline.manseau@ec.gc.ca)

Bridget Redquest

Laboratory/Project Manager Trent University

2140 East Bank Drive Peterborough, ON K9L 1Z8  
Phone: (705)748-1011 ext 6657/7313

Bridget Redquest <[bridgetredquest@trentu.ca](mailto:bridgetredquest@trentu.ca)>

[bridgetredquest@trentu.ca](mailto:bridgetredquest@trentu.ca)

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## TU Munich ParasiteDormancyCoevolution

Dear Evoldir community,

The Professorship for Population Genetics welcomes applications for one PhD position.

Title: “Causes and consequences of dormancy/quiescence evolution in parasites

Topic: Quiescence and dormancy evolve as a bet-hedging evolutionary strategies in many plants, animals, and micro-organisms (including parasites or pathogens) in unpredictable environments. Dormancy/quiescence determines the rate of genomic evolution (see work by the Tellier lab) but is also of practical relevance for disease

management. Indeed, dormant/quiescent parasites have the ability to escape drug treatment. It is therefore of interest to understand the evolutionary mechanisms promoting dormancy/quiescence in parasites. The central hypothesis of the project states that coevolution between hosts and their parasites promotes bet-hedging. We have previously shown that 1) seed banking and dormancy can evolve in hosts due to coevolutionary dynamics, and 2) depending on the germination function, the seed bank itself can slow down or even damp off the coevolutionary oscillations. As allele frequency oscillations are critical to promote bet-hedging evolution, a complex eco-evolutionary interplay occurs between the evolution of dormancy and coevolutionary dynamics (Verin and Tellier, *Evolution*, 2018). The goal of this theoretical project is to understand and predict the conditions for parasites to evolve dormancy or quiescence as bet-hedging strategies in response to coevolution and hosts' life-history traits. We will study the conditions for bet-hedging to evolve under coevolutionary (epidemiological) dynamics by using models of short and very long dormancy. We will use analytical methods of adaptive dynamics to derive analytical solutions for the ESS of dormancy/quiescence under different parameter regimes.

We look for a PhD candidate with strong foundations in mathematics/theoretical physics (deterministic and stochastic modelling) and/or theoretical population genetics. The doctoral candidates will be part of the TUM Graduate School ([www.gs.tum.de](http://www.gs.tum.de)) and work in an interdisciplinary project team. The PhD candidate will be based in the Professorship for Population Genetics (supervisor Prof. A. Tellier) at the School of Life Sciences ([www.popgen.wzw.tum.de](http://www.popgen.wzw.tum.de)), with interactions at the TUM Department of Mathematics (Prof. J. Müller).

#### Your profile

Excellent Master's degree (or equivalent) in mathematical biology / theoretical population genetics or in mathematics / theoretical physics with strong interest to learn evolutionary biology,

Expertise in programming (Python, C++, R),

Highly motivated and keen on working in an international and interdisciplinary team,

Very good knowledge of English language.

#### We offer

PhD funded by the German Science Foundation, 36 months starting in 2022, salary E13 (75%),

Membership in the TUM Graduate School,

Interdisciplinary research environment applying mathematics to evolutionary questions,

Extra funding for international travel and research stay.

TUM is an equal opportunity employer. Qualified women are therefore particularly encouraged to apply. Applicants with disabilities are treated with preference given comparable qualification.

#### Contact

Please send your application materials, including a cover letter, a CV, your degree including a detailed transcript of records, and contact information of two referees to Silke Bauer ([silke.bauer@wzw.tum.de](mailto:silke.bauer@wzw.tum.de)) and informal enquiries can be sent to Prof. A. Tellier ([aurelien.tellier@tum.de](mailto:aurelien.tellier@tum.de)). The deadline for application is 12.06.2022.

Prof. Aurelien Tellier, PhD Assoc. Prof. for Population Genetics Dept of Life Science Systems School of Life Sciences Technical University of Munich Liesel-Beckmann Strasse 2 85354 Freising - Germany [www.popgen.wzw.tum.de](http://www.popgen.wzw.tum.de) Aurelien Tellier <[aurelien.tellier@tum.de](mailto:aurelien.tellier@tum.de)> Aurelien Tellier <[aurelien.tellier@tum.de](mailto:aurelien.tellier@tum.de)>

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## UGeneva Two ExtraterrestrialExperimentalEvol

Adaptation through natural selection of terrestrial life to extra-terrestrial conditions Bas Ibelings, Mridul Thomas, Daniel McGinnis (Earth Sciences and Environment Section, Department F.-A. Forel, UniGE), Emeline Bolmont (Department of Astronomy, UniGE)

Following the 2019 Nobel prizes for Profs Major and Queloz, the University of Geneva is developing a Centre for Life in the Universe. Within this new Centre 2 PhD positions are available to study experimental evolution of life forms from Earth under conditions found on planets elsewhere.

Life is defined by the capacity of Darwinian evolution. Experimental evolution has proven to be one of the most powerful tools to study the mechanisms of evolution on Earth. Evolution that drove the diversification of life from a simple and homogenous beginning. We aim to perform experimental evolution and observe which genotypic and phenotypic traits will be favored under conditions found on different planets. For this we assume that there is a core to life that is similar on Earth and elsewhere, so that presently the best model system to study Life in the Universe are life-forms found on Earth. There are many organisms (facultatively) adapted to life in the

absence of oxygen (e.g. methanogens, yeast). Some of these function with very simple substrates, for example methane production occurring from hydrogenotrophic processes, where the substrates could be from expelled biogases of other organisms or by carbonate rock erosion ( $4\text{H}_2 + \text{CO}_2 \rightarrow \text{CH}_4 + 2\text{H}_2\text{O}$ ). These processes also alter the balance of the stable C isotopes in the system ( $\delta^{13}\text{C}$ ). From this perspective, we propose conducting experiments on organism evolution in alternative environments (various substrates and initial atmospheres, such as  $\text{H}_2 + \text{N}_2$  mixture or  $\text{CO}_2$ ). Besides quantifying the organism's evolutionary trajectory, we propose to monitor - using existing equipment in Department Forel - the various gases consumed or produced by these organisms, i.e. to investigate what types of atmospheric gas compositions could suggest the presence of life on extra-terrestrial worlds. Studies have shown growth of unicellular prokaryotes and eukaryotes under conditions found on other planets, like the  $\text{H}_2$  dominated atmosphere of rocky exoplanets, so the potential for experimental evolution is present. Questions of main interest:

What are the key traits that evolve when life adapts to non-earth like conditions and what is the nature of the underlying mutations? What are the biosignatures found as a consequence of the evolution of new traits? Are they unique signatures of life? The 2 PhD positions are available for 4 years. A 50 % technician is available to support the work. Salary ca 3,000 CHF / USD per month. These positions remain open until filled. If you are interested please send a motivation letter and brief CV to Daniel.McGinnis@unige.ch and Bastiaan.Ibelings@unige.ch. Looking forward to hear from you.

Bastiaan W Ibelings Professor

Microbial Ecology Director Department F.-A. Forel for Environmental and Aquatic Sciences

Faculty of Sciences, University of Geneva

Tel +41223790313 / +413790302 (secretary) Uni Carl Vogt (room C211) 66 Blvd Carl Vogt Geneva 1205 Switzerland

Bastiaan Willem Ibelings  
<Bastiaan.Ibelings@unige.ch>

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## U Glasgow Animal Reproduction Genetics

PhD opportunity at the University of Glasgow fully funded for UK residents (stipend, tuition fees, research budget).

Supervisors: Prof Kathryn Elmer Prof Maureen Bain

PhD project summary: Reproduction is key to the physiology, development, and life history of animals and the biological bases are deeply shared across amniotes. Viviparity has evolved more than 100 times in mammals and reptiles and its evolutionary novelty is how mothers modulate duration of pregnancy and reduction in offspring number. These are presumed to be genetic but are also affected by proximate and long-term environmental context. To date, experiments to deconstruct environmental from intrinsic and extrinsic genetic components of female reproductive investment were not possible and therefore the molecular basis of pregnancy duration and its evolution is not known.

In this project we will identify genetic determinants of reproductive investment and pregnancy duration, including partitioning the influence of maternal vs paternal effects. This is uniquely possible using an emerging model organism for amniote live-bearing - the common lizard, *Zootoca vivipara*. We will quantify the variation in gestation time using a combination of developmental biology and genetic approaches. Further, we will use genome-wide pedigrees to determine the contribution of paternal genetic variation on i) maternal reproductive strategies and ii) offspring investment and outcome. The experiments will involve new field collections, microscopy and developmental biology, and genomic analyses for high resolution parentage reconstruction. Demonstrating the genetics of reproductive timing and investment is key to identifying how major changes in reproductive mode occur, resolving genetic and evolutionary conflicts between sexes and generations, and improving knowledge of influences to pregnancy outcomes. <https://www.gla.ac.uk/colleges/mvls/graduateschool/-mvlsdtp/supervisorsandprojects-2022/mvlsdtp/-#geneticdeterminantsofreproductivemodeandinvestment> The project involves a breadth of skilled and approaches including fieldwork in Europe, genomic data generation and analysis, and histochemistry and microscopy.



Note applications are to the University programme, not the supervisors directly. Please see the webpage and the link at the bottom for how to apply. Informal inquiries to Kathryn Elmer in advance of application are encouraged.

Kathryn Elmer <Kathryn.Elmer@glasgow.ac.uk>  
Kathryn Elmer <Kathryn.Elmer@glasgow.ac.uk>

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## ULethbridge Canada:BirdEvolutionNeurobiology

Our lab currently seeking applications from students interested in pursuing a MSc or PhD starting in September 2022 or January 2023.

We offer a range of research topics that combine field and lab based approaches to understand the evolution of diversity in the anatomy and behaviour of birds. Our lab houses one of the largest comparative brain collections in the world with over 190 species represented. Dedicated lab facilities include: microtomes, dissection microscopes, fluorescent microscope, high-resolution digital slide scanner, and state-of-the-art software for image analysis. As a member of the Department of Neuroscience, we also have ample wet lab space, access to additional imaging techniques, and animal housing. Field research is supported by an array of field equipment, a dedicated 4x4 field vehicle, and a lab trailer for preparing samples.

Previous students have worked on a range of subjects, such as wing morphology in grouse, the effects of domestication on brain anatomy, olfactory system anatomy in vultures, and reconstructing the brain of the endangered night parrot. Several projects are available, but we also welcome students to develop their own thesis ideas related to avian neuroanatomy. Some examples of potential projects for new graduate students include:

\* the neuroanatomical effects of artificial selection for behaviour in pigeons \* sensory systems of hawks and falcons

All students in the lab gain valuable skills in dissections, histology, microscopy, and statistical analyses. Depending on the specific project, students can also gain experience in bioacoustics, morphometrics, microCT scanning, field techniques (e.g., trapping methods, bird handling), and behavioural analysis as well as international travel to museums. Students are also strongly encouraged to present results at conferences, typically at least one

major national or international conference per year.

Our lab maintains a diverse and inclusive lab that embraces a cooperative, team-based approach to research. Lab members work together and cooperate to solve problems, collect data, and communicate our findings. The successful applicant will not only be a member of our research team, they will also have opportunities to develop professional skills through the neuroscience graduate seminar course and workshops offered by the School of Graduate Studies.

Applicants must have a background in biology or neuroscience, some hands-on research experience (of any kind) and a valid driver's license.

To apply, please send to [andrew.iwaniuk@uleth.ca](mailto:andrew.iwaniuk@uleth.ca) the following by 10 May 2022:

- 1) a cover letter outlining your research interests and reason for applying
- 2) c.v.
- 3) unofficial copies of academic transcripts
- 4) names and contact details of at least 2 references

Andrew N. Iwaniuk Associate Professor Canada Research Chair in Comparative Neuroanatomy Canadian Centre for Behavioural Neuroscience University of Lethbridge Lethbridge AB T1K 3M4 Canada office: +1 403 332 5288 <http://scholar.ulethbridge.ca/iwaniuk/home> Bird-brain (b?rd br?n)1. a person regarded as silly or stupid.

[andrew.iwaniuk@uleth.ca](mailto:andrew.iwaniuk@uleth.ca)

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## WageningenU PlantVirusBioinformatics

The Evolutionary (Meta-)genomics group in the Bioinformatics Group at Wageningen University invites applications for a bioinformatics PhD student in 'Virus diversity and evolution in natural plant ecosystems'.

You might share our view that wild plant communities might act as viral reservoirs that are also connected to agricultural plants. Since viruses can spill over from natural to agricultural systems, it is highly relevant to characterize virus diversity in wild plants. Plant virus genomes are highly diverse and evolve rapidly. To know which role plant viruses play in shaping natural plant communities, we must characterize their biodiversity and evolution.

You might be familiar with the phenomenon that plant virus infections are often asymptomatic, i.e., they do not cause overt disease, and can even be beneficial for the host. Recently, plant virus research expanded from the study of individual virus-host systems into characterizing global diversity using metagenomics, i.e., sequencing the genetic content of environmental samples without the need for prior virus isolation. Metagenomics led to the surprising observation that virus infections are ubiquitous, that there is a high incidence of mixed infection, and that most plant viruses identified in crops also occur in wild plants. There is growing evidence that viruses can impact plant ecosystems, which calls for a reappraisal of the role of viruses in natural ecosystems and accentuates the need to understand virus genomes and their function and evolution.

The aim of this project is to develop bioinformatics methods to analyze plant virus metagenome data that has been sampled from wild plants in the Netherlands. This (and potentially your) project will contribute to understanding plant virus diversity and evolution in natural Dutch ecosystems. You will contribute to developing bioinformatics methods to discover and reconstruct virus genomes from high-throughput plant virus sequencing data and to analyze ecological and evolutionary properties of these viruses. To this end, we aim to analyze the effect of host range and mixed infections on intra-host diversity and estimate how recombination and selection impact virus genome evolution.

Beyond the scientific and potentially application merits, you will build a wide network for your future career

both within and outside Wageningen University.

The research is embedded within the chair group of Bioinformatics at Wageningen University which is led by Prof. Dick de Ridder (<https://www.bioinformatics.nl/>). You will be supervised by Dr. Anne Kupczok (<https://-annecmg.github.io/>). The research will be carried out in close collaboration with Dr. Mark Zwart at the Netherlands Institute of Ecology (NIOO-KNAW) (<https://-nioo.knaw.nl/nl/employees/mark-zwart>). The position is for four years and funded by the graduate school Experimental Plant Sciences (<https://www.graduateschool-eps.info/>).

We ask - a successfully completed MSc degree in bioinformatics or a related field; - excellent background in high-throughput sequencing analysis and comparative genomics; - affinity with ecology, evolution, and population genomics; - interest in close collaborations with experimental biologists and ability to work effectively as a team member and to carry out individual research; - very good level of oral and written English.

Please find all details and instructions how to apply here: <https://www.wur.nl/en/vacancy/PhD-position-Virus-diversity-and-evolution-in-natural-plant-ecosystems-2.htm> For enquiries regarding the position and research topic, please contact Anne Kupczok: [anne.kupczok@wur.nl](mailto:anne.kupczok@wur.nl)

Dr. Anne Kupczok Assistant Professor Bioinformatics, Department of Plant Sciences, Wageningen University

“Kupczok, Anne” <[anne.kupczok@wur.nl](mailto:anne.kupczok@wur.nl)>

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## Clermont France 5yr Eco-Evolution

### Announcement: 5 years Position in Eco-Evolution

The Laboratoire Micro-organismes: Genome et Environnement (UMR-CNRS 6023 LMGE, Clermont Auvergne University) seeks to fill a 5 year position to develop research at the interface of Ecology and Evolution in the field of microbial aquatic ecology, at the interface of the environment and human health.

<https://emploi.cnrs.fr/Offres/CPJ/CPJ-2022-018/-Default.aspx?Lang=EN>

**Context** The position aims at strengthening the synergies between evolutionary ecology and functional ecology to investigate, understand and quantify the functioning of our environments under multiple constraints (climatic and anthropic) and predict their evolutions in the context of two major societal challenges: Climate Change and Health & Environment.

The Lab Focussing on the microbial compartment, the LMGE (Micro-organisms: genome and environment) consists in the association of competences from the levels of genomics and post-genomics to population and ecosystem to investigate the relationships between environmental changes and the dynamic of communities diversity to better understand microbial processes that govern the functioning and sustainability of our environment. Our approach aims at bringing together genome, environment and health, by putting the concepts and tools of genomics and post-genomics at the service of scientific questions related to the functioning of ecosystems and health ecology. The scientific strategy of the unit is built around 3 main scientific fields: (i) parasitism and microbial ecosystems, (ii) trophic and functional ecology, (iii) health ecology and ecotoxicology.

Within the lab, the research activities of the MEB team focusses on the dynamics and structuring of microbial assemblages in aquatic ecosystems, their functional interactions over space and time and their emerging properties within ecosystems. To achieve this goal, we use environmental genomics (e.g. metagenomic coupling, single cell genome, metatranscriptomic, culturomic) and bioinformatics.

**Scientific projet** The recognition that evolutionary processes can occur on time scales as short as ecological processes, promotes the development of integrative approaches coupling ecological and evolutionary dynamics, in times of marked environmental change and loss of biodiversity on a planetary scale, which strongly affects multiple dimensions of both ecological and evolutionary dynamics, with repercussions on resilience, conservation and management of populations, communities and ecosystems. The applicant will develop such an integrative approaches, through the analyzes of their reciprocal retroactions, in the context of lake ecosystem functioning in link with climate changes or at the interface of the environment and human health.

**Teaching project** The recruited candidate will be involved in teaching units combining Ecology and Evolution, covering topics in link with i) adaptations of aquatic organisms to their environments, ii) Emergence and diffusion of pathogenic microorganisms, iii) Genomics of microbial communities iv) Bioinformatics and integrative omics.

Do you recognize yourself in the job profile? Please contact us for further discussion to built a convincing scientific project.

Cecile Lepere : [cecile.lepere@uca.fr](mailto:cecile.lepere@uca.fr) <https://lmge.uca.fr/version-francaise/annuaire/cecile-lepere/#/> Corinne Petit : [corinne.petit@uca.fr](mailto:corinne.petit@uca.fr) <https://lmge.uca.fr/version-francaise/annuaire/corinne-petit/#/> Gisele Bronner : [gisele.bronner@uca.fr](mailto:gisele.bronner@uca.fr) <https://cv.archives-ouvertes.fr/gisele-bronner>

Deadline for submitting the application : 31/08/2022

Gisele BRONNER <[gisele.bronner@uca.fr](mailto:gisele.bronner@uca.fr)>

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## CWRU Ohio DeptChair EvolutionaryBiol

The Department of Biology invites applications for Professor and Department Chair. The department currently has 23 tenured/tenure track research faculty, 7 instructional faculty, approximately 500 undergraduate majors and more than 50 graduate students in our PhD and

MS programs.

The successful candidate is expected to have an active research program in the biological sciences with a focus in neurobiology, ecology and evolution, cell biology and development, or a related, complementary field. The successful candidate will have earned international recognition in their field, and will appreciate the range of needs present in a broad biology department. As Chair, the successful candidate will also be expected to broaden participation throughout the department by among members of underrepresented groups; demonstrate effective leadership in a diverse community of faculty, students and staff; and become an articulate and vigorous spokesperson for the department's scientific and educational missions.

The Biology faculty are involved in research across a wide range of sub-disciplines of biology with high national and international visibility and active collaborations, and a strong record in securing external funding. Further information about departmental research can be obtained from <http://biology.case.edu/> and the individual websites of the faculty members. In addition to our excellent colleagues within the College of Arts and Sciences, our proximity to the prestigious CWRU School of Medicine, Cleveland Clinic, Case School of Engineering and the strong network of researchers within the Bio-Science Alliance (comprising CWRU Biology, Cleveland Museum of Natural History, Cleveland Metroparks Zoo, and Holden Forests & Gardens) provides a uniquely supportive environment for interdisciplinary research.

**Minimum Qualifications:** Applicants must have a Ph.D. or equivalent foreign degree in biology or a relevant subdiscipline in the biological sciences; a distinguished record of research accomplishments; evidence of excellent teaching; a record of administrative, managerial, and/or service experience demonstrating readiness for the role of Chair; and a record of promoting diversity. For appointment as Professor, the candidate should have received recognition as an international leader in their chosen area.

**Preferred Qualifications:** An outstanding research program in an area that complements the research activity in the department; a record of attracting external funding; and administrative experience in academic settings, in addition to the Minimum Qualifications listed above.

**To Apply:** Submit a cover letter; curriculum vitae; a research and scholarship statement; a teaching statement (including teaching philosophy and experience); and a diversity statement (see online submission site for details). Arrange to have 3 letters of recommendation sent independently. Applications may be submitted online at <http://apply.interfolio.com/105855>. Review of

applications will begin 6/24/2022 and will continue until the position is filled.

Case Western Reserve University strives to maintain a diverse and inclusive work environment. All applicants are protected under Federal law from discrimination based on race, color, religion, sex, national origin, disability, age and genetics.

Case Western Reserve provides reasonable accommodations to applicants with disabilities. Applicants requiring a reasonable accommodation for any part of the application and hiring process should contact the Office of Equity by phone at 216.368.3066 or by email at [equity@case.edu](mailto:equity@case.edu). Determinations as to granting reasonable accommodations for any applicant will be made on a case-by-case basis.

Ryan Martin <[ram225@case.edu](mailto:ram225@case.edu)>

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## EvolutionLetters EditorInChief

Editor in Chief, Evolution Letters

The Society for the Study of Evolution (SSE) and the European Society for Evolutionary Biology (ESEB) are looking for a new Editor in Chief for the journal Evolution Letters. Evolution Letters was established in 2017 and is jointly run by the two societies. An Open Access journal, it aims to publish leading research from across the field of Evolutionary Biology.

The EiC is expected to be an established evolutionary biologist with a broad overview of the field. Main responsibilities are building on the initial success of the journal, fostering continued growth, with a focus on maintaining its quality and encouraging submission of the best research articles in the field. The EiC will oversee and work hand in hand with a board of Associate Editors, our publishers, a social media/communications editor and a Managing Editor. The EiC is responsible for:

Managing, recruiting and interacting with a board of dedicated Associate Editors to guarantee high quality publications; Contributing to policy decisions on publication strategy and quality control, in liaison with the publisher and societies; Making final publication decisions based on scientific merit; Soliciting or commissioning suitable manuscripts, Special Issues and other publishing opportunities, and overseeing social media and other publicity; Wherever possible, attending and contributing to the ESEB and SSE congresses; Promot-

ing equity, diversity, and inclusion in all aspects of the journal's operations. An estimated average of 10-15% of weekly time is dedicated to this position. Appointments are for a 4-year term. Location is flexible as most communication occurs electronically. An honorarium is paid. Academic publishing is undergoing significant changes, and we would wish the candidate to be enthusiastic in support of a Society journal and its aims by pursuing opportunities to improve its popularity, impact and strength during this period.

ESEB and SSE have an Evolution Letters Oversight Committee that has meetings with the EiC and the publisher. Ultimately, the EiC is managed by this committee, in interaction with the senior committees of the societies. There is considerable independence and freedom to develop the journal. The current (inaugural) EiC, Jon Slate, has established the journal successfully, but will be standing down in 2022. Ideally the new appointee will be in place to shadow Jon before replacing him in the summer.

Further information about the journal and societies are available via the links below and further particulars are available from anyone on the appointments committee.

Evolution Letters: <https://onlinelibrary.wiley.com/journal/20563744> Society for the Study of Evolution: <http://www.evolutionarysociety.org/> European Society for Evolutionary Biology: <https://eseb.org/>

A formal application should be sent to Michael Ritchie (mgr@st-andrews.ac.uk) by June 15th . Your letter should provide an explanation of why you would be interested in taking on this exciting role at this stage of your career, and a brief outline of your vision for the journal over the next four years. It should also include a very brief CV.

Interested candidates are welcome to contact anyone listed below. Appointments committee: Michael Ritchie mgr@st-andrews.ac.uk Corrie Moreau corrie.moreau@cornell.edu Jacintha Ellers j.ellers@vu.nl Chris Caruso carusoc@uoguelph.ca Current EiC: Jon Slate j.slate@sheffield.ac.uk

Mike Ritchie Centre for Biological Diversity, School of Biology,

University of St Andrews, Fife. Scotland KY16 9TH UK I do not expect people to answer e-mails outside of office hours

Michael Ritchie <mgr@st-andrews.ac.uk>

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## Hawaii CoralReefConservation

DQoNCiRoZSBIYXdhacq7aSBJbnN0aXR1dGUgb2YgTWFyaW5lIEJp aGF3YWlpLmVkdS9oaW1iLz4NCihISU1CKSBpbmZpdGVzIGFwcGxp d2x5IGVzdGFibGlzaGVkIFJ1dGggRC4gR2F0ZXMNckVuZG93ZWQg ZiBTeXN0ZW1zLCB3aGljaCBob25vcnMgdGhIIGRpc3Rpbmd1aXNoZ dXRyZWVjaCBvZiB0aGUgbGF0ZSBECi4gR2F0ZXMuIFdlIGludml0Z Y2FudHMgZnJvbSBhbnkgZGlyY2lwbGluZS9zIG9mIGNvcnF5IHJlZ W aCB3aXR0dDQphIHZpc2lubiBmb3IgaW5ub3ZhdGl2ZSwaW50ZWdyY c2NpcGxpbnFyeSBiYXNpYw0Kb3IgaW5ub3ZhdGl2ZSwaW50ZWdyY bHVkaW5nIGJ1dCBub3QgbGltaxRIZCB0bw0Kc29jaW8tZWVnbG9n cm9ubWVudGFsIGVuz2luZWVyaW5nLCBzb2x1dGlubiVcmllbnRlZA dWRpbmcgYXJ0aWZpY2lhbCBpbmRlbGxpZ2VvY2U5IHJlZWYgZmlz ZCBodW1hbiBoZWFsdGgsIHJpZGdlLXRvLXJlZWYgcHJvY2Vzc2Vz dHkgc2NpZW5jZSwnCmluIGFkZG10aW9uIHRvIGJpb2xvZ3kvZWVn IGVjb3N5c3RlbXMuDQoNCiRoZSBIYXdhacq7aSBJbnN0aXR1dGUgb 2YgTWFyaW5lIEJp aXMgY29tbW10dGVkIHRvIHN1cHBvcnRpbmNcmRpdmVyc2l0eSwg aW9uIGluIHJjaWVvY2UgY2V5kIHRvIFVIE3EgW5vYeKAmXMgc3F0 bmQgaW5zdG10dXRpb25hbCBnb2FsIG9mIGJlY29taW5nIGEGTmF0a IG9mDQpMZWFybmlyZy4gQW4gaW5jbHVzaXZlIHdvcmtwbGFjZSB bXVuaXR5LiBxZSBibmNvdXJhZ2UNCmFsbCB0byBhcHBseS4NCg0l b246DQpodHRwczovL3d3dy5oaW1iLmhhhd2FpaS5lZHUvMjAyMi8wNS LXJ1dGgtZC1nYXRlcy1lbmRvd2VklWNoYWlyLXBvc2l0aW9uLWlu cy8NCiRvIGFwcGx5Og0KaHR0cHM6Ly93d3cu2Nob29sam9icy5jb20v ZHUvam9icy8zNTI3NTcwL2Fzc29jLWZ1bGwtdmVzZWVyaW5lci0xMS ZW5kb3dlZC1jaGFpci1wb3MtMDA4NjQ5Nz9wYWdlHlwZT1qb2JpDQ oNCg0KZHZHJ1cnljQGhhd2FpaS5lZHUuNCg0K

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## Innsbruck EvolutionaryDynamics

Dear EvolDir Community!

Announcement: Tenure Track Position in Eco-Evolutionary Dynamics

The Research Department for Limnology, Mondsee, at the Faculty of Biology at the Leopold-Franzens University Innsbruck seeks to fill a

Tenure Track Position in Eco-Evolutionary Dynamics at the earliest convenience.

Responsibilities include

Conducting independent research and teaching on the subject of "Eco-Evolutionary Dynamics" in the field of

aquatic ecology.

Research focus should be on interactions between ecological and evolutionary processes.

Cooperation with the research groups of the department, participation in the cross-faculty research area “Mountain Regions”, teaching in the Faculty of Biology, (co-)supervision of theses, acquisition of third-party funding, and participation in academic self-governance are expected.

Employment Requirements include

doctoral degree in Biology (or a related discipline) with an emphasis on ecology, evolution and/or aquatic science;

post-doc experience and/or relevant professional experience; output beyond the PhD, documented by publications in international peer reviewed journals;

interdisciplinary research; integration in the international research community; involvement in research projects and in acquisition of competitive grants; excellent didactic skills and experience in (co-)supervision of students; good communication skills and ability to work in a team; organizational and management qualities; fluency in English is required; knowledge of German is desirable (level B1 is required for teaching in the BSc program).

Format of the Position

This ‘tenure-track position’ enables pursuit of a career to full professor at the University of Innsbruck.

The successful applicant will enter a six-years’ work contract as Assistant Professor on the basis of the ‘Angestelltengesetz’ (Employees Act; extent of employment: 100%) with ‘Qualification Agreement’ according to § 27 of the ‘Kollektivvertrag’ (Austrian Collective Labor Agreement for university personnel).

Once the targets of the ‘Qualification Agreement’ are reached, the position will be tenured, thus promoting the holder of the position to Associate Professor.

Subsequently, a full professor position according to § 99 (4) of the ‘Universitätsgesetz’ (Austrian University Act) will be opened, for which the Associate Professor is eligible to apply.

Your application must have arrived by

June 8, 2022

At Leopold-Franzens-Universität Innsbruck Fakultäten Servicestelle Standort

Technikerstraße 17, A-6020 Innsbruck (fss-technik@uibk.ac.at).

Leopold-Franzens-Universität Innsbruck seeks to increase the proportion of female scientists in the faculty - so that applications from top-qualified female scientists are especially encouraged. With equal ranking, female applicants will be given priority.

In line with the ‘Kollektivvertrag’ (Austrian Collective Labor Agreement for university personnel) scientists who have entered a ‘Qualification Agreement’ are in remuneration group A2 with an initial wage of euro 4.782,30 / month (14 month year). After fulfillment of the Agreement, the salary rises to euro 5.175,50 / month (14 month year). Moreover, the university offers attractive additional benefits (see <http://www.uibk.ac.at/-universitaet/zusatzleistungen>).

The application must contain a full CV, including scientific and professional career stages; a list of scientific publications, talks and other scientific activities (seminars, conferences, etc.); description of completed, ongoing and planned research projects; the five most important works of the applicant; research and teaching concepts; and a statement of the qualification goals, which the applicant wishes to reach at this position. Qualification goals are to be explained at the hearing and subsequently represent the starting point for the negotiation of the ‘Qualification Agreement’.

Application documents must be written in English and submitted by e-mail as one PDF file.

The full authoritative text in German (published in the official bulletin of the University of 04.05.2022) can be found at <https://orawww.uibk.ac.at/public-karriereportal.home>. Up-to-date information on the state of the opening can be found at

<https://www.uibk.ac.at/fakultaeten-servicestelle/-standorte/technikerstrasse/berufung/> Univ.-Prof. Dr. Dr. h.c. mult. Tilmann Märk

R e c t o r

Best Regards,

Universität Innsbruck

Forschungsinstitut für Limnologie, Mondsee Sonja Burggraf &nbsp; Institutssekretariat Mondseestraße 9, A-5310 Mondsee Telefon +43 512 507-50201 E-Mail sonja.burggraf@uibk.ac.at, office-ilm@uibk.ac.at

“Burggraf, Sonja” <Sonja.Burggraf@uibk.ac.at>

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## InstAvianBiol Germany Two Bioinformatics SeniorRes

\*\*Permanent Senior Research position (E13 TV-L) (m/w/d) at the Institute of Avian Research (Wilhelmshaven, Germany)\*\*

We are hiring - come and work with us! (pdf of the advert can be found here: <https://ifv-vogelwarte.de/fileadmin/resources/Jobs/E13.IfV.2022.en.pdf>) The Institute of Avian Research (IAR) is a research center in the portfolio of the Lower Saxonian Ministry of Science and Cultural Affairs. The headquarter is located in Wilhelmshaven and equipped with modern bird keeping facilities, indoors as well as outdoors. A separate field station with one of the world's oldest continuously operated trapping gardens is located on the island of Helgoland. In addition to outstanding field and bird keeping facilities, the IAR benefits from a modern scientific infrastructure, including molecular labs, computational facilities as well as in-house wood and electronic workshops. The IAR has also set up, and maintains, local antennae of the MOTUS system and houses the Bird Ringing Centre of Northwest Germany.

We currently combine detailed analyses of long-term (and partly longitudinal) observational data with experimental approaches. Phenotypes are assessed using ringing data and blood sampling techniques, as well as with RFID, radiotelemetry, geolocator and GPS technology. To understand the (epi)genetic basis of behaviour we combine high-throughput-sequencing data to identify sequence variants with approaches beyond the sequence level, such as gene expression profiling and characterisation of chromatin modification or epigenetic markers.

With the recruitment of a senior scientist we aim to complement our portfolio and bridge current research foci on bird migration and life-history biology with new ideas and trajectories, either in focus or through methodological approaches. The candidate would ideally make use of the facilities and/or long-term data routinely collected on Helgoland.

We encourage suitable candidates to contact us to discuss possible research ideas or learn more about available datasets and other infrastructure ([miriam.liedvogel@ifv-vogelwarte.de](mailto:miriam.liedvogel@ifv-vogelwarte.de)). Applications should include a cover letter describing motivation and relevant experience, a detailed CV with copies of relevant certificates, a 2-page description of the research you propose to carry

out at the IAR and how it integrates with current research trajectories, and contact details of two academic references.

Applications should be submitted as a single PDF file to [poststelle@ifv-vogelwarte.de](mailto:poststelle@ifv-vogelwarte.de). Applications can be sent until 17.06.2022. (First) digital interviews are planned at 04. and 05.07.2022.

The Institute of Avian Research is an equal opportunity employer, committed to inclusion and diversity and welcomes applications from people from all groups and backgrounds. In addition, the IAR is committed to (i) increase the proportion of women in successful scientific careers (ç11 of the Niedersächsisches Gleichberechtigungsgesetz), (ii) promote the equality of (severely) disabled and non-disabled people, and (iii) provide opportunities for people with a migration background. As such, it especially welcomes applications from female scientists, (severely) disabled scientists and immigrated scientists. In case of equal suitability and qualifications, these applications will be given preference. Application costs cannot be reimbursed. Application documents will be destroyed four weeks after the hiring process has been completed. Further information on our data protection policy during recruitment processes can be found at on our website: <https://ifv-vogelwarte.de/generische-navigation/datenschutz> . —

\*\*Bioinformatician (E14 TV-L, 100%) (m/w/d) at the Institute of Avian Research (Wilhelmshaven, Germany)\*\*

We are hiring - come and work with us! (pdf of the advert can be found here: <https://ifv-vogelwarte.de/fileadmin/resources/Jobs/IfV.2022.E14-IT.en.pdf>)

We are recruiting a bioinformatician for (i) the establishment of supercomputing services (HPC), (ii) the addition of bioinformatic expertise as well as support and development of services in the field of research data management, and (iii) setting up own research at the Institute of Avian Research (IAR).

The IAR is a research center in the portfolio of the Lower Saxonian Ministry of Science and Cultural Affairs. The headquarter is located in Wilhelmshaven. The main research areas are bird migration and life history biology. A field station with one of the world's oldest continuously operated trapping gardens is located on the island of Helgoland. In addition, the IAR houses the Bird Ringing Centre for Northwest Germany.

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

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## Krakow ISEA PAS Bioinformatics

The Department of Molecular Biodiversity at the Institute of Systematics and Evolution of Animals Polish Academy of Sciences invites applications for the assistant position. We seek candidates with an MSc or PhD in bioinformatics, biotechnology, biology or related fields with experience in the study of organisms at the intra- and interspecies levels using next-generation sequencing, and particularly in bioinformatics analyses and visualization of data generated using next-generation sequencing. The Department of Molecular Biodiversity (<http://www.isez.pan.krakow.pl/en/department-experimental-zoology.html>) conducts research focusing on phylogeography, phylogenetics, molecular ecology and conservation genetics of various groups of organisms (mostly insects, protists and birds).

- MS.C. or PhD in biology, bioinformatics, biotechnology, or related fields; - experience in preparing genomic libraries; - the experience in bioinformatics analyses and visualization of data generated using next-generation sequencing; - scientific achievements documented by publications are welcome; - readiness to work in a team; - initiative to improve professional qualifications; - fluency in English;

Candidates are asked to provide the following documents:

1. application for employment addressed to the Director of ISEA PAS,
2. curriculum vitae along with information about the current course of employment,
3. copies of a university diploma,
4. copies of certificates confirming qualifications.
5. the candidate's cover letter presenting research interests and achievements (publications, conference presentations, participation in research projects).
6. the candidate's declaration that ISEA PAS will be the primary place of work (in the case of employment),
7. two opinions on the candidate's predispositions and qualifications for research work prepared by independent researchers.

The application documents (i.e. the Application and CV), need to be attached with the following clause: 'I consent to the processing of my personal data provided in the application documents for the purposes of the recruitment process conducted by the Institute of Systematics and Evolution of Animals of the Polish Academy of Sciences, for the position indicated in the

announcement. I have been informed that providing the consent is voluntary and that I have the right to withdraw my consent at any time. I have also been informed that the withdrawal of my consent will not affect the legality of the processing that was carried out on its basis prior to its withdrawal. Furthermore, I declare that I have read the information clause regarding the processing of personal data in accordance with the Regulation of the European Parliament and of the Council of 27 April 2016, included in the recruitment announcement of the Institute of Systematics and Evolution of Animals of the Polish Academy of Sciences'.

Documents should be submitted by e-mail to: [rekru-tacja@isez.pan.krakow.pl](mailto:rekru-tacja@isez.pan.krakow.pl) and to the information of dr hab. ukasz Kajtoch: [kajtoch@isez.pan.krakow.pl](mailto:kajtoch@isez.pan.krakow.pl) (in the subject of the e-mail, please provide "DMB - Call") by 1 June 2022.

The results of the competition will be announced by 17 June 2022.

ISEA PAS reserves the right to answer only selected offers and to close the call without selecting a candidate.

The call organizer may invite candidates for an interview directly or on-line. Candidates will receive an invitation to the e-mail address indicated in the call documents.

ISEA PAS does not provide housing.

Âr., 9 mar 2022 o 15:25ukasz Kajtoch  
lukasz.kajtoch@gmail.com napisaÅ³(a):

ukasz Kajtoch <[lukasz.kajtoch@gmail.com](mailto:lukasz.kajtoch@gmail.com)>

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## LinkopingU EvolutionBehaviour

IFM Biology SE-581 83 Linköping Mobile: +46 (0)736 569323 <https://liu.se/en/research/jensengroup> <https://liu.se/en/research/avian-behavioural-genomics-and-physiology-group> Associate professor in Ethology at Linköping University, Sweden (Permanent position)

We are looking for a researcher with relevant expertise in ethology, cognition and animal psychology to further develop the department's profile in these and related subject areas. We are looking for a relatively established researcher with experience of working with several different research fields to illuminate behavior and evolutionary events, both from a basic and applied perspective. The candidate we are looking for must have a great interest in developing both research and teaching in basic and applied ethology, cognition and



animal welfare.

Teaching will be in Swedish and English. Please see the full job description with details on the application process here: <https://liu.se/en/work-at-liu/vacancies>  
Per Jensen Professor of Ethology

IFM Biology SE-581 83 Linköping Mobile: +46 (0)736 569323 <https://liu.se/en/research/jensengroup> <https://liu.se/en/research/avian-behavioural-genomics-and-physiology-group> Per Jensen <per.jensen@liu.se>

per.jensen@liu.se per.jensen@liu.se

## Mainz LabManager SocialEvolution

The Institute of Organismic and Molecular Evolution at the Faculty of Biology, Johannes Gutenberg University Mainz, Germany invites applications for the position of a

Lab Manager full-time (100 %)

This position supports the research group with a focus on evolution, behavior and ecology of social insects in research and teaching. More information on this position: <https://stellenboerse.uni-mainz.de//HPv3.Jobs/jgu//stellenangebot/24622/1?lang=en-US>  
Are you ready for a new challenge and interested in this varied and responsible position?

Then submit your complete application [cover letter, resume, references] until June 6th, 2022

For questions and further information, please contact: Prof. Dr. Susanne Foitzik: foitzik@uni-mainz.de

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

“Foitzik, Susanne” <foitzik@uni-mainz.de> “Foitzik, Susanne” <foitzik@uni-mainz.de>

## NatureCommunications Editor

Nature Communications is hiring a full time editor with a background in evolutionary biology: <https://career5.successfactors.eu/sfcareer/-jobreqcareer?jobId=42632&company=C0001215517P>  
Job Title:Associate or Senior Editor (Evolution)

Organisation:Nature Communications

Location:London, New York or Berlin

Closing date:6th June 2022

Nature Research is the world’s leader in publishing high-quality research from across the natural sciences. Its journals includeNature, the Nature Research journals, the Nature Reviews journals andNature Communications.

Do you love science but feel that a career at the bench isn’t enough to sate your desire to learn more about the natural world? Do you enjoy reading papers outside your chosen area of research? If the answer is ‘yes’ to any or all of these questions, you could be the person we’re looking for to join the editorial team ofNature Communications.

Nature Communicationsis the leading multidisciplinary Open Access journal, publishing high-quality scientific research. To help us to build on the success of this journal, we’re seeking an editorwith experience in evolution who has a critical eye, a deep understanding of their subject and interests beyond, and who can think on their feet. Knowledge of genomics and/or phylogenetics is desirable.

The responsibilities include:

§Handling original research papers, and working closely with other editors on all aspects of the editorial process, including manuscript selection and overseeing peer review.

§Making well-reasoned editorial decisions on submitted manuscripts in the light of expert advice.

§Determining the representation of their subject in the journal.

§Liaising extensively with editors at other journals in the Nature family and with experts in the international scientific community.

§Attending conferences and visiting research institu-

tions.

§Commission and edit Reviews, and write Editorials

To be considered for the position, you will have:

§A PhD (or equivalent) in a field related to evolution

§Significant research experience is preferred.

§A thorough understanding of recent trends and developments in the field is essential.

§A passion for science and a thirst to learn more. You must be able to demonstrate the breadth of your interest in scientific research, both within and beyond your speciality.

§Excellent communication and interpersonal skills and be fluent in English (written and spoken).

§The ability to read and assess the novelty, context and implications of research submitted to the journal from different areas of this discipline.

§Be eager to travel and meet scientists worldwide, learn more about them and their research, and help them learn more about us and what we are looking for in the papers we seek to publish.

§Editorial experience is not required, although applicants with significant editorial experience are encouraged to apply and will potentially be considered for Senior Editor positions.

The successful candidates will report to a Team Manager in the life science division.

This demanding and intellectually stimulating role is located in either our London, New York or Berlin office. The position is offered on a permanent basis and its starting date is envisaged as soon as possible.

At Springer Nature, we're committed to creating a great working environment which includes the benefits you receive, opportunities for you to develop your skills and ways to get to know your colleagues. Some of these include:

§Support networks that focus on fostering dialogue around diversity, community building, advice and advocacy

§Wellbeing initiatives to support in maintaining a healthy work life balance

§24 hour access to our learning and development platform Leap to help develop your skills

Applicants should include: a CV, a covering letter explaining their interest in the post and their preferred office of employment, and a separate concise (300-400 words) discussion of a recent scientific development that they found particularly exciting (stating why).

Closing date 6th June 2022

Candidates will be considered as they apply.

Emily Jones, PhD (they/them) Senior Editor, Nature Communications Nature Portfolio

Springer Nature One New York Plaza, Suite 4500 New York, NY 10004-1562 Email: emily.jones@us.nature.com  
ORCID: <http://orcid.org/0000-0002-0605-884X>  
<http://www.nature.com/ncomms> Emily Jones  
<emily.jones@us.nature.com>

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## NHM London Fish Curator

We in Life Sciences Fish are hiring a new permanent fish curator. Please spread the work and encourage people to come and work with us researching and looking after one of the world's most important Fish collections.

[https://careers.nhm.ac.uk/templates/CIPHR/-jobdetail\\_2458.aspx](https://careers.nhm.ac.uk/templates/CIPHR/-jobdetail_2458.aspx) Deadline June 10th.

Posted: Simon.Loader@nhm.ac.uk

Dr Simon P. Loader, Principal Curator in Charge of Vertebrates,

Natural History Museum, Cromwell Road, London SW5 5BD, UK Tel: ++44 (0) 207 942 6459 | Mobile: +44 7505912733 Skype: simon.p.loader@gmail.com e-mail: simon.loader@nhm.ac.uk gmail: simon.p.loader@gmail.com Associate Editor, The Herpetological Journal: <http://www.ingentaconnect.com/content/bhs/thj> IUCN SSC Amphibian Specialist Group Regional Chair for East Africa

Simon Loader <simon.loader@nhm.ac.uk>

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## NHM London Two Curator Fossil Animals

The Natural History Museum, London (NHM)

Curator - Fossil Reptiles

Closing date: 9am, BST, 6 June 2022

Interviews expected: week of 4 July 2022

Embedded within the Vertebrates & Anthropology Curatorial Division, this is an important role in a world-

renowned institution with a strong scientific mission and public profile.

The successful applicant will join a large science group composed of approximately 300 scientists, in an institution that houses some of the largest, most significant scientific collections in the world. The Museum is also home to an internationally important natural history library, a suite of advanced analytical and imaging facilities, and offers the opportunity to communicate science to national and international audiences.

The Curator will be responsible for acquiring, curating and making specimens within their area of responsibility in Fossil Reptiles available to facilitate research, teaching, and exhibitions. These collections are frequently accessed by internal and external researchers and are heavily used for the NHM's public engagement activities, including permanent exhibitions, temporary and touring exhibitions, and outreach events for the general public and media.

Applications are open to candidates in the field of vertebrate palaeontology, with particular expertise in an area relevant to fossil reptiles.

To access the recruitment portal please use the following link:

<https://careers.nhm.ac.uk/templates/CIPHR/-jobdetail.2442.aspx> A detailed job description (job profile document) is available for download on the NHM website.

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The Natural History Museum, London (NHM)

Senior Curator - Fossil Mammals

Closing date: 9am, BST, 6 June 2022

Interviews expected: week of 4 July 2022

Embedded within the Vertebrates & Anthropology Curatorial Division, the Senior Curator will ensure best practice in caring for a world-class collection of fossil mammal specimens. Specimens are to be acquired, curated and made available to facilitate research, teaching, training, reference and exhibitions.

An established or emerging expert in their field of collections-based science, the Senior Curator demonstrates a high level of science scholarship. The Senior Curator will have day to day responsibility for the fossil mammal collections. This is an exciting opportunity to integrate curation and collections-based research in one of the World's largest and most important Fossil Mammals collections.

To access the recruitment portal please use the following

link:

<https://careers.nhm.ac.uk/templates/CIPHR/-jobdetail.2443.aspx> A detailed job description (job profile document) is available for download on the NHM website.

Jeff Streicher <J.Streicher@nhm.ac.uk>

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## NHM London Two curators

Job opportunity, 2x Full time permanent roles at Natural History Museum, London

<https://eur03.safelinks.protection.outlook.com/?url=https://careers.nhm.ac.uk/templates/CIPHR/-jobdetail.2443.aspx> - Parasitic Worms curator

<https://eur03.safelinks.protection.outlook.com/?url=https://careers.nhm.ac.uk/templates/CIPHR/-jobdetail.2442.aspx> - Invertebrates curator

Lauren Hughes <l.hughes@nhm.ac.uk>

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## North Carolina State University Genetics Genomics Communication

Communications Specialist Essential Job Duties

The Genetics and Genomics Academy (GGA) Communications Specialist will be responsible for implementing and maintaining the internal and external communications objectives of the GGA. Reporting to the Executive Director, the communications specialist will raise the visibility of the GGA, both within the university community and with external partners. The GGA communications specialist will help coordinate new campus collaborations, support intercollegiate cooperation, and facilitate efforts to enhance the understanding of Genetics and Genomics among citizens of North Carolina. Equity, diversity, accessibility and inclusion will be fundamental design-and-development principles of the GGA. The Communications Specialist will help attract and inform partners in many sectors of business, industry,

government and non-government organizations.

The Communications Specialist will lead the GGA communication strategies as part of a team that includes students, faculty, staff and especially the GGA Programs Specialist, the Genetics and Genomics Scholars Program Director and the GGA undergraduate teaching faculty member. We will look to the Communications Specialist to develop creative approaches to sharing information about Genetics and Genomics at NC State, including email marketing, print, social/digital media, and especially video-based content.

#### Specific Responsibilities

- Building good working relationships with the GGA administrative specialist as well as GGA faculty, students, and staff
- Maintaining and updating GGA website and create other social media platforms and accounts (i.e. Twitter, Facebook, etc.)
- Developing creative videos to be used internally and externally
- Leading the writing of annual reports
- Organizing outreach and off-campus training events
- Publicizing campus seminars, retreats, symposia and workshops
- Publicizing courses for undergraduate students who are not majoring in biological sciences
- Writing and disseminating news releases and feature articles describing technical events, publications, lectures, and related activities to local and national media groups
- Assisting faculty to improve individual webpages
- Networking with and serving as a representative of GGA at local and national meetings with a focus on Genetics and Genomics topics
- Responding to requests from news media representatives for information about Genetics and Genomics

Minimum Experience/Education Bachelor's degree and understanding of the basics of Genetics and Genomics or equivalent combination of training, knowledge and experience.

#### Other Required Qualifications

- Technical and administrative skills
- Proficiency with Microsoft Word and Excel, or similar software
- Proficiency with Gmail and Google applications
- Experience with budgeting and expense tracking

Skill in developing metrics to measure growth, collect data, communicate results and adjust plans accordingly

- Specialized skills

Excellent video production skills

Ability to use Adobe or similar applications

Experience with WordPress for web design

Experience designing social media and video planning (in collaboration with graphic artists and videographers)

- General skills

Excellent written and oral communications skills, including proofreading

Strong interpersonal skills

Excellent organizational skills and ability to meet deadlines

Keen attention to detail

Ability to work independently and as a team player

Ability to multitask

Ability to interface with wide variety of staff, students, faculty and external partners

Creative problem solving

Skills and ability to maintain a positive and optimistic attitude and professional demeanor

Ability to welcome and encourage a diverse group of internal and external learners

Curiosity about Genetics and Genomics

- Physical skills

This position will involve attending events in person  
Preferred

- At least 1-3 years' experience in a similar office environment, preferably higher education or nonprofits.

- Experience in developing and implementing focused communications plans.

- Passion for enhancing knowledge about Genetics and Genomics among the public and among students, staff, and faculty at NC State.

Please send resume and cover letter to  
Fred.Gould@ncsu.edu

Fred Gould <fgould@ncsu.edu>

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## Norway AncientDNA

The Arctic University Museum of Norway and Academy of Fine Arts (UMAK) Researcher in Northern Terrestrial Ancient DNA At The Arctic University Museum of Norway (UM) a position as Researcher is available within Northern Terrestrial Ancient DNA. The position has funding for three years, with the possibility of an extended funding period. The position is affiliated to the newly established Norwegian Centre for Arctic Ecosystem Genomics (ArcEcoGen) and will be part of the terrestrial working group.

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

The workplace is at UiT in Tromsø  $\frac{1}{2}$  #tromsolove. You must be able to start in the position no later than six months after receiving the offer.

<https://www.jobbnorge.no/en/available-jobs/job/-222676/researcher-in-northern-terrestrial-ancient-dna>  
 Prof. Inger Greve Alsos The Arctic University Museum of Norway UiT - The Arctic University of Norway NO-9037 Tromsø  $\frac{1}{2}$  Norway Telephone: +47 77 62 07 96  
 Telefax: +47 77 64 51 05 Email: inger.g.alsos@uit.no  
 NOTE THAT WE ARE RECRUITING 9 POSITIONS:  
[https://uit.no/research/arcecogen#news\\_768037](https://uit.no/research/arcecogen#news_768037) <http://en.uit.no/ansatte/inger.g.alsos> <http://ecogen.no/>  
<https://www.iceagent.no/> <http://svalbardflora.no/>  
<https://orcid.org/0000-0002-8610-1085> Inger Greve Alsos <inger.g.alsos@uit.no>

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## NorwegianU GenomeBiology

Dear All,

Faculty of Biosciences at the Norwegian University of Life Sciences (NMBU) invites applications for a permanent position as administrative coordinator (senior advisor) to support work in the Genome Biology research group at Faculty of Biosciences (CIGENE: [www.cigene.no](http://www.cigene.no)). The primary goal of this position during the first 1.5yrs will be to have administrative responsibility for the international, EU funded project AQUA-FAANG (<https://aqua-faang.eu>). However, the successful candidate will also be required to support other research activities in the group during this period.

The successful candidate will join the multidisciplinary Genome Biology research group, with interests in genetics, evolutionary and comparative genomics, bioinformatics and systems biology. This group includes 3 full-time professors, 2 associate professor, 15 post-docs/researchers, 14 PhD students and 10 research technicians (see [www.cigene.no](http://www.cigene.no)). The group has a strong aqua- and agri- research profile nationally and internationally, with key strengths in application of 'omics' data to understand the genetic architecture of complex traits. Our lab includes state-of-the-art instrumentation enabling genomic research and performs service activity for commercial actors.

Main tasks Examples of specific tasks include:

- \* Help with the planning and execution of AQUA-FAANG related activities such as scientific meetings, workshops, visiting researchers etc.
- \* Take a central role in coordinating writing/proofing formal AQUA-FAANG project reports/updates required by the EU funding body.
- \* Take a central role in writing/proofing reports, media releases etc. promised by the AQUA-FAANG project under our "Dissemination and communication" activity.
- \* Provide administrative support to the research group and help to coordinate activities such as scientific meetings and workshops, visits from individuals and groups etc.
- \* Be responsible for maintaining the CIGENE web pages ([www.cigene.no](http://www.cigene.no)), responding to enquiries made via this web page, and enhancing the group's profile on social media or other avenues.
- \* Become familiar with NMBUs administrative processes and serve as a trouble-shooter to find solutions for day-to-day needs/problems related to the Genome Biology research group, from students to professors.
- \* Orga-

nize and lead the Research groups monthly information meetings, and organize logistics related to team-building exercises (1-2 times per year).

More info: <https://www.jobbnorge.no/en/available-jobs/job/226983/administrative-coordinator-to-support-research-activities> Sincerely,

Marie SAITOU, Ph.D. Tenure-Track Principal Investigator, Centre of Integrative Genetics (CIGENE), Faculty of Biosciences, Norwegian University of Life Sciences <https://sites.google.com/view/saitou-lab> Marie Saito <marie.saitou@nmbu.no>

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## PennsylvaniaStateU ResTech EvolutionaryGenomics

A Research Technologist position is available at Pennsylvania State University beginning in May 2022, with a flexible start date. The successful candidate will provide research support and perform organizational activities in the laboratory of Dr. Jesse Lasky, Assistant Professor of Biology.

[http://www.personal.psu.edu/jrl35/psu/-index\\_JRL.html](http://www.personal.psu.edu/jrl35/psu/-index_JRL.html) Apply here: [https://psu.wd1.myworkdayjobs.com/PSU\\_Staff/job/-University-Park-Campus/Research-Technologist---Lasky-Lab.REQ\\_0000029152-1](https://psu.wd1.myworkdayjobs.com/PSU_Staff/job/-University-Park-Campus/Research-Technologist---Lasky-Lab.REQ_0000029152-1)

The Lasky Lab uses lab and field experiments, physiology, and genomics to study how environment shapes genetic diversity of plants, with goals of learning about basic biology and informing management under environmental change. This Research Technologist will assist with research projects and perform tasks related to laboratory operations and maintenance. Under supervision of the Principal Investigator and senior lab members, the technologist will conduct a variety of routine experiments following established procedures and protocols, which may include plant phenotyping, DNA or RNA extraction, and other plant growth or molecular laboratory techniques.

Responsibilities may also include:

Data collection from field or growth chamber experiments

Analysis of data using basic statistics

Maintenance and organization of laboratory equipment and supplies

Plant propagation and maintenance

Essential functions include:

Conducts routine experiments following appropriate protocols and procedures

Records results and maintains accurate records of experiments

Performs limited data interpretation and assists with basic statistics and analysis

Maintains laboratory equipment and orders/keeps inventory of supplies

Prepares stock solutions, reagents and other media

Monitors plant growth, collects data or samples, and maintains records

Hands-on laboratory experience is preferred, with expertise in more than one of the following areas: plant growth/horticulture in the field, greenhouse, growth chamber, DNA & RNA extraction, plant physiology, molecular biology and genetics, data management or statistical analysis.

The successful applicant must have the ability to plan, execute, interpret, summarize, and troubleshoot independent research and collaborate effectively with members of a research team. Excellent verbal and written English communication skills are required.

Additional Information: Include a cover letter that summarizes relevant experience and reasons for interest in the job, along with a CV that includes contact information for three references (name, position title, mailing address, telephone number, and e-mail address).

Education and Experience: This position typically requires a Bachelor's degree or higher plus one year of related experience, or an equivalent combination of education and experience for a level 1. Additional experience and/or education and competencies are required for higher level jobs. This job will be filled as a level 1 or level 2, depending upon the successful candidate's competencies, education, and experience.

This is a limited-term appointment funded for one year from the date of hire with the possibility of extension.

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

mission.

#### CAMPUS SECURITY CRIME STATISTICS:

Pursuant to the Jeanne Clery Disclosure of Campus Security Policy and Campus Crime Statistics Act and the Pennsylvania Act of 1988, Penn State publishes a combined Annual Security and Annual Fire Safety Report (ASR). The ASR includes crime statistics and institutional policies concerning campus security, such as those concerning alcohol and drug use, crime prevention, the reporting of crimes, sexual assault, and other matters. The ASR is available for review here.

Employment with the University will require successful completion of background check(s) in accordance with University policies.

#### EEO IS THE LAW

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applications without regards to race, color, religion, age, sex, sexual orientation, gender identify, national origin, disability or protected veteran status. If you are unable to use our online application process due to an impairment or disability, please contact 814-865-1473.

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## RBG Kew PlantBioinformatician

Bioinformatician (Completing the Plant Tree of Life Project)

The Royal Botanic Gardens, Kew (RBG Kew) is a leading plant science institute, UNESCO World Heritage Site, and major visitor attraction. Our mission is to understand and protect plants and fungi for the well-being of people and the future of all life on Earth. We are working to end the unprecedented extinction crisis and to help create a world where nature is protected, valued by all and managed sustainably. We will achieve these goals by drawing on our leading scientific research, unrivalled collections of plants and fungi, global network of partners, inspirational gardens at Kew and Wakehurst, and our 260 years of history.

RBG Kew is establishing a new benchmark in plant biology by completing the plant tree of life, mining Kew's collections with novel genomic methods and generating DNA data unprecedented in scale and diversity. Over the past six years, we have assembled genomic data for over half of the 13,600 genera of flowering plants, making them publicly available on-line and using them in an extensive scientific research programme. We have recently secured major new funding and are now building a team to finish the job. We're looking for a highly motivated, collaborative expert to play a central role in delivering the bioinformatic requirements of the project.

The successful candidate will join an established, vibrant, multi-disciplinary team of scientists. In collaboration with existing project informaticians, you will be responsible for analysing and managing project data, as well as developing software to enable the construction of a complete tree of life for plants.

You will be an excellent bioinformatician or software engineer with appropriate professional experience and a proven background in genomic data manipulation and management, ideally in a research environment. You will have a track record of helping to design and build robust bioinformatics pipelines, with experience of high-performance computing, relevant programming languages (such as Python) and relational databases. Expertise in phylogenomics is desirable but not essential. You will be a proven team player, with the ability and appetite to deliver project outputs, outreach, and to train and support researchers and students as required.

The salary will be  $\pounds 32,000 - \pounds 37,000$  per annum (pro rata), depending on skills and experience.

This role is based at Kew with the option of regular home working, subject to operational requirements.

Our fantastic benefits package includes opportunities for continuous learning, a generous annual leave entitlement, flexible working to help you maintain a healthy work-life balance, an Employee Assistance Programme and other wellbeing support such as cycle to work scheme and discounted gym membership. We also offer a competitive pension, an employee discount scheme and free entry into a wide range of national museums and galleries, as well as access to our own beautiful gardens at Kew and Wakehurst.

If you are interested in this position, please submit your application through the online portal, by clicking "Apply for this job". <https://careers.kew.org/vacancy/-bioinformatician-completing-the-plant-tree-of-life-project-483936.html> We are committed to equality of opportunity and welcome applications from all sections of the community. We guarantee to interview all

disabled applicants who meet the essential criteria for the post.

In addition to completing the online form, applicants must also upload 1) a letter of motivation and 2) a full CV, including details of publications and software.

Closing Date: 24/05/2022

Dr William J. Baker Senior Research Leader Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3AE, UK [www.kew.org](http://www.kew.org) | [treeoflife.kew.org](http://treeoflife.kew.org)

The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, United Kingdom.

Any views expressed in this email do not necessarily reflect the opinions of RBG Kew.

William Baker <W.Baker@kew.org>

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## Senckenberg Frankfurt Biodiversity Computer Scientist

The Senckenberg Society for Nature Research was founded in 1817 and is one of the most important research institutions around biological diversity. At its eleven sites throughout Germany, scientists from over 40 nations conduct cutting-edge research on an international scale. The company's headquarters are in the Main metropolis of Frankfurt in the heart of Germany. It is also home to one of Senckenberg's best-known facilities, the Senckenberg Natural History Museum.

The Senckenberg Society for Nature Research headquartered in Frankfurt am Main, is seeking to fill a vacancy as soon as possible for the central coordination office of the BMBF-Research Initiative for the Conservation of Biodiversity (FEEdA) at the Frankfurt site.

Biodiversity Computer Scientist (m/f/d)

(full-time position)

Your tasks include

Support of the head of the central coordination office and the scientific spokesperson of the research initiative in the field of biodiversity informatics; this includes in particular:

Contributing to the development of a sustainable, coordinated, and demand-oriented data management concept for the research initiative  
Design and implementation of

user interfaces (web-based) for database applications  
Design and implementation of ETL processes  
Technical support/implementation of a local cloud solution for research data  
Design, implementation and maintenance of an expert database, a meta-database for the research initiative data, as well as the visualization of the data  
Development and maintenance of a literature database for collaboration partners of the research initiative  
Professional and technical support on data related topics for the project partners of the research initiative  
Implementation and maintenance of interfaces to the federal Research Data Infrastructure via APIs (e.g. generic: DOIP, gRPC, OAI-PMH, REST; domain specific: ABCD/BIOCASE)  
Implementation of the technical tasks of the data management concept  
Scientific, technical and organizational support for data issues of the synthesis work for the collaborative and project partners of the research initiative.

Your profile

A university degree with IT-relevant reference or related disciplines  
Proven professional experience in the field of software and web development  
Programming experience in Python or other programming languages (e.g. Go, Java)  
Experience in the operation and administration of Linux systems  
Experience with relational databases (PostgreSQL, MariaDB) as well as database queries (SQL)  
Experience with standard web application development (JSON, XML, REST APIs)  
Knowledge of CI/CD pipelines, Docker, Git and/or shell scripting is a plus  
Knowledge of document-oriented databases and processing (e.g. Solr, Elasticsearch, SPARQL, Neo4J, MongoDB) is a plus  
Relevant experience with ecological or biodiversity data.  
Experience in interdisciplinary research environments  
Confident speaker of German and English, both written and spoken  
Team worker with both excellent communication skills and a service- and goal-oriented working style

We offer you

An attractive and challenging job in a globally renowned research institution  
salary commensurate with the importance of the tasks and the requirements of the position  
Flexible working hours - a discounted job ticket - support with childcare or caring for family members (certified by the "audit berufundfamilie") - Senckenberg badge in connection with free admission to many municipal museums - special annual payment according to the collective agreement - vacation entitlement according to the collective agreement - company pension plan

Location: Frankfurt am Main

Scope of employment: Full-time (40 hours/week)

Type of contract: Initially limited for a period of 2 years;



Subject to the extension of the project, an extension of the employment relationship will be sought.

The position can be filled as soon as possible.

Senckenberg aims to increase the proportion of women. Qualified female candidates are therefore particularly encouraged to apply. Senckenberg is certified by the "audit berufundfamilie". Compliance with the guidelines for the severely disabled and the provisions of the law on part-time work is guaranteed.

You would like to apply?

Then please send your complete and meaningful application documents (CV, training and work references, certificates and credentials, letter of motivation), in electronic form (as one continuous PDF file) by 30.06.2022, quoting the reference number #01-22021 to:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

E-Mail: [recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)

If you have any questions, please do not hesitate to contact the Head of the Central Coordination of the BMBF Research Initiative for the Conservation of Biodiversity, Dr. Julian Taffner, [julian.taffner@senckenberg.de](mailto:julian.taffner@senckenberg.de), phone: +49/ (0) 69 / 7542-1302.

Thank you for your consideration. We look forward to your application!

Yours sincerely

Isabel Gajcevic, M.A.

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

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## Smithsonian NMNH MarineEvolutionaryBiol

Please see the below announcement of an exciting new opportunity. The target I believe is a mid-career to senior scientist but anyone interested should apply or at least inquire.

Dear all, The search for the next Sant Chair in Marine Sciences has launched. The link to the posting on USA

Jobs is here USAJOBS - Job Announcement < <https://www.usajobs.gov/job/654610800> > and the paid ad that will appear in Science, Nature, and GSA Today, follows below. Please share widely!

Sant Chair in Marine Sciences, National Museum of Natural History, Smithsonian Institution The National Museum of Natural History (NMNH), Office of the Associate Director for Science and Chief Scientist, is seeking an international leader in marine science to fill the position of Sant Chair in Marine Science (Supervisory Research Biologist). The Sant Chair conducts and oversees exceptional interdisciplinary or collaborative scholarly research at the Smithsonian and will advance a cohesive ocean science strategy that includes research, education, exhibits, major public programs, media contacts, publications, and lectures. Increasing the public's awareness of science is at the core of the Smithsonian's mission to increase and diffuse knowledge. The Sant Chair will develop and participate in research programs related to their area of marine science, will conduct fieldwork on a global level with a focus on enhancing the National Collections, and will oversee major, synthetic research products of exceptional scope and originality that have significant impact across disciplines.

The Sant Chair will provide leadership, stimulate new collaborations, and enhance communication across the Museum's ocean-science portfolio including the Smithsonian Marine Station in Fort Pierce Florida (SMSFP) and the NMNH Ocean Science Center (OSC). The Sant Chair must also be able to advise Smithsonian leadership at all levels on scientific matters involving national and international scope, and they will represent the Smithsonian on marine initiatives and partnerships such as the United Nations Decade of Ocean Science for Sustainable Development.

The Sant Chair will join a vibrant community of research scientists at the NMNH and around the Smithsonian, a community that also includes highly specialized collections, conservation, laboratories, field stations, exhibits and education colleagues. The museum's collections hold over 147 million biological, fossil and mineral specimens, genomic samples, cultural objects and archival materials, representing over 90% of the Smithsonian's holdings across its 19 museums.

This is a full-time, permanent executive level position to be filled as Trust (private sector, U.S. citizenship not required, proof of eligibility to work in the U.S. required). Salary starts at \$ 135,468 per year, commensurate with experience. The Smithsonian Institution offers a comprehensive package of benefits. For complete requirements and application procedures, please visit: [www.si.edu/ohr](https://www.si.edu/ohr) < [https://www.si.edu/ohr/jobs\\_public](https://www.si.edu/ohr/jobs_public)

> and refer to Announcement # EX-22-23 (<https://www.usajobs.gov/job/654610800>). Applications must be received online by 6/27/22. Resumes should include a description of your paid and non-paid work experience that is related to this position; starting and ending dates of job (Month and year); and average number of hours worked per week. Applicants will be notified by email when their applications are received. For more information about the position, please contact Ellen Strong, Search Committee Chair and Chair of the Department of Invertebrate Zoology, at [stronge@si.edu](mailto:stronge@si.edu).

We encourage all qualified candidates to apply.

The Smithsonian Institution is an Equal Opportunity Employer.

Ellen E Strong Research Zoologist and Chair Department of Invertebrate Zoology w 202.633.1742 f 202.357.2343 [StrongE@si.edu](mailto:StrongE@si.edu)

SMITHSONIAN INSTITUTION NATIONAL MUSEUM OF NATURAL HISTORY Facebook < <https://www.facebook.com/nmnh.fanpage/> > | Twitter < <https://twitter.com/NMNH> > | Instagram < <https://www.instagram.com/smithsoniannmnh/> >

“Osborn, Karen” <[OsbornK@si.edu](mailto:OsbornK@si.edu)>

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## Smithsonian Tech microCTscanner

Hi Everyone, The Smithsonian National Museum of Natural History in Washington DC is hiring a technician to maintain our microCT scanner, train our users, and sometimes operate the machine. The position is currently a contract for 1 yr, renewable for 2 additional years, but we are working on making that a permanent position within that 3 yr timeframe.

The deadline is very short for submitting a contract bid (5pm EST June 6, 2022) for this contract, but we would like to consider as many candidates as possible for the permanent position and next year’s contract. So, if you are interested or know someone who could be interested, please contact me to learn more about the position [osbornk@si.edu](mailto:osbornk@si.edu) and for information about how to apply (the RFQ is here as an attachment but may get stripped off).

Here is the current ad: Contract micro-CT Specialist at the Smithsonian Institution National Museum of Natural History. NMNH is searching for an individual who has the requisite skills and experience to operate a micro-

computed tomography scanner, including sample preparation x-ray imaging, tomography, volume data processing and analysis at the National Museum of Natural History (NMNH) mCT Imaging Center (mCTIC). The mCTIC is part of a larger advanced imaging core facility with equipment to support scanning electron microscopy, optical microscopy, x-ray micro-computed tomography, and 3D scanning primarily serving the research interests of the NMNH. The mCTIC is a multi-user core facility where individuals are trained to prepare and analyze their samples, ultimately operating the equipment independently. The position will involve collaborative teamwork in planning and executing analysis of a wide variety of materials reflective of the vast collections of the NMNH. It will involve extensive collaboration with the head of NMNH Scientific Imaging, curatorial, post-doctoral, and visiting scientists for experimental design, training, execution of analyses, segmentation, 3D rendering of projections and volume analysis. Candidate should have a team spirit and demonstrate excellent communication and organizational skills and good command of the English language. Contract is for one year with the option to extend for up to 2 more years. Closing date is 5pm EST June 6, 2022

Thanks for helping spread the word, Karen

Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 [osbornk@si.edu](mailto:osbornk@si.edu) <http://orcid.org/0000-0002-4226-9257> Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012, Washington, D.C. 20013-7012 USA

Courier Address: Smithsonian Institution, MR 0163, Natural History, West Loading Dock, 10th and Constitution Ave NW, Washington, D.C. 20560

“Osborn, Karen” <[OsbornK@si.edu](mailto:OsbornK@si.edu)>

[OsbornK@si.edu](mailto:OsbornK@si.edu)

## UGroningen Four Evolutionary Biol

Dear Sirs,

The Groningen Institute for Evolutionary Life Sciences/GELIFES (University of Groningen, the Netherlands), is currently recruiting four Assistant and/or Associate Professors in the following fields:

1. Molecular Genetics of Adaptation -
2. Theoretical Biology
3. Evolutionary Plant Eco(physio)logy
4. Ecology & Evolution

\*Tenure Track Assistant or Associate Professor in Molecular Genetics of Adaptation \*

\*(0.8-1.0 FTE)\*

The aim of this position is to establish an independent research line for fundamental and/or applied research on molecular genetics of adaptation, and to contribute to education in molecular genetics of eukaryotes as part of GELIFES' educational programmes in biology and life sciences. The focus for the position is to understand the adaptive biological function at the cellular level applied to multicellular eukaryotic organisms.

\*Deadline\*: until 15 May 2022, 11:59pm CET. The text of the vacancy is available here <<https://www.rug.nl/about-ug/work-with-us/job-opportunities/?details>

Tenure Track Assistant or Associate Professor in Theoretical Biology (0.8 - 1.0 FTE) The successful candidate is expected to set up an independent research line within the field of theoretical biology, complementary to ongoing research in the institute and may reinforce the current emphasis on theory development in ecology and evolution, for instance, by bringing in expertise in evolutionary developmental biology, systems ecology modelling, evolution of culture and language. Alternatively, she/he may bring in expertise in other fields such as computational neuroscience, integrative biology or complex adaptive systems theory. Deadline: until 15 May 2022, 11:59pm CET. The text of the vacancy is available here <<https://www.rug.nl/about-ug/work-with-us/job-opportunities/?details>

Tenure Track Assistant or Associate Professor in Evolutionary Plant Eco(physio)logy (0.8 - 1.0 FTE) The new staff member is expected to set up an independent research line within the field of Evolutionary Plant Eco(physio)logy, with an emphasis on global

change biology, complementary to ongoing research in the institute. The successful candidate is expected to take an evolutionary, integrative approach and develop a strong research programme in plant biology at the organismal level, focusing on the adaptive traits enabling plants to cope with changing conditions. Deadline: until 15 May 2022, 11:59pm CET. The text of the vacancy is available here <<https://www.rug.nl/about-ug/work-with-us/job-opportunities/?details>

Tenure Track Assistant Professor (education profile) in Ecology & Evolution (0.8 - 1.0 FTE)

GELIFES is seeking for an early-career academic who is interested to start a tenure-track that focuses on education in the field of ecology and evolution. As Assistant Professor with an education profile, the successful candidate will teach in the degree programs BSc Biology, BSc Life Science & Technology and MSc Ecology and Evolution, and possibly the MSc Marine Biology, and is expected to contribute to current research lines in the GELIFES institute and/or develop her/his own research line. Deadline: until 15 May 2022, 11:59pm CET. The text of the vacancy is available here <<https://www.rug.nl/about-ug/work-with-us/job-opportunities/?details> \*Recognition and rewards\*

These positions are inspired by the national initiative recognition and rewards. One of the core aims of this initiative is to create a more diverse and dynamic career system at Dutch universities, so that excellence in education, research and societal impact is promoted. At the Faculty of Science and Engineering where GELIFES is embedded we embrace these ideas and have therefore introduced this new career path.

The positions we offer will be embedded in the Groningen Institute for Evolutionary Life Sciences < <https://www.rug.nl/research/gelifes/> >. GELIFES aims to enhance the understanding of adaptive processes and the maladaptive consequences of their limitations, across all levels of biological organization (from molecules and genes to individuals and ecosystems), to inform the society and contribute solutions to societal problems. GELIFES specifically aims at the integration of mechanistic, evolutionary and ecological approaches. The institute is coordinating one of the four Faculty strategic themes called Adaptive Life < <https://www.rug.nl/research/fmns/themes/adaptive-life/> >. The institute

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

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## UNorthCarolina Charlotte MolecularLabManager

The Department of Bioinformatics and Genomics is searching for a career-level molecular lab tech. Masters or equivalent work experience strongly preferred. We hope to find candidates who can facilitate sequencing projects across the department. The lab manager will help coordinate junior lab techs in our department and manage shared equipment. The position has stable funding for long term renewals.

The ideal candidate will have a BS (MS preferred) in biological science with at least five years of molecular biology lab experience and three years of personnel management. Candidates should have direct experience with sample preparation and sequencing workflows for Illumina and Oxford Nanopore sequencing platforms as well as quantitative molecular detection methods such as ddPCR and qPCR.

Applications close May 31st.

Candidates can apply via the link below. <https://jobs.charlotte.edu/postings/42210> Rebekah Rogers Assistant Professor Department of Bioinformatics UNC Charlotte

Tw: @evolscientist

Rebekah Rogers <Rebekah.Rogers@unc.edu>

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## UPennsylvania HumanEvolutionaryGenomics

Human Genomics Research Positions at the University of Pennsylvania The Tishkoff lab at the University of Pennsylvania is seeking candidates for research positions at multiple levels (postdoc and staff positions are available-MD and/or PhD required). Candidates working with non-human or model organisms who want to obtain experience working with human data are also encouraged to apply. We are integrating genomic, transcriptomic, metagenomic, metabolomic, and epigenomic datasets generated from a large sample of ethnically

diverse Africans, African Americans, and African immigrants in the US (<http://www.med.upenn.edu/tishkoff/>). We use evolutionary, statistical, population genetics and functional genomics approaches to understand the genetic architecture of a number of anthropometric, cardiovascular, metabolic, and immune related traits for which we have detailed phenotype data.

Position 1 (Computational scientist studying human evolution/genetics of complex traits) The candidate will be involved in inferring the demographic history of African populations, determining the genetic basis of adaptation during human evolutionary history, characterizing genetic and epigenetic factors influencing gene regulation in tissues and single cells in humans, characterizing variation from whole genome short and long-read sequencing data, and/or studying genotype/phenotype associations for complex traits. The ideal computational candidates will have strong computational/statistical skills with experience in handling large genomic datasets, population genetics analyses and/or quantitative analyses of complex traits. Position 2 (Scientist to conduct functional genomics studies) The candidate will use functional genomics approaches to determine the impact of candidate causal variants identified by GWAS and selection scans on protein function, gene regulation and chromatin interactions. The ideal functional genomics candidate would have expertise in using cutting edge techniques for characterizing gene regulation and chromatin structure (e.g. single cell sequencing, massively parallel reporter assays, chromosome conformation capture, RNA-seq, ATAC-seq, ChIP-seq). Position 3 (Scientist to study human immune response) The candidate will use single cell sequencing techniques (RNA-seq and ATAC-seq) to study genetic and epigenetic factors influencing immune response in populations with diverse ancestries and environments. The ideal candidate for studying immune response would have a background in immunology and extensive cell culture experience. Experience with library construction or single cell data analysis is a plus. Benefits

\* Candidates will receive excellent salaries commensurate with qualifications and experience. \* Candidates will have an opportunity to develop creative, independent projects. \* Candidates are encouraged to present their work at conferences and meetings. \* We offer a collaborative and supportive environment and welcome applications from candidates with diverse backgrounds. The Department of Genetics is centrally located at the School of Medicine within the UPenn campus and is within short walking distance to the Children's Hospital of Pennsylvania as well as the Departments of Biology, Computer Science, Bioengineering and Anthropology located on the main campus. Outstanding core

facilities are available for high throughput sequencing, genotyping, and gene expression studies and for bioinformatics and computational biology analyses. Philadelphia is a vibrant city with excellent cultural events and plenty of parks and hiking/biking trails. It is also centrally located between New York City and Washington DC, with easy access via a short train or bus ride. Candidates should send curriculum vitae, a statement of interest, and contact information for three references via e-mail to Dr. Sarah Tishkoff, Departments of Genetics and Biology, University of Pennsylvania,

tishkoff@penmedicine.upenn.edu. The starting dates of positions are flexible.

Sarah Tishkoff, Ph.D. David and Lyn Silfen University Professor Departments of Genetics and Biology University of Pennsylvania Tel: 215-746-2670 tishkoff@penmedicine.upenn.edu <http://www.med.upenn.edu/tishkoff/> Director, Center for Global Genomics & Health Equity <https://globalgenomics.med.upenn.edu/index.html> tishkoff@penmedicine.upenn.edu

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### CallForEditors MolecularEcology

Molecular Ecology is accepting applications to work as a co-editor for our upcoming special issue on the Ecology of Gene Expression (<https://onlinelibrary.wiley.com/doi/10.1111/jeb.1365294x/homepage/acceptingapplications>)

In an effort to increase diversity and support the inclusion of our colleagues from equity-deserving groups and intersections (including but not limited to, women, racialized or visible minorities, Indigenous Peoples, persons with disabilities, members of the LGBTQ+ communities), the co-editors of this Special Issue are welcoming applications from researchers to serve as a co-editor for this special issue. Appointed co-editors will help shape the special issue by handling submitted manuscripts, co-authoring a peer-reviewed editorial, and championing processes that include equitable and inclusive practices in editing, review and collaboration. Applicants from any global region, at any career stage, with a doctoral degree in a field related to Molecular Ecology are invited to apply.

Please include a short statement about your area of expertise in association with the special issue (250 words), a statement of how you would contribute to equity, diversity and inclusion (EDI) practices (e.g., Fox and Paine 2019; <https://www.rsc.org/new-perspectives/talent/inclusion-and-diversity/>) in publishing this special issue (250 words), and a list of three selected publications. For more information on Wiley's Commitment to Equity, Diversity and Inclusion: <https://www.wiley.com/network/latest-content/diversity-equity-and-inclusion-why-wiley-why-research-publishing>. Please submit applications via email to Sean Rogers (srogers@ucalgary.ca)

Sincerely, Dr. Diana Rennison (University of California San Diego) Dr. Sean Rogers (University of Calgary)

Sean Rogers <srogers@ucalgary.ca>

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## Companies Providing Metabarcoding Services

Dear All,

Does anyone have experience with sending samples or DNA extracts of bulk and/or environmental samples for DNA-metabarcoding/eDNA lab analysis and can recommend companies for that purpose? If you feel comfortable to share, I would also be interested in pricing.

I'm happy to summarize answers and post an update on EVOLDIR.

Thanks a lot in advance for your help!

Best wishes, Cornelya

Cornelya Klutsch, PhD Researcher Norwegian Institute of Bioeconomy Research Department of Ecosystems in the Barents Region Svanhovd Research Station NO-9925 Svanvik, Finnmark Email: cornelya.klutsch@nibio.no Phone: +47902 85 906

Cornelya Klutsch <cornelya.klutsch@nibio.no>

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## Mammalogist Survey

Good Afternoon,

If you are a former member of the American Society of Mammalogists (ASM), please fill out the survey below.

The Membership Committee of the ASM wants to understand the reasons that some society members decide to join for one or a few years before deciding not to renew their membership. We would also like to know what the Society could do differently to retain members or increase our membership. To help us understand these reasons, we are asking former ASM members to complete this survey: [https://fhsucahss.co1.qualtrics.com/-jfe/form/SV\\_3DHeNmGKrwoYnH0](https://fhsucahss.co1.qualtrics.com/-jfe/form/SV_3DHeNmGKrwoYnH0) Qualtrics Survey | Qualtrics Experience Management <[https://fhsucahss.co1.qualtrics.com/jfe/form/-SV\\_3DHeNmGKrwoYnH0](https://fhsucahss.co1.qualtrics.com/jfe/form/-SV_3DHeNmGKrwoYnH0)> Qualtrics makes sophisticated research simple and empowers users to

capture customer, product, brand & employee experience insights in one place. [fhsucahss.co1.qualtrics.com](https://fhsucahss.co1.qualtrics.com)

This survey is anonymous and has been exempted by the IRB at Fort Hays State University.

Thank you for your time,

Lorelei Patrick

Lorelei E. Patrick, PhD she/her/hers

Assistant Professor Department of Biological Sciences Fort Hays State University Hays, KS

Lorelei Patrick <lepatrick@fhsu.edu>

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## MolEcolPrize Nominations Jun06 deadline

Nominations for the Molecular Ecology Prize: We are soliciting nominations for the annual Molecular Ecology Prize.

The field of molecular ecology is young and inherently interdisciplinary. As a consequence, research in molecular ecology is not currently represented by a single scientific society, so there is no body that actively promotes the discipline or recognizes its pioneers. The editorial board of the journal *Molecular Ecology* therefore created the Molecular Ecology Prize in order to fill this void, and recognize significant contributions to this area of research. The prize selection committee is independent of the journal and its editorial board.

The prize will go to an outstanding scientist who has made significant contributions to molecular ecology. These contributions would mostly be scientific, but the door is open for other kinds of contributions that were crucial to the development of the field. The previous winners are: Godfrey Hewitt, John Avise, Pierre Taberlet, Harry Smith, Terry Burke, Josephine Pemberton, Deborah Charlesworth, Craig Moritz, Laurent Excoffier, Johanna Schmitt, Fred Allendorf, Louis Bernatchez, Nancy Moran, Robin Waples, Scott Edwards, Victoria Sork, and Fuwen Wei.

Please send your nomination with a short supporting statement (no more than 250 words (longer submissions will not be accepted) and the candidate's CV directly to Anne Yoder ([anne.yoder@duke.edu](mailto:anne.yoder@duke.edu)) by Monday, June 6, 2022. Organized campaigns to submit multiple nominations for the same person are not necessary and can be counterproductive. Also, note that nominations from

previous years do not roll over.

With thanks on behalf of the Molecular Ecology Prize Selection Committee

“Anne Yoder, Ph.D.” <anne.yoder@duke.edu>

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## Seminar ESEB STN Speciation May10

Dear colleagues,

A reminder that the next session of the monthly online seminar series organised by the ESEB-funded STN network « Integration Of Speciation research » ( [ <https://speciation-network.pages.ist.ac.at/> ] ) will be held on Tuesday 10th of May 2022, 5 pm CET.

The upcoming session is the second in a series of three addressing the general topic of how to understand the relative importance of different barriers to gene flow and outline best practices to measure them, with a focus on phenotypes and traits.

This session will focus on “The role of geography in generating reproductive isolation”. We will welcome as speakers Clarisse Palma-Silva (University of Campinas, Brazil) and Rosemary Gillespie (University of California, Berkeley, USA).

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

To attend the session live, please follow the link on our website: <https://speciation-network.pages.ist.ac.at/-seminar-series/> . Talks (but not the discussion session) are recorded and made available here: <https://www.youtube.com/channel/UCIEkDdE.5sDw70SQq78DIAA> . The IOS network does not only aim at scientific integration, but also integration of the community. A main objective on this front is to foster diversity and inclusion across the field. The seminar series and subsequent discussion is open to everyone, from students to established researchers and non-scientists alike. In order to maximise the geographic diversity of attendees, we will alternate between two time slots every other month: 5 pm CET and 9 am CET. Please help us to circulate this email to anyone who may be interested, especially those in countries that are typically underrepresented in scientific discourse.

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

We look forward to seeing you there!

The STN IOS organising committee

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

NERC Fellow School of Biosciences University of Sheffield [www.cooneylab.co.uk](http://www.cooneylab.co.uk) Chris Cooney <c.cooney@sheffield.ac.uk>

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## SMBE GlobalSymposia

We are excited to announce SMBE everywhere!

Dear SMBE Members,

We are excited to announce SMBE’s Global Symposia series for 2022-23, SMBE everywhere! We have a terrific slate of symposia topics and are thrilled to bring these events to our members free of charge. If you are not yet a member, please join SMBE so that you can attend. The first symposium is slated for July 11, 2022, so please mark your calendars for this event!

SMBE everywhere will be a series of ten virtual, 1-day Global Symposia which will occur in time zones across the globe starting in July 2022 and running through April 2023. Each GS will consist of plenary talks, contributed talks, a poster session, and time for discussion. Talks will be delivered via livestream, and recorded when possible. All recorded talks and posters will be available in the Gathertown space until June 2023, allowing for real-time interactions both during and between each GS throughout the year.

Please visit the

SMBE everywhere website for a glimpse of the GS themes and dates for this year. Registration will be opening May 10, 2022 and will be available throughout the year. You can register for as many events as you would like to attend! Abstract submissions are now open, and deadlines for each GS are listed, as well as the invited speakers and organizers. A special thank you to all of

our organizers, we appreciate the hard work you have already put into making SMBE everywhere happen!

Sincerely, Sarah Schaack and Stephen Wright SMBE everywhere Co-Organizers

Questions?

Please contact

smbe@allenpress.com

Society for Molecular Biology & Evolution  
smbe@allenpress.com

“smbe@allenpress.com” <smbe@allenpress.com>

## SMBE IDEA Proposal Call

Dear all,

Due to the technical difficulties with the SMBE website last week, the call for proposals to promote diversity and reduce inequities in Molecular Biology and Evolution has been extended to Monday 23rd May 2022. Please see the original call (below) for details, or check out the website (<https://www.smbe.org/smbe/HOME/TabId/37/-ArtMID/1395/ArticleID/125/-SMBE-IDEA-Inclusion-Diversity-Equity-and-Access-2022-Proposal-Call.aspx>).

Many thanks,

Ravinder Kanda (on behalf of the SMBE IDEA committee)

SMBE IDEA (Inclusion, Diversity, Equity and Access) 2022 Proposal Call

SMBE, through the IDEA (Inclusion, Diversity, Equity and Access) task force, aims to address all forms of exclusion in our society. With this in mind, a budget of up to \$25,000 per year will be dedicated to initiatives that help reduce inequities in molecular biology and evolution research. The task force would therefore like to invite members of SMBE to propose initiatives that would take place in the year 2022/2023. Examples of initiatives could include, but are not limited to, workshops, symposia, training opportunities, stand-alone featured talks, or inequity data collection in particular groups, countries, or regions (to name a few).

Guidelines and instructions for proposals

- At least one of the organizers must be a member of SMBE. Please note that you can apply for a complementary SMBE membership by contacting the SMBE council.

- A short description (between half and one full page) of the proposed idea should be submitted by email to [smbe.contact@gmail.com](mailto:smbe.contact@gmail.com) for review by 16th May 2022. This is the initial submission. Submissions should address how the proposal will help advance the goals of the SMBE IDEA task force.

- The initial submission should include the names and full contact information of all organizers and involved institutions. Universities/organizations providing additional financial support, if involved, should also be listed.

- Initial submissions will be reviewed and pre-selected by the IDEA task force, and candidates will be notified with a decision within 3 weeks after the initial submission deadline (by 6th June).

- If the initial submission is selected, organizers are expected to submit a full project plan by email to [smbe.contact@gmail.com](mailto:smbe.contact@gmail.com) by 25th July 2022. This must include a budget and time plan, as well as relevance and expected short and long-term impacts of the initiative on inclusion, diversity, equity and/or inclusion. The IDEA task force commits to aiding organizers during the development of the project plan.

- Successful proposals will be notified by 15th August 2022.

- All deadlines are 5pm local time.

Additional information

- To promote the submission of initiatives, the task force will host an open workshop (open to all SMBE members and not restricted to those who submitted an initiative) on “How to design project proposals” during the SMBE IDEA symposium (at the annual SMBE conference) on the 11th and/or 12th of July (date to be confirmed).

- Organizers should submit a report (~2 pages) of the activity to the SMBE IDEA committee within 3 months of its completion.

Dr Lulu Stader Executive Administrator, Society for Molecular Biology and Evolution  
[smbe.contact@gmail.com](mailto:smbe.contact@gmail.com) [smbe.meetings@gmail.com](mailto:smbe.meetings@gmail.com)

On behalf of the SMBE IDEA task force

Dr Lulu Stader Executive Administrator, Society for Molecular Biology and Evolution  
[smbe.contact@gmail.com](mailto:smbe.contact@gmail.com) [smbe.meetings@gmail.com](mailto:smbe.meetings@gmail.com)

“Lulu Stader (SMBE admin)” [smbe.contact@gmail.com](mailto:smbe.contact@gmail.com)  
[smbe.contact@gmail.com](mailto:smbe.contact@gmail.com)

Ravinder Kanda <[p0078006@brookes.ac.uk](mailto:p0078006@brookes.ac.uk)>



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## SORTEE Awards

Dear researchers in Ecology and Evolutionary biology, Nominations for the 2022 SORTEE (Society for Open, Transparent, and Reproducible Ecology and Evolutionary biology) awards are open and will close on 15 May. The awardees will be invited to give a short presentation at the SORTEE conference, to be held online on 11-13 July 2022.

We encourage you to apply and/or nominate someone whose work you think deserves recognition.

For more information please go to: <https://www.sortee.org/awards/> Regards,

SORTEE Awards Committee < <https://sortee.us5.list-manage.com/track/click?u=-3Da8ca1f4ea2f39ca6345f3d3e8&id=3f7e57963e&e=-511472a07c> >

Patrice Pottier | PhD Candidate Inter-disciplinary Ecology and Evolution lab (I-DEEL) Evolution & Ecology Research Centre, E&ERC Biological Sciences Building (E26) School of Biological, Earth and Environmental Sciences, BEES The University of New South Wales Randwick NSW 2052, Sydney, Australia

Contact E-mail: [p.pottier@unsw.edu.au](mailto:p.pottier@unsw.edu.au) | [patrice.pottier37@gmail.com](mailto:patrice.pottier37@gmail.com) Mobile: +61403138879  
Twitter: @Patrice\_Science <http://www.i-deel.org/-patrice-pottier.html> <https://www.researchgate.net/profile/Patrice.Pottier> pronouns: he/him/his

I may send emails out of 'normal' working hours. Please do not feel compelled to respond outside of your own working hours. < <http://www.unsw.edu.au/> > I respectfully acknowledge and pay my respects the traditional custodians of the land I work on and thank them for their ongoing custodianship; the unceded lands of the Bedegal people (Kensington campus) and all the lands where UNSW campuses are located. Sovereignty was never ceded - always was, always will be.

[p.pottier@unsw.edu.au](mailto:p.pottier@unsw.edu.au)

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## Survey Perceptions EvolutionaryBiology

Dear Colleagues,

We are conducting a survey of ecological scientists that participate in research to gauge their attitudes and perceptions towards the different sectors of their ecological research community. Our target audience includes evolutionary biologists, population biologists, systematists, etc and hence we would love to hear from you!

Have you heard opinions about which sector of your ecological research community is the most productive or impactful? Or which sector produces the highest quality research? Is it academia, government, industry, or the not-for-profit sector? Our survey aims to collect data to explore if any of these claims, among others, are justified. The results of our survey will be paired with scientific publication data to assess if peoples attitudes and perceptions of different sectors of their ecological research community match objective publication metrics. The results of our research will be published as one or more scientific journal articles.

The survey can be found here <https://www.surveymonkey.com/r/MVXRY7Y>, it takes a maximum of 10 mins to complete and we would very much appreciate if you could take the time to complete it.

Lastly, we would also greatly appreciate it if you could distribute our survey amongst your networks, to ecological scientists that participate in research.

Thank you for engaging with our survey and our research.

Kind regards and best wishes,

Pat

Dr Pat Taggart | Research Scientist Vertebrate Pest Research Unit Invasive Species Biosecurity | NSW Department of Primary Industries 11 Farrer Place | Queanbeyan NSW 2620 W: 02 6229 7708 | M: 0431 239 176 [www.dpi.nsw.gov.au](http://www.dpi.nsw.gov.au) Google Scholar < <https://scholar.google.com.au/citations?user=IAk-70MAAAAJ&hl=en> > | ORCID < <https://orcid.org/0000-0001-9523-0463> > | ResearchGate < [https://www.researchgate.net/profile/Patrick\\_Taggart](https://www.researchgate.net/profile/Patrick_Taggart) > | Publons < <https://publons.com/researcher/3388570/-patrick-taggart/> >

Pat Taggart <[pat.taggart@dpi.nsw.gov.au](mailto:pat.taggart@dpi.nsw.gov.au)>

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### Barcelona ComparativeGenomics

Postdoc position in Comparative and Structural Genomics

Ruiz-Herrera's lab is looking for a highly motivated candidate that can apply for a "Margarita Salas" post-doctoral fellowship from the Spanish Government.

The aim of the project is to study the high-structural organization of mammalian genomes combining HiC, ChIP-seq and RNA-seq data. Applicants should have a PhD in a relevant area (evolutionary biology, genomics

or genetics). We are seeking for someone with a vivid interest in evolution research. A background in bioinformatics and or population genetics/ statistical genetics is desirable, but not necessary.

Requirements:

PhD degree obtained after the 31st december 2019. Competitive publication record.

What we offer: - Two years contract that can be extended to a third year. - The total annual amount stipend will be euro 35,000 gross.

Ruiz-Herrera's lab is set at Universitat Autònoma de Barcelona (UAB). The long-term research goal of our research group is to provide a unified and encompassing view of how genomes are organized and regulated in

mammalian cells. Within this framework, the candidate will develop a project on the evolution and function of the higher-structural organization on mammalian genomes. For further information please see: <http://grupsderecerca.uab.cat/evolgenom/> . Likewise, UAB is located close to the city of Barcelona and is one of the major public universities in Spain. The UAB is internationally acknowledged for its quality and innovation in research. It coordinates a potent scientific and technological centre, which comprises all the departments, science and technology services, research centres, institutes and university hospitals affiliated with the UAB.

Complete application packages, including a CV, a brief (1-page) statement of research interests, and the names and e-mail addresses of two referees should be sent to: Dr. Aurora Ruiz-Herrera. Email: [aurora.ruizherrera@uab.cat](mailto:aurora.ruizherrera@uab.cat)

Aurora Ruiz-Herrera Moreno  
<[Aurora.RuizHerrera@uab.cat](mailto:Aurora.RuizHerrera@uab.cat)>

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## Brno Czechia FishBiology

POSTDOCTORAL RESEARCH POSITION 2-3.5 YEARS

TOPIC: Fish Evolutionary Ecology

REICHARD LAB ([www.reichardlab.eu](http://www.reichardlab.eu))

Institute of Vertebrate Biology, Czech Academy of Sciences, Brno

Full-time postdoctoral position for 2 years (+ extension until the end of 2025 possible) is available at the Institute of Vertebrate Biology, Czech Academy of Sciences, located in Brno, Czech Republic. Position may start when filled; all applications submitted until 20 June 2022 will be fully considered. Selected candidates will be interviewed online.

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

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

population genetics and phylogenetics.

Selected candidate will work along with two other post-doctoral researchers. There is flexibility in the specific focus within the broad terms of the project, although we would particularly welcome a candidate with expertise in:

1. fish morphology (dentition, gill rakers, osteology) or
2. comparative phylogenetic biology.

We expect applications from candidates with a background in ecology and evolution, ideally with a previous track record of working with fish models. For experimental work, there is access to well-equipped fish breeding facility and outdoor system of separate tanks.

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

### QUALIFICATIONS

PhD in Biology

### SALARY

at least 55 000 CZK (incl. social and health insurance and taxes), c. 2200 EUR per month (well above average for Czech living expenses), giving a net earnings of 35 000 CZK per month. May increase with qualification.

### APPLICATION PROCEDURE

Feel free to consult through informal enquires by email to [reichard@ivb.cz](mailto:reichard@ivb.cz)

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

Email your formal application to [reichard@ivb.cz](mailto:reichard@ivb.cz)

Martin Reichard <[reichard@ivb.cz](mailto:reichard@ivb.cz)>

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## CalAcademy SanFrancisco PlantSystematics

### POSITION SUMMARY:

A Postdoctoral Researcher position is available in the lab of Dr. Sarah Jacobs, within the Institute of Biodiversity Science and Sustainability (IBSS) at the California Academy of Science. Broadly, this position will conduct research on the phenomics and genomics of the plant genus *Castilleja*. The candidate will contribute to general systematic efforts in the group and help to

describe the early stages of the speciation process in this taxonomically challenging genus. The candidate will additionally contribute to the development of botanical phenomic, genomic, and bioinformatic resources, as well as the generation of extended specimens at the California Academy of Sciences. Additionally, public outreach and education through in-person and online interactions will be a component of this position and collaboration within IBSS and across the Academy is expected. This is a temporary, two-year position, with the possibility of renewal contingent on research progress and availability of funds.

The position is primarily onsite and can change as business needs warrant. The candidate must easily be able to work onsite in Golden Gate Park in San Francisco when needed. Candidates are required to have up-to-date COVID-19 vaccination, including receiving a booster shot, as a condition of employment, absent qualifying exemptions in accordance with applicable laws. Individuals receiving a conditional offer of employment from the California Academy of Sciences will be provided the full text of the vaccination policy.

#### POSITION DUTIES AND RESPONSIBILITIES:

-  
Conduct original, scientific research in collaboration with the Assistant Curator of Botany on the plant genus *Castilleja*, focusing on systematics and speciation and incorporating evidence from the genome and phenome.

-  
Contribute to building the research collections, including amassing genomic and phenomic resources, culminating in the generation of extended specimens. -

Publish and present results in scientific journals and at national and international meetings, and contribute to grant proposals. -

Contribute to and participate in educational programs at the Academy, in person and online. -

Represent the Botany Department, IBSS, and the Academy at internal and external events.

#### QUALIFICATIONS

##### EXPERIENCE and/or EDUCATION:

-  
Doctoral degree (Ph.D.) in a relevant discipline, with all requirements completed by the starting date of the position. -

Research experience in plant systematics, preferably working within and between closely related species. -

Experience working in a laboratory environment with

proper safety precautions.

##### SKILLS AND ABILITIES:

-  
Knowledge of and experience with molecular biology, next-generation sequencing procedures, and related bioinformatic tools and programming. -

Working knowledge of plant diversity and systematics.

-  
Interest in science communication/outreach and education. -

Proven track record of effective collaboration and communication with a wide diversity of stakeholders including scientists, educators, students, youth, and the general public. -

Ability to travel nationally for several weeks at a time.

-  
Ability to work as part of a team. -

Willingness to work efficiently and communicate effectively with staff, cross-functional teams and external individuals from different identities and experiences. -

Willingness to bring new ideas, create solutions and find efficiencies to transform manual or detailed processes. -

Generally contribute to a positive, enjoyable work environment.

##### APPLICATION INSTRUCTIONS:

To apply, please visit: <https://californiaacademyofsciences.applytojob.com/apply/-ay1r0hTfdg/Postdoctoral-Researcher> You will be asked to provide a CV, cover letter, three references, and to complete the online application. Applications will be reviewed as they are received, and the opportunity will remain open until filled. Ideally, the candidate will start in the fall of 2022, but alternative start dates will be considered.

The California Academy of Sciences is an Equal Opportunity Employer and is committed to ensure that all employees and applicants receive equal consideration and treatment, regardless of race, color, creed, gender (including gender identity or gender expression), religion, marital or domestic partner status, age, place of birth, national origin or ancestry, physical, mental or medical disability, height or weight, sex, sexual orientation, citizenship, military service status, veteran status, or any other characteristic protected by state or federal law or local ordinance.

##### COMPENSATION RANGE:

Please contact Dr. Jacobs with compensation inquiries.

## CONTACT INFORMATION:

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To read the entire message look it up at <http://life.biology-mcmaster.ca/~brian/evoldir.html>

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## CityTech NewYork LizardGeneFlow

The Blair lab at NYC College of Technology (City Tech/CUNY) focuses on using genomic data and sophisticated computational methods to understand evolutionary patterns and elucidate the processes giving rise to such patterns. Specific areas of focus include population genomics, molecular phylogenetics, phylogeography, species delimitation, and DNA barcoding. The lab is currently seeking a postdoctoral scholar who will work on an NSF funded project that uses multiple species of phrynosomatid lizards to understand the influence of gene flow during the diversification of arid-adapted organisms distributed throughout the major deserts of western North America. A second major goal of the project is to combine genomic data, mtDNA, morphology, and ecology to refine species limits and describe new taxa. Data will be collected from approximately 10 species/species complexes from multiple phrynosomatid genera. This project is a collaborative effort with researchers from multiple institutions with expertise in genomics, phylogenetics, and morphological analysis. The successful candidate will be given some degree of flexibility to explore related interests within the overall scope of the project. The initial appointment is for one year, with the possibility of a second year given satisfactory progress. Although the PI's laboratory is in NYC, there will be some flexibility regarding the location of postdoctoral position. However, the successful candidate must be able to periodically spend time in NYC to perform laboratory work and potentially assist in the field throughout the western US.

## Specific duties

• Assist in the collection of tissue and voucher samples in the field.

• Maintain databases pertaining to current tissue holdings.

• Collect and analyze meristic and morphometric data to aid in species delimitation.

• Perform standard molecular lab work (e.g. DNA extraction, quantification, PCR, sample prep for next-generation sequencing).

• Analyze newly obtained molecular data using recently developed software.

• Write manuscripts in collaboration with other researchers involved with the project.

• Assist in supervising undergraduate researchers.

• Present results at national scientific meetings.

• Meet with PI at least once per week to discuss progress.

## Requirements

A PhD degree in a relevant discipline is required prior to the official start date. Candidates should have previous experience with genomics, phylogenetic analysis, population genomics, bioinformatics, and cluster computing. Prior programming experience is not required, but would be beneficial. An interest and background in the biology of reptiles and amphibians would also be helpful, but is not required. Strong written and oral communication skills are required. Candidates should be available for periodic laboratory work. However, many other duties can be done remotely.

## Application

Interested candidates should submit a single pdf document containing a cover letter, CV, and research statement to [cblair@citytech.cuny.edu](mailto:cblair@citytech.cuny.edu). In addition, please include contact information for three professional references. Applications will continue to be screened until a suitable candidate is found. The official start date is somewhat flexible, but candidates who can begin sooner will be given priority. Informal inquiries can be submitted prior to a formal application.

Christopher Blair, Ph.D. Associate Professor

Department of Biological Sciences

New York City College of Technology and

Ecology, Evolution and Behavior PhD Program

Graduate Center

The City University of New York

285 Jay Street

Brooklyn, NY 11201

[CBlair@citytech.cuny.edu](mailto:CBlair@citytech.cuny.edu); [cblair@gc.cuny.edu](mailto:cblair@gc.cuny.edu)

Website: <https://sites.google.com/site/christopherblairphd/home> Office: Academic Complex 501A; Ph: 718-260-5342

Lab: Academic Complex 401

Christopher Blair, Ph.D. Associate Professor Director, Biomedical Informatics Program Department of Biological Sciences New York City College of Technology and Ecology, Evolution and Behavior PhD Program Graduate Center The City University of New York 285 Jay Street Brooklyn, NY 11201 CBlair@citytech.cuny.edu; cblair@gc.cuny.edu Website: <https://sites.google.com/site/christopherblairphd/home> Office: Academic Complex 501A; Ph: 718-260-5342 Lab: Academic Complex 401

Christopher Blair <CBlair@citytech.cuny.edu> Christopher Blair <CBlair@citytech.cuny.edu>

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## CNRS Poitiers France Evolutionary Genomics

A 24-month postdoctoral position in evolutionary genomics at CNRS (French National Center of Scientific Research) is available.

Location: lab Ecology and Biology of Interactions (UMR 7267 EBI), Poitiers, France. Team “Ecology Evolution Symbiosis” (EES).

Starting date: September 1st, 2022. Applications are welcome from now on until the position is filled.

Funding: ANR project “SymChroSex” led by Jean Peccoud.

Project title: Evolutionary genomics of a neo sex chromosome derived from a feminizing endosymbiont

Context: The mechanisms leading to the appearance of new sex chromosomes and the genes controlling sex in are unknown in most bisexual taxa. Thus, the origin and turnover of genetic determinants of sex are still mysterious. Woodlice (terrestrial isopod crustaceans) are prime models to fill this gap. Their sex chromosomes are undifferentiated (homomorphic) and heterogamy systems (XY, ZW) vary between related species. The dynamic evolution of sex determinants in these species may result in part from the action of feminizing endosymbiotic bacteria of the genus *Wolbachia*. The common woodlouse *Armadillidium vulgare* is a particularly interesting result to this evolution (Cordaux et al. 2011, Trends Genet.). In addition to *Wolbachia*, this species comprises, depending on the population: one pair of ZW-type sex chromosomes, another pair of XY-type sex chromosomes, and a fascinating feminizing element that

arose from an insertion of the bulk of the *Wolbachia* genome into the nuclear genome (Leclercq et al. 2016, PNAS). This element, called the “f-element”, feminizes its carrier in the manner of a W chromosome. Although it is of very recent origin, the f-element is already common in natural populations. The f-element is the focus of the SymChroSex project.

This project aims to: (i) characterize the f-element in terms of sequence, (ii) understand its origin and characterize its evolution in natural populations, (iii) locate the specific feminizing gene it contains, a gene probably derived from *Wolbachia* whose feminization mechanism is still unknown.

Missions: Working closely with Jean Peccoud, the post-doc will conduct tasks aimed at meeting these objectives. She/he will have access to important genomic resources (pacbio, ONT, Hi-C) to contribute to the new genome assembly of *A. vulgare*, in particular the f-element, and to analyze the transmission patterns of the f-element in controlled crosses. She/he will conduct population genomics analyses (including field samplings) to understand the origin and rapid rise of the f-element (search for selective sweep signals) and to locate the feminizing gene of the f-element (and potentially other sex determinants (ZW, XY)). Depending on the affinities of the recruited person, other areas of research may be explored, such as modeling the evolution of the different sex-determining elements in natural populations and gene expression analyses of candidate feminizing genes.

Requirements: PhD in the field of evolutionary genomics, Deep understanding of evolutionary concepts, more specifically population genetics, Skill in phylogenetic and genomic analyses, Skills in bioinformatics tools and scripting (bash, R), Ability to perform basic molecular analyses (DNA extraction, PCR), Excellent abilities in data analyses, writing, communication, teamwork and creativity.

Monthly net salary: between 2200 euro and 2450 euro according to experience.

All applications must be sent by email to Jean Peccoud (jean.peccoud@univ-poitiers.fr). They must include a CV, explain the motivations of the applicant and the adequacy with the profile sought. The names and email addresses of at least two referees are required.

Jean Peccoud <jean.peccoud@univ-poitiers.fr>

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## CornellU GeneticEpidemiology

We are seeking two Postdoctoral Associates to work on the genetic epidemiology of *Mycobacterium tuberculosis* (Mtb) at Cornell University. The project aims to develop population-genetic models and phylodynamic statistical inference frameworks and apply the developed methods to whole-genome sequencing data with its associated metadata for studying evolutionary processes and disease transmissions of Mtb. We are especially interested in candidates with experience in Bayesian inference methods. However, there is flexibility regarding the theoretical approaches used, and the postdocs will have the freedom to devise a creative computational framework for the project.

The Postdoctoral Associates will be co-advised by three Principal Investigators Jaehee Kim, Andrew Clark, and Martin Wells across the Department of Computational Biology and the Department of Statistics and Data Science at Cornell University. The postdocs will also work in close collaboration with Kyu Rhee at Weill Cornell Medicine and Lorenzo Cappello at Universitat Pompeu Fabra. In addition to the research, the Postdoctoral Associates will receive necessary training for their career development, including in the areas of teaching, mentoring, and grant writing.

The start date is ideally September 2022 but can be flexible. The initial appointment for the position is 2 years, and the continuation beyond the initial appointment will be based on the availability of funds and performance.

Cornell University sits within the vibrant and beautiful city of Ithaca in upstate New York. Ithaca offers an affordable quality of life and abundant multicultural and outdoor activities. The research environment at Cornell is friendly, highly collaborative, and interdisciplinary with numerous academic opportunities and social events that support early-career researchers.

Qualifications: - Ph.D. in a quantitative field (e.g., statistics, computer science, computational biology, or related field). - Experience with methods development for Bayesian inference and their applications. - Experience with publication writing (peer-reviewed journal articles as well as extension publications). - Strong interest in developing novel approaches to biological problems. - Programming proficiency (e.g., Python, C/C++, R). - Ability to work effectively with an interdisciplinary team. - Exemplary oral and written communication

skills. - Previous experience with biological or clinical data preferred but not required.

To Apply: Please submit the following materials to Dr. Jaehee Kim <jaehee.kim@cornell.edu>. Applications will be reviewed as received, continuing until a suitable applicant is identified. - Cover letter describing your research interests and past research experiences. - Current CV. - Contact information for three professional references. - Code samples from prior works, preferably publicly accessible (e.g., GitHub) but email attachment acceptable.

We are committed to creating learning, research, and work environments that are inclusive of all forms of diversity. We actively encourage applications from and nominations of individuals from underrepresented groups.

Jaehee Kim <jaehee.kim@cornell.edu>

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## CRG Barcelona ModelingSequenceEvolution

Postdoc position at the Centre for Genomic Regulation (CRG), Barcelona, Spain

The 'Evolutionary Processes Modeling' group at the Centre for Genomic Regulation invites applications for a postdoc position to study genetic variation and selection in human genomes using computational data analysis, population genetics and statistical methods.

<https://recruitment.crg.eu/content/jobs/position/-postdoctoral-researcher-group-evolutionary-processes-modeling-2> Deadline: 31 May 2022.

The Institute

The Centre for Genomic Regulation (CRG) is an international research institute of excellence, based in Barcelona, Spain, with more than 400 scientists from 44 countries. The CRG is composed of an interdisciplinary, motivated and creative scientific team which is supported both by a flexible and efficient administration and by high-end and innovative technologies.

In November 2013, the Centre for Genomic Regulation (CRG) received the 'HR Excellence in Research' Award from the European Commission. This is in recognition of the Institute's commitment to developing an HR Strategy for Researchers, designed to bring the practices and procedures in line with the principles of the European Charter for Researchers and the Code of Conduct for the Recruitment of Researchers (Charter and Code).

### The Role

We are looking for a postdoctoral researcher to join the 'Evolutionary Processes Modeling' group. We use computational analysis of sequencing data together with population genetics predictions and statistical modeling to answer questions about mutational processes and selective pressures in cancer cells and in the human population. The ideal candidate should be highly motivated and eager to work on evolutionary and biological problems through the use and development of computational and statistical approaches.

### About the Group

Cancer is a genetic disease, subject to population genetics forces like mutation, selection and stochasticity. Our group is particularly interested in how the evolution and survival of cancer cell populations relies on mutation influx as well as in selection inference from observed mutation data. To this end, we develop mathematical and computational approaches to estimate mutation rates and selection. Coding sequences of cancer tumors not only exhibit positively selected mutations that drive cancer ([www.nature.com/articles/s41588-019-0572-y](http://www.nature.com/articles/s41588-019-0572-y)), but there also exists a small fraction of genes that the tumor cannot afford to lose ([www.nature.com/articles/ng.3987](http://www.nature.com/articles/ng.3987)). In addition to genes, cancer driver loci can occur in the non-coding part of the genome ([www.nature.com/articles/s41467-017-00100-x](http://www.nature.com/articles/s41467-017-00100-x)). Estimates of the strength of selection in cancer allow for a prioritization of genes and non-coding regions by their disease relevance, with the ultimate goal of promoting therapeutic advances.

We are also interested in mutation rates and selection inference in the context of human genetic variation, including polymorphisms (<http://www.nature.com/articles/ng.3831>; [academic.oup.com/mbe/article-abstract/36/8/1701/5475505](http://academic.oup.com/mbe/article-abstract/36/8/1701/5475505)) and de novo variants ([www.nature.com/articles/s41467-020-17162-z](http://www.nature.com/articles/s41467-020-17162-z)). Here, a particular focus of the group lies on the description of purifying selection in humans and across species, accounting for mutational processes as well as the effects of genetic drift.

The Evolutionary Processes Modeling lab was established in October 2018 and is part of the 'Bioinformatics and Genomics' program at the CRG. Further information can be found at <https://weghornlab.net/> and at [www.crg.eu/en/programmes-groupes/weghornlab](http://www.crg.eu/en/programmes-groupes/weghornlab). Whom would we like to hire?

### Professional experience

- You are familiar with the principles of population genetics

### Education and training

- You hold a PhD degree in population genetics, physics, statistics, bioinformatics, or a related discipline

### Languages

- You are fluent in English

### Technical skills

- You have experience with computational data analysis

- You are familiar with modeling and statistical analysis

### Competences

- You have highly developed organization skills

- You have Warning: base64 decoder saw premature EOF! good communication skills

### The Offer - Working Conditions

- Contract duration: 1 year, to be extended up to a maximum of 5 years.

- Estimated annual gross salary: Salary is commensurate with qualifications and consistent with our pay scales.

- Target start date: As soon as possible.

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## Glasgow MetabolicEvolutionStickleback NewLink

We have an exciting opportunity for a Research Assistant (postdoc) to work on a BBSRC funded project ([gtr.ukri.org/projects?refi%2F%2FW002515%2F1](http://gtr.ukri.org/projects?refi%2F%2FW002515%2F1)) with Kevin Parsons and Colin Selman in collaboration with James Windmill (Strathclyde University), Bjarni Kristjansson (Holar University) and Brian Metscher (Vienna).

We aim to investigate stickleback populations from geothermally-warmed habitats and how they have evolved and metabolically adapted to this challenging environment. So far, our investigations suggest that these populations exhibit phenotypic variation in line with the symptoms of metabolic syndrome (including diabetes), but without incurring the negative consequences.



This includes evolutionary divergence in appetite levels, body composition, and glucose tolerance. The project will leverage these findings as well as wealth of existing genomic data to determine the mechanistic basis of these traits. However, this project will also embrace the reality that these populations are exposed to environmental variation which will be considered throughout our experiments.

The successful candidate should ideally have a background in one of evolutionary biology, genomics, molecular biology, animal physiology or developmental biology and will be expected to contribute to experiments and the formulation and submission of research publications as well as helping to manage and direct this project as opportunities allow. The successful candidate will also possess teamwork skills as they will work with a full-time technician and other members of the PI's group on this project as well as liaising and interacting with project collaborators.

Applications close on the 13th of June, and this post is full time and has funding up to 31/01/26.

Any further enquiries on this post may be directed to Dr Kevin Parsons, Kevin.Parsons@glasgow.ac.uk

For more information and to apply online please follow either of the links:

<https://www.jobs.ac.uk/job/CPL251/research-assistant> Research Assistant at University of Glasgow Research Assistant University of Glasgow - College of Medical, Veterinary and Life Sciences - Institute of Biodiversity, Animal Health and Comparative Medicine [www.jobs.ac.uk](http://www.jobs.ac.uk)

[https://my.corehr.com/pls/uogrecruit/-erq\\_jobspec\\_version\\_4.display\\_form](https://my.corehr.com/pls/uogrecruit/-erq_jobspec_version_4.display_form) Dr. Kevin Parsons Institute of Biodiversity, Animal Health, and Comparative Medicine University of Glasgow

Phone: +44 (0) 0141 330 5974

<https://sites.google.com/site/kevinparsonslab/-home> <http://www.gla.ac.uk/researchinstitutes/-bahcm/staff/kevinparsons/> Kevin Parsons <Kevin.Parsons@glasgow.ac.uk>

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## Helmholtz Munich Genomics

Dear All,

I have PhD and post-doctoral positions available in my new lab at Helmholtz Munich for researchers inter-

ested in planetary health, genomics, AI in genomics, and portable genomics, plus possibilities for internships:

<https://jobs.helmholtz-muenchen.de/jobposting/-78c4f8fcff04930db6edc5b3f762c4efabd827011?ref=homepage> <https://jobs.helmholtz-muenchen.de/jobposting/-426c528d35415e2d2c6a5ac7896d2c09d83833391?ref=homepage> Please share with any researcher who could be interested! Thank you very much.

Best wishes, Lara

Dr Lara Urban

Principal Investigator Helmholtz Munich & Helmholtz Pioneer Campus phone: + 49 (0) 160 92105701 email: [lara.h.urban@gmail.com](mailto:lara.h.urban@gmail.com) website: <https://www.lara-urban.com/> "Nothing in life is to be feared, it is only to be understood." - Marie Salomea Skłodowska Curie

Lara Urban <lara.h.urban@gmail.com>

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## Instituto Gulbenkian Ciencia Genome Maintenance Evolution

POSTDOCTORAL POSITION IN THE GENOME MAINTENANCE AND EVOLUTION LAB AT THEIGC (PT)

We are looking for a postdoc to join our group at the Instituto Gulbenkian de Ciência, Portugal. The project will aim to understand basic principles governing genome maintenance over evolutionary timescales. It will involve molecular, cellular, and evolutionary techniques with *S. cerevisiae*, as well as computational and genomic analyses. Specific plans for the projects will be discussed during the interview phase and will be shaped by considering the profile of the successful candidate, as well as their input and interest. Previous experience in the field or with the methods is welcomed, but not required. For more details:

Official call: [https://gulbenkian.pt/ciencia/wp-content/uploads/sites/47/2022/05/Call-Fellowship-Internal\\_MF-1.pdf](https://gulbenkian.pt/ciencia/wp-content/uploads/sites/47/2022/05/Call-Fellowship-Internal_MF-1.pdf) Lab website: <https://fumalab.github.io> Institute website: <https://gulbenkian.pt/ciencia/> Marco Fumasoni Genome Maintenance and Evolution Lab Instituto Gulbenkian de Ciência (IGC) Rua da Quinta Grande, 6, 2780-156 Oeiras, PT <https://fumalab.github.io@marcofumasoni> Tiago Paixao <searapaixao@gmail.com>

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## LEMAR MARBEC France Population Genomics

Post-doctoral project: Population genomics of common dolphins in the NE Atlantic

A 30-months post-doctoral position in population genomics is open at the University of Western Brittany as part of the DELMOGES program. The objective of the post-doctoral project is to evaluate the population structure of common dolphins in the Bay of Biscay and adjacent regions by using SNPs obtained through RAD sequencing, and using an eDNA approach. The hired post-doc will be spending the first 18 months at the LEMAR research unit located in Plouzané (RADseq approach), and the last 12 months at the MARBEC research unit in Montpellier (eDNA approach).

Scientific context: Since the 1990s, significant dolphin mortality events have occurred during the winter in the Bay of Biscay, which result in stranding peaks on the French Atlantic coast. During these events, most stranded dolphins on this stretch of coast are common dolphins (*Delphinus delphis*), which present marks caused by fishing gear, indicating these dolphins were incidentally caught. Over time, this level of incidental catch could constitute a significant threat to the common dolphin population in the northeastern Atlantic. The DELMOGES program aims at providing knowledge (from ecological data to management strategies) that is necessary to remedy the issue of common dolphin bycatch. One of the first fundamental questions that must be addressed, is the existence of distinct populations in neritic versus oceanic zones. With that aim, the post-doctoral project will evaluate population structure using two approaches: 1) by analyzing SNPs obtained through RADseq, using tissue samples collected from recently stranded neritic dolphins and biopsy samples collected in the oceanic zone of the Bay of Biscay, and 2) by developing non-invasive sampling strategies to delimit and study observed populations (eDNA approach using filtered seawater collected during the biopsy campaign).

Post-doctoral project: At the LEMAR, the hired post-doc will be in charge of DNA extractions, molecular sexing of biopsied dolphins, RAD library preparation, bioinformatic analysis of RADseq data using a calculation cluster, analyses of SNPs to evaluate population structure, and writing a scientific publication synthesizing the results. During his/her year at MARBEC, the

post-doc will analyze eDNA sequences targeting previously defined SNPs obtained in the first part of the project. For this work, the post-doc will also use a calculation cluster for bioinformatic analyses and will investigate the relevance of using an eDNA approach in this type of population genomic study. The post-doc will be in charge of writing a publication or a report on this second approach.

Candidate profile: Appointment to a post-doctoral position requires that the applicant has a PhD, or an international degree equivalent to a PhD, within the subject of the position, at the time for employment decision. The candidate must have a strong background in population genomics and bioinformatics. Experience in genomic library preparation would be a plus but is not required. Knowledge in the management of protected marine species would also be appreciated.

Working place: The postdoc will be located at the LEMAR (Laboratory of Environmental Marine Sciences) during the first 18 months. The LEMAR is situated within the IUEM (European Institute for Marine Studies) of the University of Western Brittany. The IUEM is located in Plouzané, about 8km away from the center of Brest. The LEMAR is an interdisciplinary laboratory that gathers a total of ca. 150 researchers and technicians and 50 PhD students. The LEMAR includes a molecular ecology lab, with all the necessary equipment to conduct basic labwork (DNA extraction, PCR amplification, etc..) and to construct DNA libraries. The last year of the project will be spent at the MARBEC laboratory. The postdoc will benefit from the experience in eDNA analysis of the team at MARBEC, and from the bioinformatic infrastructure from Ifremer. Both French and English are used as spoken languages in the two laboratories.

Salary: The salary is 1917 euro /month net and 46 days-off/year.

Application: The application must include: 1) a cover letter presenting the research interests and relevant experience of the applicant (max. 2 pages), 2) a curriculum vitae including the list of publications, 3) copies of academic diplomas, and 4) the names and e-mail addresses of two referees. Applications should be sent as a single pdf to [amelia.viricel-pante@univ-brest.fr](mailto:amelia.viricel-pante@univ-brest.fr). The deadline for applications is June 15, 2022. Short-listed candidates will be interviewed on June 30, 2022, in a visio-conference mode.

Expected starting date: from September 1st, 2022

Contacts : Amélia Viricel-Pante ([amelia.viricel-pante@univ-brest.fr](mailto:amelia.viricel-pante@univ-brest.fr)) ; LEMAR, University of Western Brittany) et Sylvie Lapègue ([Sylvie.Lapegue@ifremer.fr](mailto:Sylvie.Lapegue@ifremer.fr))

; UMR MARBEC, Montpellier.

Amelia Viricel-Pante <viricelpa@univ-brest.fr>

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### LoyolaU Chicago FossilSticklebackFish

I'm hiring a postdoc to collect data from a continuous 20,000yr sample of fossil Miocene threespine stickleback fish (*Gasterosteus doryssus*). We are asking questions about evolutionary tempo and mode, and the links between micro and macroevolution. This position is funded by NSF.

Here's the job ad. <https://www.careers.luc.edu/postings/19827> My institution treats postdocs as non-tenure track faculty for some reason. Hence the ask for the formal teaching and diversity statements. Teaching is optional, if the candidate has the interest, wants to bolster their CV, or to extend funding.

My website is [stuartlabloyola.org](http://stuartlabloyola.org). Those interested can find a link to the project summary there. The grant is written for a postdoc, but I would also consider preparators hired as technicians.

Please email me with questions and interest.

Yoel Stuart Assistant Professor Department of Biology  
Loyola University Chicago [ystuart@luc.edu](mailto:ystuart@luc.edu) [stuartlabloyola.org](http://stuartlabloyola.org)

"Stuart, Yoel" <[ystuart@luc.edu](mailto:ystuart@luc.edu)>

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### MaxPlanckJena UHalle InsectSocietyDiseaseDynamics

Applications are invited for a 2-year postdoctoral position in the labs of Yuko Ulrich (Max Planck Institute for Chemical Ecology, Jena, Germany) and Robert Paxton (Martin Luther University Halle-Wittenberg, Halle, Germany).

We are looking for a dynamic, creative, and collaborative postdoctoral researcher to join an interdisciplinary team working at the intersection of behavioral ecology and epidemiology. The project will take place at the Max Planck Institute for Chemical Ecology in Jena ([www.ice.mpg.de](http://www.ice.mpg.de)), in the Ulrich group

([www.ulrichlab.com](http://www.ulrichlab.com)), in close collaboration with the group of Robert Paxton in Halle. The project aims to investigate disease dynamics in colonies of the clonal raider ant by developing a virus-ant model and experimentally studying the impact of social behavior (division of labor, network structure) on viral spread in social groups.

The Max Planck Institute for Chemical Ecology provides a thriving, international, and multidisciplinary research environment. The working language of the institution and of the research group is English. We offer a competitive salary, generous holiday entitlement and pension scheme, as well as career development training. The Max Planck Society is committed to equal opportunities and diversity ([www.mpg.de/equal\\_opportunities](http://www.mpg.de/equal_opportunities)). We welcome qualified applicants from all backgrounds.

To apply, please send your CV with the names and contact details of at least of 2 references, a cover letter (2 pages) describing motivation for the project, research interests and relevant experience, and a digital copy of MSc and PhD certificates or equivalent. Please send applications as a single pdf file, quoting the reference number 4-4758/22-D, via the application portal at <https://apply.idiv.de>. Submission deadline is 09 June 2022.

Informal inquiries about the position can be addressed to Dr. Ulrich ([yulrich@ice.mpg.de](mailto:yulrich@ice.mpg.de)).

Robert Paxton <[robert.paxton@zoologie.uni-halle.de](mailto:robert.paxton@zoologie.uni-halle.de)>  
Robert Paxton <[robert.paxton@zoologie.uni-halle.de](mailto:robert.paxton@zoologie.uni-halle.de)>

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### MichiganStateU Two ComputationalGenomics

Dear colleagues,

The Lehti-Shiu lab is seeking candidates for two postdoctoral positions in Michigan State University:

Position 1: The successful candidate will work on an NSF-funded project to connect sequences to functions within and between species. The specific goals of the project are to 1) use computational modeling to predict the functions of cis-elements and genes based on features such as DNA sequence, methylation, and expression and 2) perform experimental studies to validate the computational predictions. For more details, see: <https://careers.msu.edu/cw/en-us/job/510589/-research-associatefixed-term> Position 2: The postdoctoral scientist will carry out research for the Great

Lakes Bioenergy Research Center (GLBRC), with the duty to identify the genetic basis of the bioenergy crop switchgrass' traits that are relevant for its productivity in marginal lands. The employee will use machine learning computational biology to carry out this research and works alongside other postdocs as well as undergraduate and graduate students and other scientists within the center. For more details, see: <https://careers.msu.edu/cw/en-us/job/510458/research-associatefixed-term> For more information about our lab, please visit our website: <https://shiulab.github.io/> Melissa Lehti-Shiu and Shin-Han Shiu Department of Plant Biology Department of Comp. Math. Sci., & Engr. Michigan State University "Shiu, Shinhan" <shius@msu.edu>

## MichiganTech bioinformatics

Full Job Description: Data Management Developer POSITION TITLE: Postdoc research associate (Ph.D.), Research Associate or Senior Technician (MS/BS) Duties: Development of a data management system for big data storage and retrieval LOCATION: Michigan Tech, Houghton, MI 49931, USA (Working remotely may be considered) JOB TYPE: Full-Time SALARY: \$60,000/Year based on experience QUALIFICATIONS Expected experience (Applicants with the following experience are encouraged to apply.

Applicants with MS degree with experience are also encouraged to apply) - Education - Ph.D. degree required; degree in computer science, computational Engineering, and other STEM majors preferred. MS degree in above field with experience can also be considered; - Experience with DNA sequence data preprocessing and analysis is a plus; - Know SQL, PHP, Python, Java, JavaScript, Perl, and C/C++ to develop data management system, web application, and create pipelines for queries and data retrieval; - Familiarity with relational database management systems - SQL, non- relational database (NoSQL), for example, MongoDB and Cassandra; - Manages the database, the duties include creation, alteration, deletion, and copying of schemas, databases, tables, views, indexes, stored procedures, triggers, and declarative integrity constraints; - Explore the cloud computing using AWS, Azure, or Google cloud; - Can work independently & collaboratively with limited guidance in a small team setting; - English Fluency -be able to speak, write, and understand English.

RESPONSIBILITIES - Determine how data should be

structured, stored, and integrated with existing IT systems; - Design new infrastructure, build data preprocessing pipelines, and collect and organize structured and unstructured sources of information; - Clean and check quality of data; - Develop Web application and integrate of other tools for data analysis; - Generation of statistics, reports, presentations, and visualizations; - Explore the Cloud computing and tools to analyze the data in the storage;

Contact: Prof. Hairong Wei (hairong@mtu.edu )

kristin Brzeski <kbrzeski@hotmail.com>

## NaganoU Two FishDynamics

(1) postdoctoral researcher (Ecology/River Ecological Engineering)

Job Opportunities:

Postdoctoral Researchers (temporary job)

Nagano University - Nagano, Japan

Nagano University is seeking a few trained postdoctoral researchers (Ecology/River Ecological Engineering) to work with a team on a study of the importance of habitat connectivity in rivers and its impact on riverine ecosystems and conservation measures (Project Head: Professor Hiroshi Hakoyama). The project is supported by the Ministry of Land, Infrastructure, Transport and Tourism of Japan, and is going to last for 5 years.

Duties & Responsibilities

(1) Ecology/River Ecological Engineering (field research and experiments). Research will be conducted to evaluate the function of longitudinal continuity (such as mainstream tributaries, upstream and downstream) and transverse continuity (such as riverbanks, recreational areas, open levees, and peripheral habitats) in restoring and preserving ecosystems.

Moreover, the postdoctoral researcher should cooperate and write papers with co-workers, participate in team discussions, assist the members of the team and the lab in all respects, and accept other duties as assigned.

Information

Minimum education: Ph.D. in a related field

Applications: When applying for this position, please send a CV/cover letter and letters of recommendation from the research supervisor or the department head to

Institute of Freshwater Biology, jinji@nagano.ac.jp by e-mail with the title "IFB\_2022".

Deadline to apply: Ongoing (Open until filled)

Location: 1088 Komaki, Ueda, Nagano 386-0031, Japan

Employment period: from 2022/06/01, or as soon as possible, to 2023/03/31. The employment period may be extended based on performance and availability of funding.

Regular work hours: 8:30-17:15 (Break time 12:00-13:00), Monday-Friday

Salary: 300,000-360,000 yen a month (according to research experience and achievements). The absence deduction will be calculated based on the amount of absence hours/days in accordance with the laws on employment.

Employee benefit: Employee must join the Japanese national social (health) insurance and pay employment insurance in accordance with the laws of Japan. Part of the cost is borne by the Employee and deducted from the monthly post-tax remuneration each month on payday (inquiry e-mail address: soumu@nagano.ac.jp). Nagano University will pay the cost of the LCC ticket from your country to Japan at the start of the contract and pay the cost of the return ticket at the end of the contract. Nagano University will pay the cost of a registered guarantor for your apartment.

URL: <https://www.nagano.ac.jp/outline/facilities/ifb/-ifb/> <https://www.nagano.ac.jp/artis-cms/cms-files/-20220517-135531-1489.pdf> —

(2) postdoctoral researcher (Statistician)

Job Opportunities:

Postdoctoral Researchers (temporary job)

Nagano University - Nagano, Japan

Nagano University is seeking a few trained postdoctoral researchers (Statistician) to work with a team on a study about the population dynamics and fisheries management of Japanese eel (Project Head: Professor Hiroshi Hakoyama). The project is supported by the Fisheries Agency of Japan and is going to last for at least several years. The outcome of the project is expected to contribute to discussions at FAO, IUCN, and CITES and policy design and implementation for the management of Japanese eel.

Duties & Responsibilities

(1) Statistician (time-series analysis, mixed-effects models, machine learning, fisheries management, extinction risk assessment, mathematical modeling): analyzing spatiotemporal multivariate time-series of fisheries and en-

vironmental data of Japanese eel; developing statistical and mathematical methods for fisheries management.

Moreover, all postdoctoral researchers should cooperate with each other, write papers with co-workers, participate in team discussions, assist the members of the team and the lab in all respects, and accept other duties as assigned.

Information

Minimum education: Ph.D. in a related field

Applications: When applying for this position, please send a CV/cover letter and letters of recommendation from the research supervisor or the department head to Institute of Freshwater Biology, jinji@nagano.ac.jp by e-mail with the title "IFB-postdoc\_2022".

Deadline to apply: Ongoing (Open until filled)

Location: 1088 Komaki, Ueda, Nagano 386-0031, Japan

Employment period: from 2022/06/01, or as soon as possible, to 2023/03/31. The employment period may be extended based on performance and availability of funding.

Regular work hours: 8:30-17:15 (Break time 12:00-13:00), Monday-Friday

Salary: 330,000-470,000 yen a month (according to research experience and achievements). The absence deduction will be calculated based on the

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## Norwich Bioinformatics

Postdoctoral Research Scientist (Bioinformatics)

Applications are invited for a Postdoctoral Researcher to join the Laboratory of Dr Falk Hildebrand at the Earlham Institute & Quadram Institute based in Norwich, UK.

The Hildebrand group is researching microbial communities, specifically interested in decoding the diversity, community interactions, and evolution of pro- and eukaryotic microbes. The group develops and maintains various metagenomics software tools (see [www.falk.science](http://www.falk.science)).

**Background:**

How quickly can microbes adapt to newly colonized environments?

The Hildebrand group develop tools to reconstruct novel species and delimit even closely related strains. These enable mapping the gut microbial persistence, dispersal and evolution of microbes in microbial communities (doi:10.1016/j.chom.2021.05.008) or the relative distribution of fungi & bacteria (doi: 10.1111/1462-2920.15314) in thousands of metagenomes. However, past work often pointed to the crucial impact of the bacterial pan genomes and species interactions in communities (doi:10.1038/s41586-018-0386-6, 10.1136/gutjnl-2018-317715). These are often captured at insufficient quality with the current generation of sequencing platforms & metagenomic tools (doi: 10.1128/mSystems.00881-21).

**The role:**

In both human gut and soil microbiomes, typically hundreds to thousands of microbial species can be found. By all accounts, their genome architecture seems to be incredibly dynamic, with genes frequently lost or introduced. This process is part of the constant adaptation to the microbe's environment. To understand such processes better, the postholder will develop novel pipelines in metagenomics, that can automatically combine data from PacBio, single cell and Hi-C sequencing. This will enable ultra-resolution metagenomics and be used for comparative genomics based on thousands of metagenomes.

This post will therefore require a highly motivated and experienced bioinformatician, with an interest to compare microbial genomes reconstructed from metagenomes. For this, existing pipelines will be adapted and new pipelines implemented. Datasets the candidate will conduct research are diverse, e.g. gut metagenomes or soil metagenomes. These will be sequenced using 2nd and 3rd generation sequencing platforms and advanced protocols, such as illumina, PacBio, ONT, Hi-C & single cell sequencing data. The analysis will be published in research papers that the candidate should be leading.

**The ideal candidate:**

Candidates should have a PhD in Bioinformatics or related field, with experience in either: metagenomics, population genetics, comparative genomics (eukaryotic or prokaryotic), binning algorithms, single cell sequencing and/or sequencing technologies. The candidate will work independently, with other group members, and with national and international collaborators to generate and analyse data.

Previous experience in publishing scientific results as well as bioinformatics expertise are essential. An interest in community microbiology (such as gut microbiome), genetics and evolution will be advantageous, but prior experience or knowledge of metagenomics is not a requirement. Good organisational skills and the ability to communicate and work productively within a multidisciplinary team will be crucial. Training will be available for multiple aspects of the work.

**Additional information:**

Salary on appointment will be within the range 32,578 to 39,938 per annum depending on qualifications and experience. This is a full-time post for a contract of 3 years.

For further information and details of how to apply, please visit our website <http://jobs.earlham.ac.uk/> or contact the Human Resources team on 01603 450462 or [nbi.recruitment@nbi.ac.uk](mailto:nbi.recruitment@nbi.ac.uk) quoting reference 1004217.

As a Disability Confident employer, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy.

Closing date is Sunday 27 June 2022, interviews will be held on Wednesday 6 July 2022.

Many thanks Dee Denise Pead

Senior Human Resources Advisor NBI Partnership

The NBI Partnership Ltd provides non-scientific services to the Quadram Institute Bioscience, the John Innes Centre, The Earlham Institute and The Sainsbury Laboratory

Norwich Research Park Colney Lane Norwich Norfolk NR4 7UH Tel: 01603 450295 ext 2295 Email: [denise.pead@nbi.ac.uk](mailto:denise.pead@nbi.ac.uk)

Website: <http://nbip.nbi.ac.uk/> "Denise Pead (NBI)" <[Denise.Pead@nbi.ac.uk](mailto:Denise.Pead@nbi.ac.uk)>

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## OhioU PlantEvolution

### POSTDOCTORAL RESEARCH POSITION IN FLORAL EVOLUTION

The Schenk Lab at Ohio University is looking for a Postdoctoral Researcher to start an NSF Funded project in August 1st 2022. The position will be in person in Athens, Ohio for two years and includes travel support for research and conferences.

Brief Project Overview: Flowers have experienced ex-

traordinary morphological changes through evolutionary time that includes multiple origins of novel, non-fertile structures. Because flowers are a complex network of interconnected parts, they provide an ideal system for studying integrated-trait evolution in response to functional cooption. We are investigating coopted floral structures called staminodes, which are sterile stamens that can perform novel functions, such as nectar production, pollinator attraction, or enhanced pollen dispersal or deposition. Staminodes provide an exceptional opportunity for revealing the evolutionary consequences of functional cooption in an integrated system. The project will study staminodes in *Mentzelia* (Loasaceae) to answer the question: Is there an evolutionary response to compensate for the loss of reproductive function when a structure is coopted to perform a novel function?

**Research tasks:** The postdoctoral research associate will be expected to conduct experiments, including genomic library preparation and sequencing, phylogenomics, phylogenetic comparative approaches, morphological characterization of floral traits, floral manipulation experiments with natural pollinators, and field work in the western U.S. The successful candidate will have the opportunity to attend and present work in national and international meetings and publish research results. The postdoctoral research associate will co-mentor undergraduate students and collaborate with a Ph.D. student, research associates, and the PI.

**Qualifications:** The Postdoctoral Scholar must have earned their Ph.D. in Botany, Biology, or a closely related field before August 2022. Successful candidates are preferred to have research experience in plant evolution, phylogenetic comparative approaches, floral morphology and evolution, and/or pollinator ecology.

**Application process:** Please submit a cover letter that outlines your previous research experiences, CV, contact information (name, phone number, email, and mailing address) for three professional references, and one publication that best represents your qualifications to <https://www.ohiouniversityjobs.com/postings/41476>. Applications received by June 5th, 2022 will receive full consideration; however, applications will be reviewed until the position is filled. Please see the above link for additional information about applying and qualifications.

For more information, see: Schenk Lab website: <https://schenklab.weebly.com/> Environmental and Plant Biology at OU: <https://www.ohio.edu/cas/plant-biology> Our NSF funding: [https://www.nsf.gov/awardsearch/showAward?AWD\\_ID=2117446](https://www.nsf.gov/awardsearch/showAward?AWD_ID=2117446) Application link: <https://www.ohiouniversityjobs.com/postings/41476>

Ohio University is proud of its rich history, diverse campuses, international communities, and beautiful

Appalachian settings. As part of our ongoing efforts to provide and support a transformative learning experience, we affirm our commitment to fostering a welcoming, respectful, diverse, and inclusive workforce and community. All qualified applicants are encouraged to apply and will receive consideration free from discrimination on the basis of race, color, religion, age, ethnicity, national origin, national ancestry, sex, pregnancy, gender, gender identity or expression, sexual orientation, military service or veteran status, mental or physical disability, or genetic information. Ohio University is an equal access/equal opportunity and affirmative action employer.

John J. Schenk, Ph.D. Assistant Professor Department of Environmental and Plant Biology Ohio University 401 Porter Hall Athens, Ohio 45701-2979 Office phone: ???(740) 593-0716 E-mail: [schenk@ohio.edu](mailto:schenk@ohio.edu) Lab website: <https://schenklab.weebly.com> “Schenk, John” <[schenk@ohio.edu](mailto:schenk@ohio.edu)>

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## PennsylvaniaStateU AvianGenomics

Postdoctoral Researcher in Avian Genomics / Phylogenomics

A NSF-funded Postdoctoral Scholar position is available at The Pennsylvania State University < <https://psu.edu/> > to study comparative genomic and phylogenomic patterns of North, Central, and South American wood warblers, under the supervision of Dr. David Toews (<http://www.davetoews.com>). We study the evolutionary biology, genomics, and molecular ecology of birds using a range of bioinformatic tools. The position requires a Ph.D. degree in biology, evolutionary biology, bioinformatics, genomics, or a related field. Familiarity with R and/or experience using a computing cluster environment is preferred.

This is a limited-term appointment funded for one year from date of hire, with excellent possibility of refunding.

If you are interested, applications must be submitted electronically and include a cover letter and a CV (including names of two referrals). For further information, please email Dr. David Toews at [toews@psu.edu](mailto:toews@psu.edu). Review of applications will begin immediately and continue until the position is filled.

[https://psu.wd1.myworkdayjobs.com/en-US/-PSU\\_Academic/details/Postdoctoral-Scholar—Toews-Lab\\_REQ\\_0000029155-1?q=Lab\\_REQ\\_0000029155](https://psu.wd1.myworkdayjobs.com/en-US/-PSU_Academic/details/Postdoctoral-Scholar—Toews-Lab_REQ_0000029155-1?q=Lab_REQ_0000029155)

David Toews <toews@psu.edu>

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### Royal Botanic Gardens Kew Crop Domestication Genomics

We have an exciting opportunity for a Post Doc to work on the NERC funded project “Evolutionary dynamics of vegetative agriculture in the Ethiopian Highlands: integrating archaeobotanical and genomic science” (<https://gtr.ukri.org/projects?ref=NE%2FW005689%2F1>). You will work with Dr James Borrell and Dr Philippa Ryan at Royal Botanic Gardens, Kew, in collaboration with Prof Dorian Fuller at the Institute of Archaeology, University College London.

Enset is a giant perennial herb that provides the staple food for 20 million people, but outside of Ethiopia, this remarkable banana relative is virtually unknown. Like many tropical clonal crops, which tend to preserve poorly in the archaeological record, enset’s domestication history is poorly understood. Yet today we observe over a thousand unique landraces, many with traits specialised for disease tolerance, taste, co-products and other useful attributes.

The successful applicant will make a major contribution to understanding how farmers selected and cultivated this diversity, and over what time period, helping to unravel the mystery of enset domestication. This has significant applications in supporting the adaptation of enset and other clonal crops to climate change. The successful applicant will also form part of a vibrant, dynamic and cross disciplinary scientific environment, with access to Kew’s state-of-the-art laboratory facilities and opportunities to develop professional skills for the next stage of their career. This role coincides with a major new collaboration between Kew and the UCL Institute of Archaeology as we apply novel approaches combining genomics and archeobotany.

The ideal candidate will have a PhD in genomics or a related discipline, together with a strong interest in crop evolution and domestication and a track record of research publications commensurate with their career stage. They will be excited at the opportunity to integrate archeobotanical evidence (e.g. phytoliths, macro remains) from sites across the Ethiopian highlands, together with environmental and cultural diversity data to help parameterise genomic models. They will also be confident with developing novel methodologies, bioinformatic analysis, data management and communicating

their research through publications and conferences. We particularly welcome applicants that wish to contribute their own ideas and help to shape our research direction.

For informal enquiries please contact Dr James Borrell ([j.borrell@kew.org](mailto:j.borrell@kew.org)) or Dr Philippa Ryan ([p.ryan@kew.org](mailto:p.ryan@kew.org)).

This role is based at Kew with the option of regular home working, subject to operational requirements.

The salary will be pounds 34,933 per annum (pro rata).

More info: <https://careers.kew.org/vacancy/post-doctoral-research-associate-crop-domestication-genomics-487493.html> Post doctoral Research Associate: Crop Domestication Genomics < <https://careers.kew.org/vacancy/post-doctoral-research-associate-crop-domestication-genomics-487493.html> >

The salary will be pounds 34,933 per annum (pro rata). Our fantastic benefits package includes opportunities for continuous learning, a generous annual leave entitlement, flexible working to help you maintain a healthy work-life balance, an Employee Assistance Programme and other wellbeing support such as cycle to work scheme and discounted gym membership. [careers.kew.org](http://careers.kew.org)

Dr. James Borrell

Research Fellow

Royal Botanic Gardens, Kew,

Richmond, Surrey TW9 3AE

[j.borrell@kew.org](mailto:j.borrell@kew.org)

[www.jamesborrell.com](http://www.jamesborrell.com)

The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, United Kingdom.

James Borrell <[J.Borrell@kew.org](mailto:J.Borrell@kew.org)>

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### Royal Botanic Gardens Kew Forest Conservation Genetics

Royal Botanic Gardens Kew is recruit two Post-Docs in the area Plant Health, evolutionary genomics and conservation genetics. These projects will be part of the new Centre for Forest Protection, funded by the Department for Environment, Food and Rural Affairs (Defra).



The two projects are:

Evaluating genetic bottlenecks in planted and naturally colonised young woodlands (<https://careers.kew.org/vacancy/postdoctoral-researcher-in-forest-conservation-genetics-486905.html>) The Center for Forest Protection is a major new initiative, jointly led by Forest Research and Royal Botanic Gardens Kew, that aims to enhance the future resilience of forests and woodlands (<https://www.forestprotection.uk/>). The successful applicant will form an integral part of a new project within the Center for Forest Protection, aiming to evaluate genetic bottlenecks in planted and natural colonised young woodlands in the UK. The successful applicant will also form part of a vibrant, dynamic and cross disciplinary scientific environment, with access to Kew's state-of-the-art laboratory facilities and opportunities to develop professional skills for the next stage of their career. With a major new investment in this area, this is an exciting time to join the team.

The UK has committed to establishing 30,000 ha of new woodland annually by 2050. We know that genetic diversity underpins the resilience and future adaptive potential of our tree populations, and that maintaining this diversity is a key goal of the UK Forest Genetic Resources strategy. However, as we move towards ambitious afforestation goals, there is a major knowledge gap around the resulting genetic diversity in planted versus naturally colonised woodlands and how this will influence resilience to environmental change, pests and diseases.

Where we rely on tree planting for large-scale afforestation, a significant danger is that commercial seed collection, germination, nursery cultivation and/or planting inadvertently introduces genetic bottlenecks or selection at one or more life stages. On the other hand, maximising germination and survival through the provision of highly favourable growing conditions during nursery production could result in more diverse populations, which through natural selection are better able to keep pace with emerging stressors. This project seeks to provide key evidence to address this knowledge gap and feed in to best practice for afforestation. The successful candidate will hold a PhD in a relevant discipline, with a track record of research commensurate with their career stage. They will lead research seeking to understand the population genetics of planted and naturally colonised woodlands. They will also be confident with developing sampling strategies, conducting field and lab work, bioinformatic analysis, and communicating their research through publications and conferences.

This role will collaborate extensively with scientists at Forest Research, as well as building relationships with

stakeholders in the tree production industry and policy makers via Defra. This position represents an exciting opportunity to shape future tree planting strategies, with policy implications both in the UK and internationally.

Distribution and diversity of existing UK elm trees (<https://careers.kew.org/vacancy/postdoctoral-research-associate-485419.html>)

Since 1970 Dutch elm disease (DED) has killed an estimated 60-100 million elms in Britain, with the fungal pathogen *O. novo-ulmi* spread almost exclusively by two species of Scolytus bark beetles which feed on healthy elms and but use dying elms as breeding material. Nowadays, few mature elms remain in the UK landscape although rare old survivors do occur, some of which may have natural field resistance. Young elms regenerate constantly and tend to survive 10-20 years. This means that the smaller vector beetle, *S. multistriatus* can breed successfully but the larger *S. scolytus* may have become scarce. However, there has been little study of how beetle populations may have changed in the past 30-40 years. Several breeding programmes in Europe have crossed resistant Asiatic elms with European species to produce *O. novo-ulmi* resistant cultivars. Pure U. minor clones taken from older trees that have survived DED in Spain have been propagated. Many of these putatively resistance elms have been planted in the UK.

The project aims to do the following: (1) Collect, review and combine existing key data on resistant elm plantings and older survivor elms in Britain into a single accessible database and map. (2) Evaluate the durability of already planted resistant elm cultivars under DED pressure. (3) Establish the current presence and relative frequency of

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## SGN Frankfurt Biodiversity

Job announcement ' Ref. #04-22004

For over 200 years the Senckenberg Gesellschaft für Naturforschung (SGN) represents one of the most relevant institutions investigating nature and its diversity.

Currently, scientists from more than 40 countries across 11 locations in Germany conduct research in the fields of biodiversity, earth system analysis and climate change.

Following its mission to “analyze and document biodiversity in earth system dynamics ’ to serve science and society” Senckenberg stands for curiosity-driven and application-oriented collections-based research.

The Department of River Ecology and Conservation at Senckenberg in cooperation with the Faculty of Biology at the University of Duisburg-Essen jointly invite applications for a

Postdoctoral Researcher (Ecologist) (m/f/d) (full time; 2 years with option for extension)

We are looking for an enthusiastic ecologist (m/f/d) with a background in community ecology, macroecology, metacommunities, and/or analysis of ecological time series. The applicant should have a strong track record of scientific publications.

The position is partly embedded in the International Long-Term Ecological Research (ILTER) network and the European Long-Term Ecosystem, critical zone and socio-ecological Research Infrastructure (eILTER RI). The eILTER RI comprise ~200 eILTER sites from over 20 participating European countries, providing access to a wide range of long-term biodiversity and environmental data. This provides a fantastic opportunity to become part of a global network of established researchers, post-docs, and graduate students working with long-term monitoring data.

The postdoc will investigate trends in ecological communities over time and space, and identify drivers of ecological variation. We can provide access to large-scale and long-term biodiversity and environmental datasets covering various terrestrial, freshwater and marine taxa groups depending on candidate interests. As an example, we have compiled more than 1,800 time series of stream invertebrates from 22 European countries which is among the most comprehensive biodiversity time series compilation in Europe. We encourage applications from ecologists with backgrounds in terrestrial and/or freshwater systems.

Your potential tasks:

Analyzing biodiversity time series and accompanied environmental data to elucidate temporal trends in taxonomic and functional diversity and their drivers  
Contribute to the research of the eILTER PLUS project and conduct research on global change impacts on biodiversity within the framework of other projects in the department (i.e. restoration ecology, multiple stressor analyses, long-term ecological research)  
Data analysis,

preparation of manuscripts and reports  
Involvement in national and international projects, including the support of the ILTER science chair  
Mentoring graduate students  
Your profile:

PhD in Ecology or a related field  
Solid background in (macro-) ecology and zoology (preferably invertebrates)  
Advanced skills in statistical analyses of large ecological datasets, preferably using R  
Strong track record of international publications  
Excellent written and oral communication and project presentation skills  
Salary and benefits are according to a public service position in Germany (TV-H E13, 100%). The contract should ideally start around August 1st, 2022 and will initially be initially restricted to 2 years with a possible extension.

The Senckenberg Research Institute supports equal opportunity of men and women and strongly encourages women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Gelnhausen, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application until June, 13th 2022, preferably by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref. #04-22004) and include

a letter outlining your suitability for the post, a detailed CV, certificates and credentials, contact details of 2 references, a list of publications and acquired funding to: Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt

E-Mail: [recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)

Applications can also be submitted via our online application tool: <https://www.senckenberg.de/de/karriere/-bewerbung/> For scientific enquiries please get in contact with Prof. Dr. Peter Haase. E-Mail:

[peter.haase@senckenberg.de](mailto:peter.haase@senckenberg.de)

Yours sincerely

Isabel Gajcevic, M.A.

Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung

(Rechtsfähiger Verein gemäß § 22 BGB)

Senckenberganlage 25

60325 Frankfurt am Main

Besucheradresse: Mertonstraße 17-21, 60325 Frankfurt am Main (1. OG)

Telefon/Phone: 0049 (0)69 / 7542 -

Leiterin Personal & Soziales

- 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales

- 1319 Elsen, Carina



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## SGN Frankfurt MolluscMethylation

Job Announcement ref. #12-22008

The LOEWE Center for Translational Biodiversity Genomics (LOEWE-TBG, <https://tbg.senckenberg.de/>) aims at making the genomic basis of biological diversity accessible for basic and applied research. Building on genome sequencing and analysis, LOEWE-TBG research topics range from comparative genomics, natural products genomics, and genomic biomonitoring to functional environmental genomics. LOEWE-TBG is based in Frankfurt am Main, Germany, and is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology.

The Senckenberg Gesellschaft für Naturforschung and the LOEWE -TBG invite applications for a PostDoc Candidate (m/f/d)

Epigenetics and DNA methylation in molluscs

We are seeking highly motivated PostDoc candidates with interest in epigenetics and DNA methylation. The project involves functional evaluation of DNA methylation in the sacoglossan sea slug species *Elysia timida* as a model system to understand the fundamental roles of this epigenetic mark in the phylum Mollusca and to identify potential genes important for successful chloroplast incorporation (functional kleptoplasty). Epigenetic mechanisms regulate the interpretation of genetic information and adapt gene expression patterns to changing developmental or environmental conditions. Several epigenetic mechanisms have been identified to date, with DNA cytosine methylation being the best studied and possibly the most important epigenetic mark. The project will be supported by the excellent laboratory and bioinformatics facilities of the center.

Your tasks - Establishment of a culture of the alga *Acetabularia acetabulum* and *E. timida* at LOEWE-TBG - Perform experimental time series (whole genome bisulfite sequencing (WGBS) / RNA-seq) during the life cycle of *E. timida* - Perform subsequent bioinformatic analyses of whole-genome bisulfite sequencing and RNAseq data using existing recipes/scripts - Publication of results in high-profile international journals

Your profile - PhD in evolutionary biology, molecular biology, computational biology/bioinformatics or a related subject - Experience with analyzing WGBS and RNA-seq data (scripting in R or python would be beneficial) - Teamwork oriented and excellent communication skills with proficiency in written and oral English - Interest to collaboratively work in an interdisciplinary, international team

What is awaiting you? - An interesting task in a dynamic team of researchers in an international research group and joining the new LOEWE TBG excellence centre with its 20 new research groups - A relevant and timely research topic - The possibility to create a network with scientists in interdisciplinary fields in translational biodiversity genomics - Flexible working hours - dual career service - leave of absence due to family reasons (certified by “auditberufundfamilie”) - parent-child - office - annual special payment - company pension scheme - Senckenberg badge for free entry in museums in Frankfurt - leave of 30 days/year

Place of employment: Frankfurt am Main Working hours: Full time (100% position, 40 hours/week) Type of contract: 2 years, starting as soon as possible Salary: according to the German collective agreement TV-H (pay grade E 13) The Senckenberg Gesellschaft für Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The employer is the Senckenberg Gesellschaft für Naturforschung.

How to apply Please send your application, mentioning the reference of this job offer (ref. #12-22008) until 06 June 2022 (deadline), by e-mail (attachment in a single pdf document) including a brief cover letter detailing your research interests and experience (1 page), a CV and copies of your certificates, transcripts and grades to:

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt a.M. E-Mail: [recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)

For scientific information please contact Dr. Carola Greve, E-Mail [carola.greve@senckenberg.de](mailto:carola.greve@senckenberg.de)

Dr. Carola Greve (Lab and Project manage-

ment) Zentrum für translationale Biodiversitätsgenomik (LOEWE-TBG) Tel.: +49 69 7542 1844 Mail: Carola.Greve@senckenberg.de

Senckenberg Gesellschaft für Naturforschung  
Rechtsfähiger Verein gemäß § 22 BGB Senckenberganlage 25 60325 Frankfurt

Direktorium: Prof. Dr. Klement Tockner, Prof. Dr. Andreas Mulch, Dr. Martin Mittelbach, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Karsten Wesche  
Präsidentin: Dr. h.c. Beate Heraeus  
Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Mitglied der Leibniz-Gemeinschaft

<http://www.senckenberg.de>



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## SGN Frankfurt Systematics

Job announcement ref. #01-22020

The Senckenberg Gesellschaft für Naturforschung (Senckenberg Society for Nature Research, [www.senckenberg.de](http://www.senckenberg.de)) is a member of the Leibniz Association. About 850 people, at seven institutes across Germany, work on the Earth System, exploring a systemic understanding of nature and its interactions with the Anthroposphere. Furthermore, the Senckenberg natural history museums are places of learning and wonder and serve as open platforms for a democratic dialog with society.

Senckenberg is seeking applications for the position of a Postdoctoral Researcher (m/f/d)

We are looking for a postdoctoral researcher with an excellent background in molecular systematics/evolutionary biology. Experience with laboratory techniques and phylogenetic/population genetic analysis of DNA are essential. Organisational skills, a teaching record and willingness to apply for external funds are also expected. A proficiency of English is essential. Knowledge or the willingness to acquire command of the German language is desired.

We expect the successful applicant to participate in the research programs of the department at least with

part of his/her research activities. The position entails the supervision of our “Grunelius-Möllgaard-laboratory for Molecular Systematics and Evolution” and limited teaching obligations. Your tasks

Pursue your own research on plant or fungal systematics, phylogeny and/or evolution individually and together with colleagues from Senckenberg  
Publish research results in international peer-reviewed journals  
Supervise the Grunelius-Möllgaard lab for Molecular Evolution-  
Participate in teaching and outreach activities of the department  
Your profile

A PhD degree in biology with a focus on plants or fungi-  
Experience with the generation and analysis of molecular genetic data  
Interest in the systematics and evolution of plants or fungi  
Good writing skills and command of English  
Salary and benefits are according to a full-time public service position in Germany (TV-H E 13, 100 %).  
The position is a two years-term post, starting from 1 July 2022.

The Senckenberg Research Institutes support equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany.

Please send your application, mentioning the reference of this job offer (ref.#01-22020) before May, 31st 2022 by e-mail (attachment in a single pdf document) and including a cover letter describing your motivation to apply, a detailed CV and contact details of two potential referees to:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25 60325 Frankfurt am Main

E-Mail: [recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)

For scientific questions don't hesitate to contact Dr. Christian Printzen [Christian.printzen@senckenberg.de](mailto:Christian.printzen@senckenberg.de).

Mit freundlichen Grüßen /Best Regards Maria di Biase  
Personalsachbearbeiterin SENCKENBERG Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß § 22 BGB) Senckenberganlage 25 60325 Frankfurt am Main

Besucheradresse: Mertonstraße 17-21, 60325 Frankfurt am Main (1. OG) Telefon/Phone: 0049 (0)69/ 7542 - Leiterin Personal & Soziales - 1458 Loke, Uta  
Stellv. Leiterin Personal & Soziales - 1319 Elsen, Carina  
Team Personalbeschaffung (Recruiting) -1564 di-Biase, Maria - 1204 Reitinger, Jasmin - 1478 Gajcevic, Isabel  
Fax: 0049 (0)69/ 7542-1445 Mail:

[recruiting@senckenberg.de](mailto:recruiting@senckenberg.de) Direktorium: Prof. Dr. Klement Tockner, Prof. Dr. Andreas Mulch, Dr. Martin Mittelbach, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr.

Karsten Wesche

Präsidentin: Dr. h. c. Beate Heraeus  
Aufsichtsbehörde:  
Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Mitglied der Leibniz-Gemeinschaft

Vernetzen Sie sich mit uns: [www.senckenberg.de/-socialmedia](http://www.senckenberg.de/-socialmedia)  
Maria Di Biase  
<recruiting@senckenberg.de> Maria Di Biase  
<recruiting@senckenberg.de>

## StockholmU FungalAdaptation

Postdoc-position available at the Department of Ecology, Environmental and Plant Sciences, Stockholm University

A postdoctoral research position in Fungal Biology is available at the Department of Ecology, Environmental and Plant Sciences, Stockholm University. This postdoc offers an opportunity to explore fungal adaptation to extreme environments. The postdoc-project can be developed after the interest of the applicant, and may involve genome analyses, degradation assays, lab and/or field experiments.

Motivation: Crude oil and petroleum products are of specific concern in pollution studies due to their structural complexity, slow biodegradability, biomagnification potential, and the serious health hazards associated with their release into the environment. Bioremediation, that makes use of natural microbial biodegradation activity, constitute an attractive alternative to physicochemical methods for restoration of PHC polluted environments. By the study of fungal genomics, transcriptomics, proteomics, metabolomics, and other high-throughput methods, it is becoming increasingly evident that fungi hold a wide array of characters making them able to live in extreme environments. In this project, we will investigate the microbial community in the underground mining facility in Kiruna (Kiruna underjordsgruva, KUJ), which is contaminated with pollutants because of the use of petroleum products for maintenance of machinery. Isolates from the mine are available in the laboratory, and these can be studied for their degrading capacity and genomic adaptations.

The research will be conducted within the Johannesson research group, within the Department of Ecology, Environmental and Plant Sciences, Stockholm University. Johannesson group is currently moving to Stockholm from Uppsala University, see the group-info

here: <https://www.iob.uu.se/research/systematic-biology/johannesson/> For more information about the Department, see here: <https://www.su.se/department-of-ecology-environment-and-plant-sciences/about-the-department> Required qualifications for applicants are 1) a PhD in Biology, Genetics, Evolutionary Biology, Genomics, Microbiology or related field, 2) experience in one or several of the following areas: bioinformatics, biochemistry, microbiology, mycology, and 3) demonstrated communication skills in English.

The position is a two-year scholarship, financed from Carl Trygger Foundation. Review of applications will begin immediately and continue until the position is filled.

To apply, send your CV, including contact information for two references, and a cover letter stating your research interest to: Dr Hanna Johannesson, [hanna.johannesson@ebc.uu.se](mailto:hanna.johannesson@ebc.uu.se).

Ni<sub>2</sub>r du har kontakt med oss på Uppsala universitet med e-post så innebär det att vi behandlar dina personuppgifter. För att liksom mer om hur vi gör det kan du liksom 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> Hanna Johannesson <[hanna.johannesson@ebc.uu.se](mailto:hanna.johannesson@ebc.uu.se)>

## StockholmU InsectSpermEvolution

Postdoctoral Fellow in Insect Sperm Evolution at the Department of Zoology, Stockholm University

Closing date for applications: 15 July 2022

Before applying see “Qualification Requirements” below.

The position will be held in the Department of Zoology at Stockholm University which consists of five divisions: Ecology, Ethology, Functional Zoomorphology, Population Genetics and Systematics & Evolution. The department accommodates 45-50 staff and a similar number of PhD students. The advertised postdoctoral position will be placed in the Division of Ecology at the Department of Zoology.

Project description

The successful candidate will be part of an interdisciplinary research project, based at Stockholm University

in the lab of Professor Rhonda Snook. The aim of the work is “The evolution of sperm cell shape and motion” in insects funded by the Human Frontiers Science Program with research partners at the University of Lincoln (UK) and Tulane University (USA). The overall aim in the Snook lab will involve 1) phylogenetic analyses addressing evolutionary diversity in sperm shape in insects, 2) assessing how intraspecific variation in sperm length impacts sperm movement and function within the female reproductive tract using molecular biology techniques and microscopy, and 3) testing the relationship between sperm length and sperm motility in the closed system of the female reproductive tract using experimental analogues of the female reproductive tract and biophysical modelling lead by consortium partners. This is an innovative and collaborative opportunity to combine diverse the fields of phylogenetic analysis, molecular biology, applied mathematics and biophysics to understand the evolution of the wide diversity of sperm shapes. For work in the Snook lab, a strong candidate will have a background in either evolutionary biology or molecular biology and a deep interest in microscopy and/or spermatogenesis. There is scope to develop parallel projects for an organized candidate.

**Main responsibilities** The position is 100% research within the project described above.

**Qualification requirements** Salary is provided as a tax-free scholarship stipend of 27500 SEK per month. Thus, only non-Swedish citizens with a doctoral degree or similar equivalent acquired in a country other than Sweden can apply. The degree must have been completed at latest before the employment decision is made, but no more than three years before the closing date. An older degree may be acceptable under special circumstances. Special reasons refer to sick leave, parental leave, elected positions in trade unions, service in the total defense, or other similar circumstances as well as clinical attachment or service/assignments relevant to the subject area.

**Terms of employment** The position involves full-time employment for a year in the first instance. Following satisfactory progression, another year can be appointed. There is the possibility of extension for a third year. Start date no sooner than September 1, 2022 or as per agreement after.

Stockholm University and the Snook lab strives to be a workplace free from discrimination and with equal opportunities for all.

**Evaluation Criteria** In the appointment process, special attention will be given to candidates with a strong background in either evolution or molecular biology and a willingness to learn analytical methods. Prior train-

ing in insect rearing desirable and a keen interest in microscopy and/or spermatogenesis is beneficial. It is not expected that the postdoc have prior mastery of all these elements. Given the interdisciplinary and collaborative nature of the funding, applicants should be good communicators and happy to work in an international team with biologists, biophysicists and mathematical modellers, spread across three countries, as well as work independently to solve challenging technical problems. Working language in the lab is english.

**Contact** Further information about the position can be obtained from Professor Rhonda R Snook, rhonda.snook@zoologi.su.se.

**Application** Apply for the position at jobs@zoologi.su.se It is the responsibility of the applicant to ensure that the application is complete in accordance with the instructions in the job advertisement, and that it is submitted before the deadline. Please include the following information in your application as a combined pdf file entitled “XX app Snook” where XX is your name. - Cover letter outlining why you are interested in, and what makes you suitable for, the position (no more than 2 pages) - Your CV - including contact details, degrees and other completed courses, work experience and a list of publications - Contact details for 2-3 references - Copy of PhD diploma (if you have received your PhD; you will need to provide this before starting if you have not finished yet)

You are welcome to apply!

Rhonda R Snook Professor Ecology Division Department of Zoology Stockholm University, Sweden

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## Sydney EvolutionaryBiology

**POSTDOCTORAL RESEARCH ASSOCIATE IN EVOLUTIONARY BIOLOGY** - Full time 3 years fixed term at the University of Sydney, Australia - Join an exciting collaborative research group - Base salary starts at AU\$95,047 p.a. + 17% employer contribution to superannuation - Flexible starting date

**POSITION SUMMARY** We are seeking a motivated

and enthusiastic PhD graduate to work on rates of evolution and models of macroevolutionary change. The successful candidate will be part of the Molecular Ecology, Evolution, and Phylogenetics Lab, led by Professor Simon Ho and Professor Nathan Lo. The position is funded by the Australian Research Council Discovery Project “Testing links between genomic and morphological evolutionary rates” and involves collaboration with Dr Hervé Sauquet at the Royal Botanic Gardens (Sydney).

**KEY RESPONSIBILITIES** - lead research projects on rates of evolution and models of macroevolutionary change - analyse large genomic data sets from plants, animals, and bacteria to address key questions in evolutionary biology - work effectively as part of a team and collaborate with external researchers - present the results of the research at seminars and conferences - write papers for publication in peer-reviewed journals.

**ABOUT THE SCHOOL** The School of Life and Environmental Sciences (SOLES) is a large and research-active school with expertise in ecology, evolutionary biology, conservation, microbiology, biochemistry, molecular biology, and agriculture. It brings together diverse researchers and students to improve teaching and enhance research capacity. To learn more about SOLES, see: <https://www.sydney.edu.au/science/schools/school-of-life-and-environmental-sciences.html>

**ABOUT YOU** The University values courage and creativity; openness and engagement; inclusion and diversity; and respect and integrity. As such, we see the importance of recruiting talent aligned to these values and are looking for a Postdoctoral Research Associate who has: - a PhD in Molecular Evolution, Phylogenetics, Computational Biology, or closely related discipline - strong skills in macroevolutionary analysis and Bayesian phylogenetics - experience in analysing genomic data - experience in Python and R - demonstrated independence in conducting research and other scholarly activities

**HOW TO APPLY** For further information, contact details, and a link to the application form, see: [bit.ly/sydney-postdoc-evo](https://bit.ly/sydney-postdoc-evo) or search for position 0092374 in Careers at Sydney (<https://www.sydney.edu.au/about-us/careers-at-sydney.html>) Please direct any questions about the position to Simon Ho ([simon.ho@sydney.edu.au](mailto:simon.ho@sydney.edu.au))

“[simon.ho@sydney.edu.au](mailto:simon.ho@sydney.edu.au)” <[simon.ho@sydney.edu.au](mailto:simon.ho@sydney.edu.au)>

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## TempleU ComparativeGenomics

The Liberles Research Group (<https://sites.temple.edu/liberles/>) is looking for a 1 year NSF-funded postdoctoral fellow to join the group at Temple University. This work is collaborative with David Alvarez-Ponce at University of Nevada and Krisztina Varga at University of New Hampshire. The Liberles Group works on computational comparative genomics and molecular evolution, with a focus on modeling the evolutionary genotype-phenotype map. The main project that the postdoc would work on involves characterization of selection on protein stability modulated by amino acid substitution and how various biological factors influence it. This involves a combination of evolutionary, protein structural, and statistical analysis. Other ongoing projects in the group include modeling duplicate gene retention and modeling metabolic pathway evolution, both in a phylogenetic context.

The group is embedded in the Center for Computational Genetics and Genomics, creating a high level training environment that enables interaction with other research groups working in computational genomics, molecular evolution, evolutionary ecology, and population genetics.

The ideal candidate will have strong programming and statistics skills with a background in evolutionary biology and/or protein biophysics.

The group works at Temple University in Philadelphia, PA, USA. While there is a slight preference for someone who can work locally in Philadelphia, remote applications (including international ones) will receive full and serious consideration. To apply, please send your CV, a cover letter indicating career goals and research interests, and contact information for three professional references to [daliberles@temple.edu](mailto:daliberles@temple.edu).

David A Liberles <[daliberles@temple.edu](mailto:daliberles@temple.edu)>

[daliberles@temple.edu](mailto:daliberles@temple.edu)

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## TrentU ConservationGenomicsCaribou

Dr. Paul Wilson (Trent) and Dr. Micheline Manseau (ECCC, Trent) through EcoGenomics (ecogenomicscanada.ca), a long-term national scale program, are recruiting PhDs and Post-doctoral Fellows (PDFs) focusing on genomic applications to caribou conservation. This national-scale collaborative research program on caribou conservation genomics is supported by whole-genome sequences of caribou representing diverse subspecies, ecotypes and populations, with additional genomes being planned for sequencing, and development of targeted caribou-specific loci for Population Genomic surveys of a long-term (20-year) database of samples (40,000 across Canada). The national network supporting these positions include partnerships with Environment & Climate Change Canada; Canadian Wildlife Service; Parks Canada; the Ontario Ministry of Northern Development, Mines, Natural Resources & Forestry, Ontario Ministry of the Environment, Conservation and Parks and other provincial (e.g. Alberta, British Columbia, Manitoba, Saskatchewan) and territorial jurisdictions (Northwest Territories, Yukon, Nunavut); wildlife management boards and Indigenous communities (e.g. the Sahtu Wildlife Management Board); and industry such as MB Hydro. Positions may be based out of Peterborough, Ontario at Trent University or Ottawa at the National Wildlife Research Centre, Environment & Climate Change Canada.

The following positions/projects are available:

PDF studying Demographic Parameters in caribou ranges across Canada using applications such as spatial capture-recapture (sCR); density estimation; population modelling; and network analyses. Position requires strong quantitative skills, and experience in software development will be considered an asset.

PDF in establishing metrics for large-scale and long-term Genomic Monitoring of caribou through the implementation of sequencing technologies, e.g. high/low coverage genomes and amplicon sequencing, and development of analytical pipelines. Position requires strong bioinformatic skills, and knowledge of molecular genomic protocols will be considered an asset.

PhDs supporting the above projects will be considered in addition to projects related to caribou ecotype dynamics in Ontario's Ring-of-Fire region; assessment of

genomic erosion in isolated caribou populations (natural and captive) and at the southern range margins of boreal caribou; and an assessment of rapidly evolving genomic elements in adaptive genes of caribou subspecies and ecotypes across Canada.

Starting dates flexible for all positions

<https://www.ecogenomicscanada.ca/phd-and-pdf-recruitment-may-2022/> Send a Cover Letter and CV to: pawilson@trentu.ca or micheline.manseau@ec.gc.ca

Bridget Redquest

Laboratory/Project Manager Trent University

2140 East Bank Drive Peterborough, ON K9L 1Z8  
Phone: (705)748-1011 ext 6657/7313

Bridget Redquest <bridgetredquest@trentu.ca>

bridgetredquest@trentu.ca

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## UAlgarve PoppyDomestication

Postdoc:

OpiumPoppyDomestication

Postdoctoral Position at the University of Algarve, Portugal.

**OVERVIEW** We are accepting applications for a two-years post doctorate fellow position in plant transcriptomics, to investigate the domestication and spread of the opium-poppy (*Papaver somniferum*). The candidate will investigate changes in gene expression between wild and cultivated accessions as well as analyse genotype-by-sequencing data of a global panel of poppy accessions, including different wild species. The project is a collaboration with archaeobotanists at the Muséum National d'Histoire Naturelle in Paris (France) and the Deutsches Archäologisches Institut in Berlin (Germany).

The candidate will have obtained a PhD (or concluding one before the beginning of the grant) in Biological Sciences, preferably in the field of Botany, Plant Physiology or Plant Molecular Biology. The candidate will have bench experience in analysing plant gene expression (ideally using RNA-seq), as well as in RNA extraction and quantification. Experience in the analysis of next-generation sequencing data and programming skills in R or Python are considered a plus. The position is meant to start as early as July 2022.

**HOW TO APPLY**



Applications must be accompanied by the following documents:

- Official identification document (simple copy or legal equivalent). If you have a nationality other than Portuguese, you should present a residence permit, permanent residence certificate or long-term resident status, valid on the scholarship start date, any of which may be replaced, in its absence, by a declaration of commitment. However, one of the previous must be delivered at the contracting phase, under penalty of forfeiture of the granting of the scholarship;
- Copy of the qualification certificates of the academic degrees held, specifying the final classification and, if possible, the classifications obtained in all subjects taken;
- If the doctorate has been awarded by a foreign higher education institution, it must conform to the rules established in Decree-Law no. 66/2018 of August 16, and all required formalities must be complied with up to the date of termination deadline for submission of the application. If the completed process is not found until the end of the application deadline, the candidate must prove that he / she has requested the recognition of the degree;
- Curriculum Vitae;
- Passport or identification card for European applicants (copy);
- Taxpayer Identification Number (NIF), if you have a nationality other than Portuguese, it must be submitted during the scholarship contracting phase, under penalty of forfeiture of the scholarship award;

See the link below for full details.

<https://euraxess.ec.europa.eu/jobs/763980> Review of applications begins on end-May 2022.

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

Kind regards,

Hugo R. Oliveira (PhD Cantab.) Interdisciplinary Centre for Archaeology and the Evolution of Human Behaviour (ICArEHB) Universidade do Algarve Campus de Gambelas 8005-139 Faro Portugal [http://www.icarehb.com/hugo\\_rafael\\_oliveira/](http://www.icarehb.com/hugo_rafael_oliveira/) <https://twitter.com/HugoRCOliveira> Hugo Rafael Cardoso Oliveira <hroliveira@ualg.pt> Hugo Rafael Cardoso Oliveira <hroliveira@ualg.pt>

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## UArizona TheoryDensityDependence

Postdoc position: density-dependent selection theory

A postdoc position is available with PI Joanna Masel (<http://www.eebweb.arizona.edu/faculty/masel/people/joanna/>) at the University of Arizona in Tucson. The position is amenable to remote work, and efforts will be made to accommodate all situations. That said, collaboration with an in-Tucson Ph.D. student is expected, and Tucson is located in the biodiverse Sonoran desert, surrounded on all four sides by mountainous national and state parks, with an attractive climate for most of the year. Stipend is at NIH rates, and the cost of living in Tucson is relatively low. Start date is negotiable; funding is secured through the end of July 2024.

The project is to model evolution not according to a unitary concept of “fitness”, but according to a small set of fitness-associated traits designed to capture fundamental distinctions. Previous work in our lab made progress on this for the case of competition for durable resources <https://doi.org/10.1016/j.tpb.2018.11.006>. We distinguished between absolute fecundity, relative competitiveness of juveniles to secure territories needed to reach adulthood, and absolute adult mortality. This categorization captured differences both in whether changes to a trait changed population density, and whether changes in density affected selection on the trait.

The postdoc’s role will be to apply similar concepts to consumable resources, including interference competition during which resources may grow to higher levels than allowed for within Tilman’s  $R^*$  theory ecology. Our aim is to produce a robust classification scheme for fitness-associated traits, providing a theoretical basis both for density-dependent evolution, and for a resolution of the “Grime-Tilman” debate from ecology. We also hope to incorporate plastic resource allocation strategies into the unified scheme. However, the exact direction of the work depends on the postdoc’s interests. Our inclusion in a larger initiative <https://www.biologicalpurpose.org/> offers opportunities for interdisciplinary collaborations, especially with philosophers.

Excellent mathematical modeling skills are required. Prior knowledge of either theoretical population genetics

or theoretical ecology is preferred, but strong candidates who have worked on other kinds of models will also be considered.

Contact Joanna Masel at [masel@email.arizona.edu](mailto:masel@email.arizona.edu) for more information and to apply.

“Masel, Joanna - (masel)” <[masel@arizona.edu](mailto:masel@arizona.edu)>

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## UArkansas Evolutionary Genomics

A postdoc fellow position is available in the Zhuang Lab, Department of Biological Sciences, University of Arkansas. (<https://fulbright.uark.edu/departments/biology/directory/index/uid/xz036/-name/Xuan+Zhuang/>),

We are looking for highly motivated researchers who are willing to tackle fundamental questions in both basic evolution and biomedical research. Research interests in the Zhuang Lab include Evolution of genetic novelty and diversity; Genetic basis of variation for complex traits and diseases; Molecular mechanisms of gene formation and gene loss. Investigations involve molecular evolution, quantitative genetics, genomics and bioinformatics, in model (fruit flies) and non-model organisms (polar fishes). Current projects in our lab are related to new gene and convergent genome evolution, and genetic basis of complex disease. More information is available on our website (<https://zhuangxuan.wixsite.com/home/-research-blog>).

### Qualifications

\* Ph.D. in Genomics, Bioinformatics, Evolution, Genetics, or related fields; \* Proficiency in at least one programming language (e.g. Python, Perl, etc.) and one statistical program (e.g. R, SAS, etc.); \* Experience working with and analyzing whole genomic and transcriptomic data sets (e.g. assembly, annotation, comparative genomic analyses, etc.); \* Good understanding of evolution and genetics theory and methodology; \* Basic molecular biology wet lab skills (desired but not required); \* Strong written and oral communication skills, and ability to work independently and in collaboration with others.

**Responsibilities** The primary responsibilities of this position are developing and implementing bioinformatics pipelines to carry out comparative genomic analyses, interpreting and organizing results into publishable papers and grant proposals. Other responsibilities include data management, mentoring students, and providing

bioinformatics support for the lab.

**Application Instructions** Please email Dr. Zhuang ([xz036@uark.edu](mailto:xz036@uark.edu)) the following materials: (1) CV (includes publications and pre-prints), (2) a cover letter outlining previous research experience and future plans, specifically how it is related to research focus in our lab, (3) contact information for two references.

About the University Founded in 1871, the University of Arkansas is a land grant institution, classified by the Carnegie Foundation among the nation's top 2 percent of universities with the highest level of research activity (R1 University). The University of Arkansas campus is located in Fayetteville, a welcoming community ranked as one of the best places to live in the U.S. The growing region surrounding Fayetteville is home to numerous Fortune 500 companies and one of the nation's strongest economies. Northwest Arkansas is also quickly gaining a national reputation for its focus on the arts and overall quality of life. Arkansas is a natural wonder of forests, mountains and lakes framed by picturesque rivers and streams. Some of the best outdoor amenities and most spectacular hiking trails are a short drive from campus.

Xuan (Shaine) Zhuang, PhD Assistant Professor

Department of Biological Sciences

Science and Engineering (SCEN) 422

University of Arkansas

Fayetteville, AR 72701

<https://zhuangxuan.wixsite.com/home> Xuan Zhuang  
<[xz036@uark.edu](mailto:xz036@uark.edu)>

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## UBrest France Marine Fishes Pop Genomics

Postdoc: Population genomics of pollack and red mullet in NE Atlantic, using RAD sequencing

A 39 months Post-Doc is proposed at the University of Brest, UBO (LEMAR laboratory) to perform a population genomics study of two fish species of high commercial interest in European fisheries, the pollack, *Pollachius pollachius*, and red mullet, *Mullus surmuletus*, in the North-East (NE) Atlantic. A particular attention will be paid to the population structure in the Bay of Biscay and adjacent waters. This project is based on a collaboration between UBO, the National Museum of Natural History (MNHN), Ifremer, and professional fishermen.

**Background and scientific context:** The development of relevant fisheries management plans relies on the accurate assessment of stock boundaries. In the Bay of Biscay, the management of a certain number of exploited species, known as 'Data Poor Species', is largely hampered by a significant lack of knowledge concerning their biology and ecology, notably concerning their population structure. This is particularly the case for the pollack, *Pollachius pollachius*, and the red mullet, *Mullus surmuletus*. In this context, a population genomics study will be conducted to explore the spatio-temporal structure of pollack and red mullet populations in the Bay of Biscay and surrounding waters. With this aim, a RAD-seq (Restriction site Associated DNA sequencing) will be conducted on both species, which is highly relevant to discover a sufficient number of genetic variants on non-model species, and in fine to evaluate fine-scale structuring patterns in populations. These investigations will be combined with previous data obtained by a Pool-Seq approach. About 700 individual pollack samples and 800 red mullet samples collected from Portugal to northern Scotland are expected to be RAD-sequenced individually. These samples include temporal samples that cover a period ranging from 10 years (red mullet) to 20 years (pollack). Additional samples will be collected in 2023 and added to the dataset.

**Detailed post-Doc project:** The Post-Doc will be in charge of conducting the preparation of RAD libraries and all analysis downstream to sequencing at LEMAR laboratory. Sequencing will be conducted on external platforms. Bioinformatic analysis will be conducted using a calculation cluster located at Ifremer (Datarmor). This genomic study will aim at addressing two issues: — 1. Firstly, the population genetic structure of both pollack and red mullet will be investigated over the distribution range of both species from Portugal to northern Scotland. The goal of this first task will be to assess the level of evolutionary divergence among the populations of both species in their— Atlantic distribution area. — 2. Secondly, genomic data will be applied to assess connectivity patterns between the Bay of Biscay and surrounding waters. A particular effort will be conducted to apply genomic data to management issues of both species in the Bay of Biscay.

**Profile of the candidate:** The candidate must have a strong background in population genomics and bioinformatics. A significant experience in DNA libraries preparation (RAD-seq or other methods) will be appreciated. In addition, the post-doc is expected to be particularly interested into the application of population genomics data in fisheries management.

**Working place:** The post-doc will be hosted at Laboratory of Environmental Marine Sciences (LEMAR;

<https://www-iuem.univ-brest.fr/lemar/?lang=en>).

This laboratory is located in the European Institute for Marine Studies (IUEM; <https://www-iuem.univ-brest.fr/?lang=en>), which is a pluridisciplinary institute dedicated to the field of marine and coastal sciences. The IUEM is located in Plouzané, about 8km away from the center of Brest. The LEMAR is an interdisciplinary laboratory that gathers a total of ca. 150 researchers and technicians and 50 PhD students. The LEMAR includes a molecular ecology team, with all the necessary equipment to conduct most of the labwork (DNA extraction, PCR amplification, etc..) and construct DNA libraries. Both French and English are used as spoken languages in the laboratory.

**Salary:** The salary is 1 917,12 euro /month net and 47 days-off/year.

**Application:** This will include 1/ a cover letter presenting the research interests and relevant experience of the applicant (max. 2 pages), 2/ a curriculum vitae including the list of publications, 3/ copies of academic diplomas, and 4/ the names and e-mail addresses of two referees. Applications should be sent as a single pdf to [gregory.charrier@univ-brest.fr](mailto:gregory.charrier@univ-brest.fr). The deadline for application is May 18, 2022. Short-listed candidates will be interviewed on May 30th, 2022, in a visio-conference mode.

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## UBuffalo PregnancyEvolution

POSTDOC - Evolution of pregnancy

Applications are invited for a postdoctoral position (up to 4 years) to study evolution of human-specific pregnancy traits using organoid models of the maternal-fetal interface, which is supported by a Burroughs Wellcome Fund 'Next Gen Pregnancy Initiative' grant. The postdoc position is in lab of Vincent Lynch in the Department of Biological Sciences at the University at Buffalo, SUNY. The Lynch lab uses evolutionary genomics and comparative cell biology to investigate the genetic and molecular mechanisms that underlie the developmental and evolutionary origins of endometrial stromal fibroblasts and decidual stromal cells, and how

gene expression evolution in these cell-types give rise to adverse reproductive outcomes such as infertility, preeclampsia, and preterm birth.

Specific research involves comparative genomics to identify gene expression changes at the maternal-fetal interface in humans compared to other species, particularly other primates, and modeling the consequences of these gene expression changes using organoid models of the human maternal-fetal interface. The postdoc can also develop new research directions consistent with these projects, such as the development of CRISPR genome editing and iPSC methods. Specific skills needed for this position vary, but experience with cell culture is essential; Experience in generating iPSC cells is preferred but not required. The postdoc will also receive guidance and support for career development, tailored to long-term goals including both academic non- academic careers.

The University at Buffalo, SUNY offers an exceptional environment for research and training in, with strong interaction among genomics research groups across schools and departments. The Department of Biological Sciences also offers numerous opportunities for collaboration.

Qualifications:

- Ph.D. in biology (required)
- Experience in cell culture (required)
- Experience with CRISPR genome editing
- Experience in developing iPSC cells
- Record of research productivity, including publications/preprints demonstrating skillsets (required)

Application materials:

- CV (preprints encouraged to demonstrate skillsets)
- Brief description of past and future research interests
- Contact information for three references, upon request

Recent related publications:

<https://www.biorxiv.org/content/10.1101/2021.09.27.461980v1> <https://www.biorxiv.org/content/10.1101/2021.10.25.465769v1> <https://elifesciences.org/articles/69584> <https://elifesciences.org/articles/61257>

The University at Buffalo, SUNY is committed to active recruitment of a diverse

Faculty, research support specials (including post-docs, research technicians, and research specialists), as well as a diverse student body. The University is an Affirmative Action/Equal

Opportunity Employer of women, minorities, protected

veterans and individuals with disabilities and encourages applications from these and other protected group members.

The position is open immediately until filled, with a flexible start date, and anticipated to last for up to four years. Applications, questions, and informal inquiries are welcome and directed to Vincent Lynch <[vjlynch@buffalo.edu](mailto:vjlynch@buffalo.edu)>.

Vincent J. Lynch, Ph.D. Associate Professor Department of Biological Sciences University at Buffalo, SUNY 551 Cooke Hall Buffalo NY, 14260

[vjlynch@buffalo.edu](mailto:vjlynch@buffalo.edu)

"These days the most useful thing we can do is to repudiate, and so we repudiate" - I. Turgenev, Fathers and Sons (1862)

"There is a grandeur in this view of life, with its several powers, having been originally breathed into a few forms or into one; and that whilst this planet has gone on cycling according to the fixed laws of gravity, from so simple a beginning endless forms most beautiful and most wonderful have been, and are being, evolved." -C. Darwin, 1859

[vjlynch@buffalo.edu](mailto:vjlynch@buffalo.edu)

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## UCincinnati HostParasiteEvolutionaryEcology

POST-DOCTORAL ASSOCIATE POSITION IN  
HOST-PARASITE BIOLOGY

Location: Department of Biological Sciences, University of Cincinnati, Cincinnati, Ohio, USA

Description: An NSF-funded post-doctoral position for 1 year is available in the laboratories of Dr. Michal Polak and Dr. Joshua Benoit on host-parasite interactions at the University of Cincinnati. The post-doctoral scientist will collaborate with the co-principal investigators to study the genetic bases of ectoparasite resistance and of associated life-history trade-offs in naturally occurring Drosophila-mite model systems. These studies will be strongly multi-disciplinary, and include host behavioral and physiological assays, bioinformatics and functional genomics. The post-doc will train in a vibrant and nationally recognized academic setting and will be supported to develop their own research directions. The position offers a competitive salary and will help defray relocation costs. The participant will be provided with

effective mentoring aligned with their individual career goals.

Qualifications: Ph.D. in Entomology, Biology or related field; publications in peer-reviewed journals; experience with bioinformatics analyses, functional genomics, basic molecular biology/physiology techniques, and/or host-parasite systems, is desired.

Start date: The target start date, though flexible, is September 1, 2022. Applications received by July 1, 2022, will receive full consideration.

Interested individuals should send, as a single PDF document, a cover letter, CV, a short statement of research interests, unofficial academic transcripts, and the contact information for 3 to 4 references to Dr. Polak (michal.polak@uc.edu) and Dr. Benoit (joshua.benoit@uc.edu).

For more information regarding the position, please contact either Dr. Benoit or Dr. Polak.

Relevant Links: <http://www.artsci.uc.edu/departments/biology.html> <http://insectphysiology.uc.edu/> <https://polaklab.org/>  
Michal Polak, PhD Professor University of Cincinnati Cincinnati, Ohio USA Email: polakm@uc.edu Tel: +1 (513) 556-9736

polakm@ucmail.uc.edu

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## UExeter Cornwall QuantGenLifeHistoryEvolution

\*\*\* An experimental test of the role of selection, drift and gene flow in shaping evolution in the wild \*\*\*

More information and link to apply: <https://tinyurl.com/3rjtndjm> Application closing date: 06/06/2022

Dr Erik Postma (University of Exeter), Prof Jon Slate (University of Sheffield) and Prof Marcel Visser (Netherlands Institute of Ecology) are recruiting a Postdoctoral Research Fellow for a NERC-funded project investigating the role of selection, genetic drift and gene flow in shaping contemporary life-history evolution in wild populations.

This 4-year post will involve the processing and analysis of long-term individual-based life-history data for a Dutch island population of great tits, as well as whole-genome sequence data for 1000+ individuals, using state-

of-the-art analytical tools. This population has been displaced from its adaptive optimum by means of artificial selection on clutch size (Postma et al. 2007. J. Evol. Biol.), providing a unique opportunity to study life-history evolution-in-action and to gain a better understanding of the adaptive potential of natural populations.

The PDRF will be responsible for primary results write-up, the presentation of results at scientific conferences, and they will contribute to public outreach. This will involve annual visits to Wageningen and Sheffield, and data collection on the island of Vlieland for a number of weeks each spring (circumstances permitting).

\* About you \*

The successful applicant will possess a relevant PhD or equivalent qualification/experience in evolutionary biology or a related field, with a broad knowledge in the discipline. They have excellent quantitative skills, demonstrable expertise in biostatistics, and a strong interest in quantitative genetics and life-history evolution. They are expected to prepare data for analysis, write up results for publication and give presentations at conferences and other events. They are a team player capable of working independently, have excellent organisational ability, and are willing to assist in training of graduate students.

The ideal candidate will have a strong background in evolutionary ecology, quantitative genetics and/or bioinformatics. They possess sufficient specialist knowledge in the discipline to apply existing and develop new analytical tools to individual-based life-history, pedigree, and sequence data. Furthermore, an affinity for field work and experience working with birds would be of advantage.

\* More information \*

Anyone considering applying is encouraged to contact Erik Postma by e-mail at [e.postma@exeter.ac.uk](mailto:e.postma@exeter.ac.uk)

– Erik Postma Senior Lecturer in Evolutionary Biology University of Exeter

[https://twitter.com/erik\\_postma](https://twitter.com/erik_postma) [https://biosciences.exeter.ac.uk/staff/profile/-index.php?web\\_id=Erik\\_Postma](https://biosciences.exeter.ac.uk/staff/profile/-index.php?web_id=Erik_Postma) <https://www.lifelovedeath.net/> Centre for Ecology and Conservation, College for Life and Environmental Sciences Penryn Campus, Treliever Road, Penryn, Cornwall, TR10 9FE

Erik Postma <[postma.erik@gmail.com](mailto:postma.erik@gmail.com)>

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## UFlorida PopGen

The McGuire Center for Lepidoptera and Biodiversity, Florida Museum of Natural History, University of Florida, is seeking a postdoc to study population genetics/genomics.

The position will work in a diverse and highly collaborative environment across three labs maintained by Drs. Jaret Daniels, Akito Kawahara, and Keith Willmott.

Position is initially for 1 year with the possibility of additional years depending on funding.

Required: 1) PhD in genetics, population biology, conservation biology, or relevant field, 2) lab skills relevant to library prep and sequencing, 3) experience with programming/scripting/data analysis (e.g. R, Python), 4) good communication/writing skills.

The McGuire Center is committed to creating a safe, inclusive, diverse, and equitable work environment. Candidates from groups underrepresented in science are encouraged to apply.

Salary: \$50,000.

How to apply: Submit a single pdf that includes the following: 1) cover letter detailing relevant experience and fit for this position, 2) curriculum vitae, and 3) names and contact information of at least 3 references familiar with your work. The pdf should be emailed to Dr. Jaret Daniels (jdaniels@flmnh.ufl.edu) with the subject line: "Postdoc\_UF"

Application deadline: May 15, 2022.

Questions should be directed to Dr. Jaret Daniels at jdaniels@flmnh.ufl.edu.

kawahara@flmnh.ufl.edu

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## UFreiburg ForestGenetics

The working group of Forest Genetics at the University of Freiburg is looking for a

Postdoctoral researcher (w/m/d)

\* Application deadline: 05.06.2022 \* Start-date: At the

earliest possible date. \* Fulltime position

The full announcement can be found here: <https://uni-freiburg.de/universitaet/jobs/00002252/> In the Forest genetics group at the Albert-Ludwigs-Universität Freiburg, we are investigating the genomic and epigenetic basis for the adaptation and acclimation of temperate and tropical tree species. To this end, we analyze genetic and genomic data together with phenotypic and environmental data. Our research is carried out in natural populations as well as in greenhouses and climate chambers. For our team, we are looking for a postdoctoral researcher with experience in analyzing genomic data sets in non-model species and with an interest in working with trees. The postdoctoral researcher will support the chair in research, teaching, and administration and will have the opportunity to establish his/her own profile in forest genetics research and teaching. An integration into ongoing projects on the genomic characterization of European forest tree species and on the molecular phenology of tropical tree species is planned. More information on current projects can be found here: <http://katrin-heer.de>. The position has a teaching obligation of four semester hours per week. Participation in a course on forest genetics and research skills for MSc students is planned. In addition, a course on bioinformatic analysis of genetic datasets for Master students should be established independently.

Your profile A very good Master's degree in biology, bioinformatics, or similar subjects, and a completed Ph.D. are required. Experience with genomic dataset analysis (in a Unix environment and with R and Python), RNAseq data, and de novo assembly and annotation of transcriptomes and genomes is required. You are familiar with the specifics of working with non-model species. Further, experience working on clusters and local servers is required and you will support the working group with establishing the local server infrastructure is expected. Experience in working with plants and in the laboratory (DNA and RNA extraction, creation of sequencing libraries) is an advantage. You are able to carry out scientific work independently and can demonstrate this through your publications. You enjoy working in a team and have experience in supervising BSc and MSc theses. Lectures at the MSc level are in English as is the working language in the group. Therefore, a very good knowledge of English is required. Good knowledge of German is an advantage for administrative support of the group.

What we offer You will be integrated into a newly established working group at the University of Freiburg working on forest genetics and genomics in temperate and tropical regions. The position offers the possibility of scientific qualification. The postdoctoral researcher

will be supported in writing his/her own research proposals. The salary is the standard salary for postdoctoral positions in Germany including social security and health insurance.

Your application Your application should include a letter of motivation, an academic CV (including an overview of your research and teaching activities, an overview of data analysis and software skills, and a publication record), copies of academic transcripts, and contact details for two academic references. The position is limited to four years and can be extended for another two years after a successful evaluation. The salary will be determined in accordance with TV-L E13 We are particularly pleased to receive applications from women for the position advertised here. Please send your application in English including supporting documents mentioned above citing the reference number 00002252, by 05.06.2022 at the latest. Please submit your application via the online portal of the university via the link below or to our team assistant Jessica Sun ([jessica.sun@forgen.uni-freiburg.de](mailto:jessica.sun@forgen.uni-freiburg.de)) For further information, please contact Prof. Dr. Katrin Heer on the phone number +49 761 203-3647 or E-Mail [katrin.heer@forgen.uni-freiburg.de](mailto:katrin.heer@forgen.uni-freiburg.de).

Prof. Dr. Katrin Heer Forest Genetics

Albert-Ludwigs-Universität Freiburg Faculty of Environment and Natural Resources Bertholdstraße 17, 79098 Freiburg i. Br., Germany

Phone: +49 761 203 3647 [www.katrin-heer.de](http://www.katrin-heer.de) Katrin Heer <[katrin.heer@forgen.uni-freiburg.de](mailto:katrin.heer@forgen.uni-freiburg.de)>

## UHelsinki Three FishEcoEvoGen

Up to 3 post-doctoral positions are available at the University of Helsinki, Finland working in Prof. Craig Primmer's research group (<http://www.helsinki.fi/evolution-conservation-and-genomics>) as a part of a recently funded ERC project entitled "Life history genes in fishes: bridging functional and evolutionary genetics for understanding life history trait evolution".

Successful applicants will likely have a strong background in research related to the themes listed below, but the specific combination of expertise is flexible, with the overall composition of the team being most important.

Reaction norms and quantitative genetics of fitness-related traits (morphological, physiological, behavioral) linked to large effect loci in Atlantic salmon and Rainbow

trout in common garden and semi-natural conditions, and associated data analyses (some data already available). Relevant group publications: Debes et al. 2021; Åsheim et al. 2022; Bangura et al. 2022

Population and evolutionary genetics of large effect life history-linked genes in long-term time series, links to life-history variation, and associations with environmental factors across a latitudinal gradient of 12 European Atlantic salmon populations. Relevant group publications: Czorlich et al. 2018, 2022

Reproductive fitness and strength of selection on large-effect life history-linked genes in natural salmon populations. Relevant group publications: Czorlich et al. 2018; Mobley et al. 2019, 2020

Molecular functions underlying genotype-life history associations: Functional genomic (including CRISPR), cellular and/or physiological approaches for understanding how the candidate genes, and genes they interact with, influence life history traits in salmon, trout and cod, and their sex-specific effects. Relevant publications: Kurko et al. 2020; Verta et al. 2020; Ahi et al. 2022

Appointees to the positions shall hold a doctoral degree and have the ability to conduct independent scholarly work. Suitable applicants will likely have a strong background in at least some of the approaches listed above, although the species/system with which they have experience is less important. The ability to work as a part of a larger research team addressing related questions is also important.

Informal inquiries can be directed to Professor Craig Primmer ([craig.primmer\(at\)helsinki.fi](mailto:craig.primmer(at)helsinki.fi)). Formal applications should include as a single pdf file: - a CV including a list of publications and with names and contact details of at least two referees - a max. 2 page letter of motivation

To apply, please submit your application using the University of Helsinki electronic recruitment system by clicking on Apply for job via <https://www.helsinki.fi/en/open-positions> The deadline for applications is 16:15 EEST on Tuesday 21 June 2022. The positions are available immediately but start dates up until the beginning of 2023 will be considered (although an earlier start is preferred).

The positions are initially available until 12/2025, but a 1-2 year extension may be possible. The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal performance with the overall starting salary amounting to c. 3200-3600 EUR per month, depending on the previous relevant

research experience of the candidate.

Finland is a member of the EU, has high quality free schooling (also in English), very affordable childcare, generous family benefits and healthcare, and has been ranked as the world's happiest country three years running and the best country in the world for expat families. The University of Helsinki is a top 100 ranked university in most ranking lists, and is currently investing heavily in life science research (see <https://www.helsinki.fi/en/helsinki-institute-of-life-science>) and the City of Helsinki is in the world's top ten most livable cities. Primmer's research group currently consists of 2 post docs, 7 PhD students and 3 research assistants with 9 different nationalities. The salmonid fish research field has traditionally lacked gender and cultural diversity, but the group is committed to helping to influence a change and we therefore strongly encourage applications from researchers with diverse backgrounds. Successful applicants are expected to adhere to the university and research group's codes of conduct

The University of Helsinki is an international scientific community of 40,000 students and researchers. It is one of the leading multidisciplinary research universities and ranks among the top 100 international universities in the world.

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## UInnsbruck OrganismicAnimalEvolution

PostDoc: UInnsbruck.OrganismicAnimalEcology

MOLECULAR ECOLOGY, DEPARTMENT OF ECOLOGY, UNIVERSITY OF INNSBRUCK PostDoc position, 20 hours/week, 6 years

The Molecular Ecology group (<https://molecular-ecology.at/>) of the Department of Ecology seeks to hire a PostDoc with experience in organismic animal ecology. The position starts in summer/autumn 2022 (exact starting date flexible; 20 h/week employment for 6 years). Centering on the Alpine Space, the group's mission is interdisciplinary research, embedded in international collaboration networks. A list of research topics can be

found at: <https://molecular-ecology.at/research-topics/>.  
 \*\*\*Responsibilities\*\*\* 1. Participation in organisation and administration 2. Independent research; publishing 3. Contact and cooperation with academics nationally and internationally 4. Independent teaching

\*\*\*Selection criteria\*\*\* A. PhD degree in life sciences B. proven research experience with organismal animal ecology, preferably on arthropods (ideally social insects) or vertebrates C. creative problem-solving skills D. ability to work as part of a team as well as independently E. organisational talent F. ability to work under pressure G. very good knowledge of English and ideally German  
 \*\*\*Salary\*\*\* The monthly gross salary is 2031 EUR (to be paid 14 times a year) for a 20 h/week employment (for 6 years). The contract includes health insurance and 5 weeks of holidays annually.

\*\*\*How to apply\*\*\* To apply, please submit online ([https://lfuonline.uibk.ac.at/public-karriereportal.details?asg\\_id\\_in=12712](https://lfuonline.uibk.ac.at/public-karriereportal.details?asg_id_in=12712)) the following materials: a cover letter, systematic point-by-point replies as to your readiness for the responsibilities and how you meet the selection criteria, brief statement of research interests, curriculum vitae, a complete list of publications, and - if possible - two reference letters.

Applications must be submitted until 27 June 2022.

The University of Innsbruck is striving to increase the percentage of female employees and therefore invites qualified women to apply. In the case of equivalent qualifications, women will be given preference. An offer of employment is contingent on a satisfactory pre-employment background check.

\*\*\*The research institution and its environment\*\*\* The University of Innsbruck has a long-standing and internationally renowned tradition in life sciences and offers a vibrant research atmosphere. It has 28,000 students and 5,500 staff members. Innsbruck is situated in the Alps and very close to Switzerland, Germany and Italy; scenery and outdoor recreation are fantastic.

\*\*\*More information needed?\*\*\* For more information, please contact: Birgit C. Schlick-Steiner <[birgit.schlick-steiner@uibk.ac.at](mailto:birgit.schlick-steiner@uibk.ac.at)>

“Schlick-Steiner, Birgit Christiane” <[Birgit.Schlick-Steiner@uibk.ac.at](mailto:Birgit.Schlick-Steiner@uibk.ac.at)>



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## UKonstanz AvianSocialEvolution

\*\*\*Short deadline\*\*\*

Post-doc position in avian social evolution at the Centre for the Advanced Study of Collective Behavior, University of Konstanz.

The Griesser lab invites application for a postdoctoral position as part of a project at the interdisciplinary Centre for the Advanced Study of Collective Behavior. The project investigates the consequences of the interplay between individual and group social phenotype in a wild bird species. Not only individuals but also groups vary in their social phenotype. Although the latter component is rarely considered, it is potentially quite important: successful groups should be better at coordinating their behaviours, e.g., during foraging or predator encounters, and thus influence the fitness of group members.

This project will investigate these links in a wild population of Siberian jays (*Perisoreus infaustus*) in Swedish Lapland, monitored since 1989. This bird species lives in stable, enduring groups composed of a breeding pair and up to 4 non-breeders, and we follow individuals in up to 90 groups throughout their life to collect life-history and behavioural data. The project will combine field experiments with existing long-term data to investigate the interplay between individual and group social phenotype, and its consequences. A short description of our past research can be found here: <https://www.youtube.com/watch?v=JaH6wjAYAiE> You will join the Griesser lab and the interdisciplinary team at the Excellence Cluster for the Advanced Study of Collective Behaviour at the University of Konstanz. The position should begin 1st July 2022 and will be fully funded for 22 months (salary scale 13/3 TV-L).

Your qualifications: - PhD in behavioural ecology, evolutionary biology, or similar; - Field experience of behavioural observations and experimental work; - Bird handling experience (including mist netting); - Highly motivated and sociable personality; - Project management skills; - Ability to work both independently and in a team; - Driver's license (manual transmission); - Basic knowledge of X-country or downhill skiing is an advantage.

Deadline: 18<sup>th</sup> May 2022; application will be reviewed as soon as received. Applications should be sent to

michael.griesser@uni-konstanz.de and include a short motivation letter, a CV including publications, and names of two referees.

The University of Konstanz is an equal opportunity employer that is committed to providing employment opportunities to all qualified applicants without regard to race, colour, religion, age, sex, sexual orientation, gender identity, national origin, or disability. It seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourage women to apply (see equal opportunity).

If you have questions, contact michael.griesser@uni-konstanz.de

Michael Griesser Heisenberg Fellow Department of Biology University of Konstanz

<https://scholar.google.com/citations?user=-IEIH0xkAAAAJ>

Michael Griesser  
<michael.griesser@uni-konstanz.de>

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## ULausanne AntPopulationGenomics

University of Lausanne: Postdoctoral position in ant population genomics/phylogenomics

A Postdoctoral position is available in the group of Prof. Michel Chapuisat at the Department of Ecology and Evolution, University of Lausanne, Switzerland. The group studies social evolution. We are currently investigating the origin, evolution, and mechanisms of action of a supergene controlling social organization across *Formica* ants (see <http://www.unil.ch/dee/page7000.html>). Recent research showed that some species have three supergene haplotypes. *F. selysi* and *F. cinerea* commonly hybridize, raising the possibility of supergene introgression. The postdoctoral researcher will generate and analyse population genomics data to uncover key processes governing supergene evolution, including selection, genetic load, drive and introgression. This project will shed light on how supergenes arise, spread and shape complex alternative phenotypes.

Your responsibilities: You will study the evolution of a social supergene. This will involve field sampling of multiple ant species, population analyses (e.g. sex-ratio, male production), sequencing, population genomic, comparative genomic, and phylogenomic analyses. Depending on your personal interests and skills, projects on genome evolution, molecular evolution, behavioural genetics and ecological genomics are also possible.

Your qualifications: We are seeking to recruit an early career post-doctoral researcher with a PhD degree in evolutionary biology, genetics, genomics, bioinformatics or related fields. The ideal candidate should have skills and experience in one or more of the following fields: population biology, population genetics, comparative genomics, phylogenetics, ecological genomics, molecular evolution. The candidate should have a convincing publication track-record, excellent inter-personal skills and a strong ability to work in a team.

Job information: Expected start date in position: 01.08.2022 (or at earliest convenience) Contract length: 1 year, renewable for up to 5 years depending on funding available Activity rate: 100% Workplace: Lausanne - Dorigny

What the position offers you: We offer a nice working place in a multicultural, diverse and dynamic academic environment, with opportunities for professional training. The Department of Ecology and Evolution in Lausanne University hosts research groups working on a broad range of topics, producing a rich intellectual and social life. The working language in the group and in the Department is English for all scientific matters. Good command of English is needed, some knowledge of French would be a plus, but is not mandatory. The University of Lausanne offers state-of-the-art facilities, including excellent computer facilities and molecular labs.

Contact for further information: Prof. Michel Chapuisat: Michel.Chapuisat@unil.ch

Your application: Deadline: 01.06.2022. Incoming applications will continue to be considered until the position is filled. To apply, please upload a single pdf document containing: a cover letter with a short description of your research interests, research experience, and why you are interested in joining our group; Your CV; The contact details of 2-3 referees; A copy of your PhD degree. Ideally, you should have received your PhD within the last 2 years or be about to obtain it in the next four months.

To receive full consideration, application documents should be uploaded online through the University of Lausanne recruitment platform. Please apply through this webpage: <https://bit.ly/3vV1FwX> Michel.Chapuisat@unil.ch

## ULiege Evolutionary Neuroethology

A postdoctoral position in Evolutionary Neuroethology is open to join the 'Laboratory of Evolutionary Neuroethology' led by Dr. Jean-Marc LASSANCE within the Unit GIGA-Neuroscience at the campus Sart-Tilman of the University of Liège in Belgium. The GIGA ([https://www.giga.uliege.be/cms/c\\_4113263/en/giga](https://www.giga.uliege.be/cms/c_4113263/en/giga)) is an interdisciplinary biomedical research center offering access to core facilities including animal facilities, imaging, sequencing and viral vector production platforms. GIGA and the University of Liège welcome applicants with diverse backgrounds and experiences.

Subject description Olfaction 'the sense of smell' plays a fundamental role in the life of animals and humans alike. Indeed, the detection of olfactory stimuli is a key determinant of many innate behavioral responses, from aggression to parental care. A central goal of our research is to understand how an animal's innate interpretation of odors drives behavior, how this representation evolves, and how genetic variation modulates the neural architecture of odor information processing in the mammalian olfactory system. We are seeking to recruit a highly motivated post-doctoral fellow for an interdisciplinary project at the interface between evolutionary biology and neurobiology. The project focuses on performing behavioral experiments in rodents and profiling the sensory responses to stimuli corresponding to various ethological contexts using high-throughput sequencing approaches. The project will be conducted at GIGA, a cross-disciplinary environment which will provide the candidate with ample possibilities to learn new skills and methods ranging from imaging to single-cell sequencing.

Work duties The main duties involved in this post-doctoral position is to conduct research. Work duties include: - Perform behavioral experiments and expose animals to ethologically relevant cues. - Work in tight collaboration with the GIGA Genomics platform to coordinate the preparation and sequencing of samples. - Work in collaboration with the GIGA Bioinformatics platform to analyze Next-Generation Sequencing data. - Actively contribute to a positive and creative working atmosphere in the group. - Possibility to develop own research questions within the project aims.

Qualification requirements Appointment to a post-doctoral position requires that the applicant has a PhD,

or an international degree deemed equivalent to a PhD, within the subject of the position, at the time for employment decision. The doctoral degree should have been obtained no more than five years before the last date for applications. Extensions are possible under certain circumstances such as childbirth and adoption. Importantly, the candidate should be a situation of international mobility: he/she should not have worked or lived in Belgium for more than 24 months during the 3 years preceding his/her start date.

Additional requirements: - PhD certificate in a relevant field such as biology, neurobiology, evolutionary biology. - Very good proficiency in written and oral English. - Good communication skills. - Ability to work well individually and as part of a team.

Assessment criteria and other qualifications This is a career development position primarily focused on research. The position is intended as an initial step in a research career, and the assessment of the applicants will primarily be based on their research qualifications and potential as researchers. Particular emphasis will be placed on research skills within the topic.

For appointments to a post-doctoral position, the following shall form the assessment criteria as merits: Experience in conducting behavioral experiments with laboratory animals ' Experience in molecular biology techniques ' Experience in analysis of  $\frac{1}{2}$ omics' data (i.e. genomics, transcriptomics including single-cell sequencing) and data visualization ' Documented ability to develop and carry out high-quality research ' Documentation of successful completion of research projects ' High intellectual capacity and problem-solving ability ' Technical and analytical know-how, organization skills ' Enthusiasm, dedication and an ability to work both independently and embedded in a team Consideration will also be given to good collaborative skills, drive and independence, and how the applicant's experience and skills complement and strengthen ongoing research within the unit, and how they stand to contribute to its future development.

Terms of employment This is a full-time, fixed-term employment of two years (initial contract for one year renewable). Starting date is September 1st 2022. Any questions related to the position should be directed to Jean-Marc Lassance (jmlassance@uliege.be).

Instructions on how to apply

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

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## UMassachusetts Boston MutualismCoevolution

The Vidal Lab at UMass Boston invites applications for a postdoctoral position on mutualism coevolution. This postdoc position is currently funded for a total of 4 years. The current position is to work on a newly NSF-funded collaborative project using budding yeast to test the coevolutionary dynamics of multispecies mutualisms. The lab also has active research in insect herbivore-plant interactions. Thus, a researcher interested in understanding broad questions in the ecology and evolution of species interactions would fit well in this position. You can learn more about the Vidal Lab here: [vidallab.weebly.com](http://vidallab.weebly.com)

Preferred start date: August 2022, but I'm willing to delay the start date until January 2023 for ideal candidates.

Qualifications: PhD in Ecology, Evolutionary Ecology, Community Ecology, Evolutionary Biology, or a closely related field is required. Experience with basic molecular techniques (mainly pipetting) and data analysis. Proficiency in basic microbiology skills such as making solutions, culturing microorganisms, and sterile techniques is preferred, but not necessarily required. Applicants should have demonstrated knowledge of concepts and theories related to species interactions, with a preference for mutualisms. A strong publication record is preferred.

Please direct any questions to Dr. Mayra Vidal ([mayra.cadorinvidal@umb.edu](mailto:mayra.cadorinvidal@umb.edu)) and view the full job description and apply at

<https://employmentopportunities.umb.edu/boston/en-us/job/513877/post-doctoral-research-fellow> Mayra C. Vidal, PhD

Assistant Professor

Department of Biology

University of Massachusetts Boston

100 Morrissey Blvd.

Boston, MA 02125, USA.

Pronouns: she, her, hers

<http://vidallab.weebly.com/>  
<[mayracvidal@gmail.com](mailto:mayracvidal@gmail.com)>

Mayra Vidal

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## UMemphis InsectGenomics

A 4-year postdoctoral fellowship in insect genomics & evolution is available in the lab of Dr. Duane McKenna at the University of Memphis (<http://www.duanemckenna.com>).

**Position Summary:** The successful applicant will be primarily responsible for data analysis and wet lab work associated with genomic and evolutionary studies of insects, and will work closely with Dr. McKenna and others in his lab. All applicants with relevant background will be considered, regardless of the organism(s) previously studied. The position offers opportunities for mentoring students and for being mentored, building new collaborations, writing grants and scientific papers, and learning and developing cutting-edge analytical and laboratory methods and tools. The position offers a competitive salary plus benefits. The initial appointment is for one year, and is renewable for at least 3 additional years, contingent upon outstanding annual performance evaluations and availability of funding. Applications must be submitted online at <https://workforum.memphis.edu/> and should include a cover letter, CV, two representative publications, and contact information (not letters) for at least three professional references. **Required Qualifications:** A Ph.D. in bioinformatics, computational biology, data science, ecology, evolution, genetics, genomics, phylogenomics, systematic biology, or similar. A strong record of scientific publication. Experience generating and analyzing various kinds of genomic/molecular data. Strong communication and interpersonal skills, including a proven ability to work both independently and as part of a team.

**The McKenna Lab:** Lab members study insect systematics, genomics, ecology, evolution and diversity. Focal areas of study include the phylogeny and evolution of beetles and other insects, the evolution and genomic basis of plant-feeding, and interactions between insects and plants on ecological and evolutionary time scales. The lab hosts a highly-collaborative group of postdocs, PhD research associates, a research assistant professor, graduate and undergraduate students, and volunteers. We are part of a large community of biodiversity scientists associated with the Center for Biodiversity Research ([www.umbiodiversity.org](http://www.umbiodiversity.org)) in the Department of Biological Sciences (<https://www.memphis.edu/biology/>) at

the University of Memphis a leading metropolitan research and teaching institution in Memphis, TN, U.S.A.

**Application deadline:** The position is open until filled. Screening of applications begins June 3, 2022. For more info. and to apply, visit: <https://workforum.memphis.edu/postings/31418> Contact for questions: Duane McKenna ([dmckenna@memphis.edu](mailto:dmckenna@memphis.edu))

Duane McKenna PhD William Hill Professor of Biology Department of Biological Sciences University of Memphis Director, Center for Biodiversity Research Director, Agriculture & Food Technologies Research Cluster, FedEx Institute email: [dmckenna@memphis.edu](mailto:dmckenna@memphis.edu) <http://duanemckenna.com> [www.umbiodiversity.org](http://www.umbiodiversity.org) [dmckenna@memphis.edu](mailto:dmckenna@memphis.edu)

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## UMinnesota GenomicsPopulationGenetics

**Position:** Postdoctoral Research Associate

**Location:** University of Minnesota, Department of Agronomy and Plant Genetics, St. Paul, MN

**Research Area:** Genomics and population genetics

**Qualifications:** PhD in evolutionary, population, or quantitative genetics, plant breeding, or related field. Proficiency in UNIX shell, Python, or other programming languages is preferred. A demonstrated ability to publish original research in peer-reviewed journals is preferred. Basic molecular biology skills, including DNA extraction and PCR, are preferred.

We are seeking a postdoctoral research associate in the area of genomics and population genetics. The successful candidate will examine the genomic and nucleotide sequence-level effects of biotech treatments, including mutagens, tissue culture, and targeted genetic modifications (CRISPR) in soybean. There will be potential to contribute to related research projects in the host labs.

There are opportunities to improve your biocomputing skills through tutorials hosted by the Minnesota Supercomputing Institute <https://www.msi.umn.edu/tutorials> and local Software Carpentry workshops <https://dash.umn.edu/events/software-carpentry>.

There are several faculty members on the St. Paul campus with research programs in genomics (including Candy Hirsch, Gary Muehlbauer, and Ruth Shaw) and evolutionary genetics (including Yaniv Brandvain, Suzanne McGaugh David Moeller, and Peter Tiffin).

To apply, send a cover letter and curriculum vitae to Peter Morrell (pmorrell@umn.edu) and Robert Stupar (stup0004@umn.edu). The review of applications will begin on 10 June 2022 and continue until the position is filled.

Peter Morrell <pmorrell@umn.edu>

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### UMontana ASU PopulationGenomics

Postdoctoral Research Associate -Population Genomics, University of Montana and Arizona State University

A joint postdoctoral position on viral and bacterial population genetics is available to work in collaboration with Jeff Good and Brandon Cooper's research group at the University of Montana (Missoula) and Jeff Jensen's research group at Arizona State University (Phoenix). We seek a postdoctoral colleague interested in collaborating on ongoing projects focused on viral and bacterial evolution, with an emphasis on developing population genetic methods and theory suitable for understanding molecular evolution from viral and bacterial timeseries data. Candidates for this position would also have opportunities to develop and apply cutting-edge population genetic models and methodology for the analysis of both RNA and DNA-based viruses (cytomegalovirus, SARS-CoV-2) and intracellular bacteria symbionts (Wolbachia bacteria).

The successful candidate will have the opportunity to lead analysis of several large existing genomic datasets, including the NIGMS-funded SARS-CoV-2 Surveillance Sequence Network, and to develop new research directions that complement our current research projects. No previous experience in viral or bacterial systems required. A strong background in population genetics theory and application, analysis of large-scale genomic data, and a Ph.D. in computational or evolutionary/population genetics or a related field is required. This position is available immediately and is centered at the University of Montana, with flexibility for full remote employment working with Dr. Jensen at Arizona State or centered at another institution (restrictions on remote international appointments may apply).

Our labs value diversity and we encourage candidates with unique backgrounds and skills to apply, especially candidates from backgrounds that are traditionally underrepresented in STEM. We value prior con-

tributions that candidates have put towards diversity, equity, and inclusion initiatives. The University of Montana and Arizona State University offers vibrant research communities. The Good and Cooper labs share newly constructed molecular and office space along with the UM Genomics Core and three other outstanding research groups, as part of an entire floor dedicated to evolutionary genomics research. The Jensen lab is in the School of Life Sciences at Arizona State University, and is part of a large and collaborative group in evolutionary genomics at ASU - see ASUpopgen.org, the Center for Evolution & Medicine <<https://evmed.asu.edu/>>, and the Center for Mechanisms of Evolution <<https://biodesign.asu.edu/mechanisms-evolution>>. For further information on this position and our research please visit our lab websites (thegoodlab.org; cooper-lab.org; jjensenlab.org) and email Drs. Good (jeffrey.good@umontana.edu), Cooper (brandon.cooper@mso.umt.edu), or Jensen (Jeffrey.D.Jensen@asu.edu). All applicants are strongly encouraged to contact us prior to applying.

To apply, please visit <https://bit.ly/3353umjobs> Candidates must apply online and will be asked to upload the following application materials: a cover letter describing your research interests and qualifications, a CV, and the names and contact information for three references. Applications will be reviewed upon receipt. Candidates should apply by May 27, 2022 for full consideration, and the position will remain open until filled. The position start date will be flexible contingent on the needs of the preferred candidate.

ADA/EOE/AA/Veteran's Preference Employer  
Jeffrey.Good@mso.umt.edu

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### UNSW Sydney ModellingPathogenEvolution

Postdoctoral Research in Mathematical/Computational Biology at The University of New South Wales, Sydney Australia

A 2-year postdoc position is available in Mark Tanaka's group at UNSW Sydney to start around July/August 2022. The project aims to understand the emergence of new infectious diseases as a function of both microbial evolution and cultural shifts in human populations. It combines the development of new mathematical models with the analysis of epidemiological and anthropological

data. This project is funded by the Australian Research Council and will be conducted in collaboration with Jeremy Kendal at Durham University UK.

Apply online at the UNSW jobs website <https://external-careers.jobs.unsw.edu.au/cw/en/job/509044/-research-associate> <https://www.jobs.unsw.edu.au/>

For further information please contact Mark: [m.tanaka@unsw.edu.au](mailto:m.tanaka@unsw.edu.au) See also: <http://www.tanakalab.unsw.edu.au/> [m.tanaka@unsw.edu.au](mailto:m.tanaka@unsw.edu.au)

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## UOtago LifeHistorySexualSelection

Seminal fluid and life-history responses in mammals

This project seeks to test how seminal fluid exposure during mating influences a female mammal's future fertility and rate of ageing. Previous research from our team has shown that female sexual experience, without pregnancy, enhances fertility and growth but reduces lifespan in mice. Other research in invertebrates and humans suggests that seminal fluid exposure could be the cause of these long-lasting effects, which will be directly tested in this project. The project will use a number of approaches to manipulate exposure to seminal fluid during mating, assessing how this influences the gestational development of subsequent offspring, total female fecundity and effects on ageing. Research in this project will provide insight into how male seminal fluid proteins influence female reproductive physiology and fitness, with relevance to both human fertility and the evolutionary roles of these proteins in sexual selection and conflict

The Candidate is expected to have a background in evolutionary biology, reproductive biology, ageing or a related field. It is expected that they will have experience working with rodents, or a very strong desire to learn.

The student will be primarily supervised by Dr. Michael Garratt, whose interests lie in understanding the links between reproduction and ageing. They will be housed within The Department of Anatomy at the University of Otago, a department with diverse and complimentary research interests. These interests include reproduction, genomics, development, neuroscience, neuroendocrinology, clinical anatomy and biological anthropology. The University of Otago is located in the beautiful town of Dunedin in the South Island of New Zealand.

Please address any questions to Mike Garratt

([mike.garratt@otago.ac.nz](mailto:mike.garratt@otago.ac.nz))

For more information and to apply: <https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=en&job=2200889> Dr. Michael Garratt

Senior Lecturer

Department of Anatomy

School of Biomedical Sciences

University of Otago

New Zealand

Email: [mike.garratt@otago.ac.nz](mailto:mike.garratt@otago.ac.nz)

<https://www.otago.ac.nz/anatomy/people/staff/profile/index.html?id=2975>

<https://scholar.google.co.nz/citations?hl=en&user=Q3aOKlgAAAAJ> Mike Garratt

<[mike.garratt@otago.ac.nz](mailto:mike.garratt@otago.ac.nz)>

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## UPennsylvania HumanPrimateEvolutionaryGenetics

The Kamberov lab in the Department of Genetics at the UPenn School of Medicine in Philadelphia USA, is recruiting to fill a postdoc position investigating the genetic changes and developmental mechanisms that made humans the “naked” ape, which is a key thermoregulatory adaptation of our species and differentiates us from all other primates. Applicants should hold a Ph.D. in biology or related field. Applicants with a background in developmental biology, mouse genetics, evolutionary genomics, and expertise in working with large-scale transcriptomic data are encouraged to apply. Interested applicants should send a letter detailing your interest in the position and a CV to Yana Kamberov ([yana2@penmedicine.upenn.edu](mailto:yana2@penmedicine.upenn.edu)).

[yana2@penmedicine.upenn.edu](mailto:yana2@penmedicine.upenn.edu)

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## UToronto EvolutionPlantMicrobeInteractions

\*Postdoctoral Position in Evolution of Plant-Microbe Interactions\* A fully funded postdoctoral research fel-

lowship is available in the collaborative laboratories of \*David Guttman\* and \*Darrell Desveaux\* in the

\*Department of Cell & Systems Biology at the University of Toronto, Canada.\*The candidate will contribute to a project focused on identifying new immune receptors in soybean and studying how host immunodiversity has changed during the course of soybean domestication. This project builds on our recent publication, \*Lafamme et al. 2020. The pan-genome effector-triggered immunity landscape of a host-pathogen interaction. Science. 367(6479):763. \*

The candidate will be responsible for the following objectives:

1. Screen for \*Pseudomonas syringae\* type III effectors that elicit immunity in multiple soybean accessions and \*Glycine soja\*, the closest wild relative of soybean. This screen will use the PsyTEC system developed in Lafamme et al. 2020.
2. Use comparative and evolutionary genomic analyses to identify highly conserved immune receptors among soybean and \*G. soja\*.
3. Create and screen CRISPR/Cas9 knock-outs of the most highly conserved soybean immune receptors to determine how the immunodiversity has changed during the course of domestication.

Interested applicants should have a Ph.D. (or be close to completion) in an appropriate discipline and experience working in plant-microbe interactions, plant biology, or microbiology. Some computational experience is also highly desired, although training is available in the research group. The position is available for a minimum of two years, subject to annual review, and can be started immediately.

The Guttman and Desveaux collaboration includes a highly motivated and diverse group of graduate students and postdocs broadly focused on host-microbe interactions with particular specializations in bacterial evolution and plant immunity using approaches that include plant pathology, microbiology, comparative and functional genomics, genome editing, high-throughput functional screens, experimental evolution, statistical genomics and machine learning, and of course molecular and cellular biology.

The Guttman lab is also closely associated with the Centre for the Analysis of Genome Evolution & Function (CAGEF), which is a genomics core facility with particular expertise in microbial and plant genomics. The genomic and bioinformatic resources afforded by CAGEF are easily accessible to anyone working in the Guttman and Desveaux collaborative group.

To apply, the applicant should send the following to [david.guttman@utoronto.ca](mailto:david.guttman@utoronto.ca) & dar-

[rell.desveaux@utoronto.ca](mailto:rell.desveaux@utoronto.ca)

1. A cover letter outlining your previous experience and research and career goals.
2. CV
3. Contact information for three references

More information about the Guttman and Desveaux laboratories and affiliated units can be found at: [guttman.csb.utoronto.ca](http://guttman.csb.utoronto.ca), [desveaux.csb.utoronto.ca](http://desveaux.csb.utoronto.ca), [www.cagef.utoronto.ca](http://www.cagef.utoronto.ca), [www.csb.utoronto.ca](http://www.csb.utoronto.ca).

The University of Toronto is the top university in Canada and ranked within the top 20 world-wide. It provides an outstanding scientific environment with a highly interactive community of researchers. The Guttman lab and University of Toronto are strongly committed to diversity and especially welcomes applications from racialized persons, persons of color, women, Indigenous / Aboriginal People, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas. Toronto is a diverse, vibrant, and cosmopolitan city; one of the most desirable in the world in which to work and live.

David S. Guttman Professor, Department of Cell & Systems Biology Director, Centre for the Analysis of Genome Evolution & Function University of Toronto Toronto, Ontario, Canada

Darrell Desveaux Professor, Department of Cell & Systems Biology Director, Centre for the Analysis of Genome Evolution & Function University of Toronto Toronto, Ontario, Canada

David Guttman <[david.guttman@utoronto.ca](mailto:david.guttman@utoronto.ca)>

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## WashingtonStateU FungalBiocontrol

Link to full job post: [https://wsu.wd5.myworkdayjobs.com/WSU\\_Jobs/job/-Pullman-WA/Post-Doctoral-Research-Associate\\_R-5618](https://wsu.wd5.myworkdayjobs.com/WSU_Jobs/job/-Pullman-WA/Post-Doctoral-Research-Associate_R-5618)

Summary of Duties: The Han Lab in the Department of Entomology at Washington State University is seeking a postdoctoral research associate to support a project involving biocontrol of arthropod pests. The successful candidate will assist with laboratory and field research concerning the selection of fungal biocontrol agents towards specific pest species, including Varroa mites. They will participate in projects involving molecular biology, genome sequencing and analysis. Responsibilities include maintaining fungal cultures and performing laboratory growth experiments, rearing or collecting pest species for

testing, and working with honey bee hives. They will mentor graduate and undergraduate students, prepare project reports and manuscripts for publication, and present research results at professional and industry meetings.

The position is located in Pullman, WA, however, work at the Othello Honey Bee and Pollinator Research and Extension Center or remote field sites is possible. The position is initially available for one year, with renewal dependent on need and/or if additional funding is secured. The position is available immediately and will remain open until filled.

**Required Qualifications:** - Candidates should have a PhD or equivalent degree in Mycology, Entomology, Crop Sciences, or a related field in the biological sciences, good written and oral communication skills and the ability to work collaboratively across disciplines. - Candidates who have not yet completed their PhD but have a scheduled defense date in the near future may be considered. - The candidate must possess a valid driver's license or have the ability to obtain one by the date of hire. - They must have excellent organizational, interpersonal, and communication skills.

**Preferred Qualifications:** - Ideal candidates will have experience using microbial biocontrol agents, working

with fungi in the laboratory, raising arthropod pests, and/or working with honey bees. - Prior experience with molecular biology, genomics, and/or bioinformatics is also preferred. - The ideal candidate will be proficient in statistics and the scientific publication process.

**Application Instructions:** Please visit: [https://wsu.wd5.myworkdayjobs.com/WSU\\_Jobs/job/-Pullman-WA/Post-Doctoral-Research-Associate\\_R-5618](https://wsu.wd5.myworkdayjobs.com/WSU_Jobs/job/-Pullman-WA/Post-Doctoral-Research-Associate_R-5618) to apply. Applicants must attach the following documents to their online application: 1) Copy of their curriculum vitae and 2) cover letter. Application materials should clearly communicate how the applicant meets the required qualifications and additional requirements. Applicants are required to include contact information for 2-3 professional references within the application.

**Required Documents:** 1) Curriculum Vitae 2) Cover Letter 3) Professional references. Please Note: references will be embedded in the application. Please also include your references in an attached document.

Jennifer Han, PhD Assistant Professor Department of Entomology

Washington State University

"Han, Jennifer Okhyun" <jennifer.o.han@wsu.edu>

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## AarhusU GWAS and Prediction Jul

Hi All

In July 2022, Aarhus University is running a 5ECTs course on Analysis of GWAS data with a Focus on Prediction. The course is aimed at MSC and PhD students. The deadline for registering is the end of May. The main objectives are:

- 1 - teach students the methods being used to analyse GWAS. These will include both basic analyses (e.g., quality control and single-SNP tests of association) and advanced methods (e.g., heritability analyses).
- 2 - teach students how to construct prediction models (i.e., to be able to predict an individual's risk of developing a disease, given their genetic information).
- 3 - teach students how to use popular genetic software.

At the end of the course, students should be able to:

- 1 - Explain the aims of a GWAS, and all the steps required to perform a basic association analysis.
- 2 - Discuss how heritability analyses can be used to improve our understanding of complex traits.
- 3 - Explain how prediction models are constructed and used within personalized medicine.

The course involves classroom teaching from 4th to 8th July, and then approximately two weeks working on an assignment (to be submitted at the start of August). Students must be in Aarhus for the classroom teaching (AU will arrange accommodation), but will generally complete the remainder of the course remotely.

See this link for more details of the course <https://kursuskatalog.au.dk/en/course/114031/Analysis-of-GWAS-Data-with-a-Focus-on-Prediction-of-Complex-Phenotypes> And this link for details of how to apply <https://international.au.dk/education/admissions/-summeruniversity> If you have any questions, please contact me (doug@qgg.au.dk)

Doug

Doug Speed <doug@qgg.au.dk>

## Lisbon cE3c AdvancedCourses

cE3c Advanced Courses 2022/2023 - List already available

The detailed program of the Advanced Courses organized by cE3c - Centre for Ecology, Evolution and Environmental Changes

<http://ce3c.ciencias.ulisboa.pt/> - for the academic year 2022/2023 is already available.

These courses are aimed for students enrolled in Doctoral Programmes in Biology or related area. They can also be attended by post-graduate students of other Doctoral Programmes or Masters in Biology, or others with basic biology formation (such as BSc in Biology or related areas).

These courses are free for 1st year PhD students of several Doctoral Programmes of the Faculty of Sciences of the University of Lisbon (FCUL) or institutions in partnership with FCUL, counting credits for their formation:

- Biology, Ciências do Mar or other PhD programmes at FCUL;
- Biodiversity, Genetics and Evolution - BIODIV (ULisboa and UPorto);
- Biology and Ecology of Global Changes - BEAG (ULisboa and UAveiro).

The courses have in general an intensive format, with one week of duration, with 5-6 ECTs recognition for the above mentioned Doctoral Programmes. Some have a shorter format (see details in each course's programme).

We present below the list of courses of more interest for evolutionary biologists or development of soft skills. More details of these and other courses (including programmes, fees and procedures for applications) can be found at:

<https://ce3c.ciencias.ulisboa.pt/training/> Advanced Courses cE3c 2022/2023 November 7th - 11th 2022 -Scientific Writing and Communication(Gabor Lövei).Deadline for applicationsOctober 3rd 2022.

November 21st- 25th2022 -Production of Science Communication Activities(Cristina Luís & Patrícia Garcia Pereira).Deadline for applicationsOctober 28th2022. (ONLINE)

January 9th - 13th 2023 -Bioinformatics analysis of biological sequences - from sequence to structure(Teresa Nogueira, Rita Ponce &Eva Pinho).Deadline for applications December 9th 2023. (ONLINE)

January 16th - 20th 2023 -Science and the Media: bringing together scientists, journalists and society(Marta Daniela Santos). Deadline for applications December 16th 2023.

March 6th- 10th2023-Strategies for citizen engagement in science communication(Cristina Luís, Esther Marin et al.).Deadline for applications February 10th2023. (ONLINE)

May 3rd- 5th2023-Introduction to R programming and biological data analysis(Inês Fragata & Vitor Sousa). Deadline for applications April 3rd 2023.

May 8th- 12th2023-Advanced R for Ecology and Evolutionary Biology(Inês Fragata & Vitor Sousa). Deadline for applications April 3rd 2023.

May 22nd-26th2023-Climate Change Adaptation(Silvia Carvalho et al.). Deadline for applications April 21st 2023.

May 29th- June 2nd 2023 -Experimental Design and Reproducibility in Science(Inês Fragata, Leonor Rodrigues & Diogo Godinho). Deadline for applications April 28th2023.

July 17th- 21st 2023 -Measuring Biodiversity:How to get data, assess its quality and measure different aspects of diversity(Joaquín Hortal). Deadline for applications:May 18th2023.

Margarida Matos

Executive Committee of Centre for Ecology, Evolution and Environmental Changes

Faculdade de Ciências da Universidade de Lisboa

Margarida Matos <mmmatos@fc.ul.pt>

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## Lisbon FishGenetics Nov7-11

Dear colleagues,

The deadline for submitting abstracts to the \*2022 Small Pelagic Fish Symposium\* has been extended to \*May 29, 2022\*.

The Symposium will held November 7-11 in Lisbon, Portugal. Please check the Symposium website and details here: <https://meetings.pices.int/meetings/>

[international/2022/pelagic/scope](https://meetings.pices.int/meetings/-international/2022/pelagic/scope). The Symposium Scientific Program will include six workshops scheduled for Nov. 7, immediately prior to the main 4-day program, and will be half-day long.

We are hosting workshop \*W1: Application of Genetics to Small Pelagic Fish\* will include four major talks by workshop conveners, 3-4 oral communications (12 min presentations + 3 min Q&A), and 1 hour of open Q&A session to allow ample time for workshop participants to brainstorm and discuss the application of molecular tools in fisheries science and management, and of specific applications to questions relevant to Small Pelagic Fish resources.

Plenary talks: 1. Background on the knowledge of Small Pelagic Fish genetics - Rita Castilho (University of Algarve & CCMAR - Portugal) 2. Overview of Molecular Genetics Methods - Jan McDowell (VIMS - U.S.A.) 3. Case-studies on the use of molecular genetic tools to specific questions of SPF: a. From allozymes to neutral molecular markers: population genetics of sardines and anchovies - Malika Chlaida (INRH - Morocco) b. The potential of Next-Generation-Sequencing: from genes to genomes, and from single to multiple markers - Ana Veríssimo (CIBIO - BioPolis, Portugal).

We welcome oral and poster contributions to the workshop and especially encourage early-career researchers and PhD students to present their results on using molecular genetic/genomic tools to address key questions relevant to Small Pelagic Fish biology, ecology, evolution and fisheries management.

Hope to see you in Lisbon! The workshop conveners, Ana Veríssimo Jan McDowell Malika Chlaida Rita Castilho

Ana Verissimo <verissimoac@gmail.com>

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## Lisbon PelagicFishEvolution Nov7-11

Dear colleagues,

We would like to announce the \*2022 Small Pelagic Fish Symposium\* to held November 7-11 in Lisbon, Portugal. Please check the Symposium website and details here: <https://meetings.pices.int/meetings/-international/2022/pelagic/scope>. The Symposium Scientific Program will include six workshops scheduled for Nov. 7, immediately prior to the main 4-day program, and will be half-day long.

The workshop \*W1: Application of Genetics to Small Pelagic Fish\* will include four major talks by workshop conveners, 3-4 oral communications (12 min presentations + 3 min Q&A), and 1 hour of open Q&A session to allow ample time for workshop participants to brainstorm and discuss the application of molecular tools in fisheries science and management, and of specific applications to questions relevant to Small Pelagic Fish resources.

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We welcome oral and poster contributions to the workshop (\*deadline for submission is May 22\*). We especially encourage early-career researchers and PhD students to present their results on using molecular genetic/genomic tools to address key questions relevant to Small Pelagic Fish biology, ecology, evolution and fisheries management.

Hope to see you in Lisbon!

The workshop conveners, Ana Verissimo Jan McDowell Malika Chlaida Rita Castilho

Ana Verissimo <verissimoac@gmail.com>

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## Maine Biodiversity Oct14-18

Workshop: Integrating macro-ecology & macro-evolution for biodiversity assessment

14-18 October 2022, at Schoodic in Maine

The workshop aims to connect across scales to understand factors dictating patterns of biodiversity. We plan to address a major gap in our field, connecting large-scale understanding of biodiversity at a given time period in a spatially variable environment (macroecology) with the understanding of how the integrated structure of biodiversity changes through time (macroevolution). What are the spatial and temporal drivers of biodiversity, and what aspects impart resilience to perturbations

such as those from invasive species or climate change? The biggest challenge in studying biodiversity processes is the spatial and temporal scales involved. However, there are several research avenues emerging that demonstrate ways to circumvent these limits, one theoretical and three empirical. First, several modeling approaches are under way that provide a predictive framework for how communities might respond to change. The data to test such models must come from communities in which we can actually measure change through extended time periods and large space. We have identified three such areas: Paleobiology directly observes at the spatiotemporal scales of biodiversity dynamics of macro-organisms; island biogeography provides a stage where macroecology plays out within islands and macroevolution plays out between islands; and microbial ecology makes experiments feasible at the spatiotemporal scales of biodiversity dynamics for those organisms. The workshop will bring together researchers from these different disciplines, with the goals of explicitly modeling processes that bridge macroecology and macroevolution. The primary goal is to identify commonalities across systems to build a common framework and unified theory of the processes that generate, maintain, and conserve biodiversity and create resilience therein.

The meeting organizers are Rosemary Gillespie, Michael Hickerson, and Brian McGill, together with Luke Harmon, Oskar Hagen, Stephanie Kivlin, Evan Economo, and Jessica Blois. An additional 15 scientists have been invited to participate.

We encourage graduate students based in the US to apply here for a travel grant to participate in this workshop (link address <https://forms.gle/xYtafakWPS1dNaBw7if> needed)

Please feel free to email Rosemary Gillespie [gillespie@berkeley.edu](mailto:gillespie@berkeley.edu) with any questions

Rosemary GILLESPIE <[gillespie@berkeley.edu](mailto:gillespie@berkeley.edu)>

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## Norway Bergen Systematics Marine Invertebrates Sept 26-Oct 7

ForBio - Research School in Biosystematics and the University of Bergen Norway (UiB) jointly offer the course: Systematics and Evolution of Marine Invertebrates

Time and place: Sep. 26, 2022-Oct. 7, 2022 5:00, Biological Institute (BIO), University of Bergen

Course scope: Systematics and Evolution of Marine Invertebrates is a voyage through the tree-of-life of metazoans offering a comprehensive overview of the diversity of invertebrate phyla, morphological traits, and latest hypotheses of evolutionary relationships based on molecular phylogenetics. A suit of laboratory activities gives students a truly hands-on experience and opportunity to explore the morphology of a large ensemble of major representatives of the Animal Kingdom, through the observation of life and preserved specimens, anatomical dissections, interpretation of anatomical slides, and optical microscopy.

#### Course instructors

Prof. Manuel Malaquias (University Museum of Bergen, UiB, Norway; course coordinator) Ass. Prof. Nataliya Budaeva (University Museum of Bergen, UiB, Norway; course coordinator) Prof. Andreas Hejnol (University of Jena, Germany / University of Bergen, Norway) Ass. Prof. Aino Hosia (University Museum of Bergen, UiB, Norway) Dr. Luis Martell (University Museum of Bergen, UiB, Norway) Prof. Elena Temereva (Lomonosov Moscow State University, Russia) Dr. Nina Mikkelsen (University Museum of Bergen, UiB, Norway) Ass. Prof. Andreas Altenburger (The Arctic University of Norway) Prof. Henrik Glenner (University of Bergen, Norway) Dr. Kenneth Meland (University of Bergen, Norway) Ass. Prof. Nicolas Straube (University Museum of Bergen, UiB, Norway) Dr. Jon Hestetun (NORCE Norwegian Research Centre AS) Dr. Antonina Kremenetskaia (P.P. Shirshov Institute of Oceanology, RAS, Russia) Dr. Francisca Carvalho (University Museum of Bergen, UiB, Norway)

#### Learning outcomes

- 1) To describe the morphology and anatomy of the different phyla of invertebrate animals and how they are adapted to the living environment.
- 2) Acquire knowledge on taxonomy and phylogeny of marine animals, from sponges to protochordates.
- 3) Explain the concepts and terms that underlie phylogenetic classifications and hypotheses.
- 4) Acquire competences on basic anatomical dissection and drawing techniques.
- 5) Acquire competences to understand and discuss conflictive hypotheses on the evolution of the Metazoa tree-of-life.
- 6) Develop a critical attitude towards scientific literature (papers).
- 7) Understand the dynamics of the scholar process that underlies the “making” of Science.

Application deadline: June 17th 2022

More information and registration: <https://www.forbio.uio.no/events/courses/2022/-Systematics%20and%20Evolution%20of%20Marine%20Invertebrates>  
Please feel free to contact nataliya.budaeva@uib.no

with any questions.

Nataliya Budaeva, Associate Professor Department of Natural History Section of Taxonomy and Evolution University Museum of Bergen University of Bergen PB 7800 5020 Bergen Norway

<https://www.uib.no/en/persons/Nataliya.Budaeva> Coordinator of ForBio - Research School in Biosystematics <https://www.forbio.uio.no> Nataliya Budaeva <Nataliya.Budaeva@uib.no>

## Online GradStudentProfDevel May19-20

Calling all graduate students working in animal behavior and related fields!

Please join us for a motivating and inspiring two-day virtual workshop focused on peer coaching; community building; and justice, equity, diversity, and inclusion.

REGISTER HERE BY MAY 10: <http://tinyurl.com/-2p8y5n5p> < <https://t.co/Sq76pe9hsi> >

Peer-mentoring circles: A major goal of the workshop is to build peer-mentoring circles, which create supportive environments and provide networking opportunities, and also allow scientists, especially those from under-represented groups, to learn how to navigate the culture common to the sciences and to academia. These circles provide support for you as a grad student and your next career steps.

Keynote speakers will address strategies for thriving in STEM. We are delighted to have two excellent keynote speakers:

Dr. Adriana Maldonado-Chaparro (<https://adrianamaldonadoc.wixsite.com/home> < <https://t.co/0aSIwAz8RK> >) and

Dr. Charissa Owens (<https://cofc.academia.edu/CharissaOwens/CurriculumVitae>)

Career panel: We will also have a career panel to provide insights into a wide variety of different careers, including industry, government, non-profits, and academia.

Graduate students who identify as members of minoritized groups across a variety of axes (e.g., racial or ethnic group, gender identity, sexual orientation, first-generation college student, disability, neurodivergence, veteran status, and other disadvantaged backgrounds) are strongly encouraged to apply.

Workshop details

May 19 and 20, 2022

1:00 - 4:30pm EST each day

If you have any questions, please contact the organizers: Drs. Delia Shelton (shelton.delia@gmail.com), Alex Trillo (ptrillo@gettysburg.edu), Beth Reinke (eareinke@neu.edu), Elizabeth Hobson (hobsonh@ucmail.uc.edu), Caitlin Wells (cpwells@rams.colostate.edu), Alycia Lackey (alycia.lackey@louisville.edu), and Ginny Greenway (egreenway@ufl.edu).

Alycia CR Lackey Assistant Professor Department of Biology University of Louisville alyciarlackey.weebly.com

“Lackey,Alycia Carolyn Reynolds”  
<alycia.lackey@louisville.edu>

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## Online IntroAncientMetagenomics Aug1-5

/Last reminder of the announcement below. Application form shuts in one week on June 1st!/  
Dear colleagues,

The SPAAM Community is offering a new 5 day virtual summer school course sponsored by the Werner Siemens Foundation: \*Introduction to Ancient Metagenomics\*.

DATE AND SCHEDULE: Online from Monday 1st to Friday 5th of August from 09:00 to 17:00 (CEST, Leipzig time zone).

ORGANISERS: Dr. Christina Warinner (Harvard University, Max Planck Institute for Evolutionary Anthropology) and James Fellows Yates (Max Planck Institute for Evolutionary Anthropology, Leibniz Institute for Natural Product Research and Infection Biology Hans Knöll Institute).

INSTRUCTORS: Dr. Aida Andrades Valtueña, Dr. Theodor C. Lamnidis, Dr. Arthur Kocher, Dr. Alex Hübner, Dr. Irina Velsko, Dr. Alexander Herbig, Megan Michels, Alina Hübner, Clemens Schmid, Maxime Borry (and more TBC)

COURSE OVERVIEW: Ancient metagenomics applies cutting-edge metagenomic methods to the degraded DNA content of archaeological and paleontological specimens. The rapidly growing field is currently uncovering a wealth of novel information for both human and natu-

ral history, from identifying the causes of devastating pandemics such as the Black Death, to revealing how past ecosystems changed in response to long-term climatic and anthropogenic change, to reconstructing the microbiomes of extinct human relatives. However, as the field grows, the techniques, methods, and workflows used to analyse such data are rapidly changing and improving.

In this \*hands-on summer school (block praktikum)\* we will go through the main steps of ancient metagenomic bioinformatic workflows, familiarising students with the command line, demonstrating how to process next-generation-sequencing (NGS) data, and showing how to perform de novo metagenomic assembly. Focusing on host-associated ancient metagenomics, the course consists of a combination of lectures and hands-on exercises, allowing participants to become familiar with the types of questions and data researchers work with. Round table discussions with experts at each stage of the workflow will be held to allow participants to get advice on their own projects and research.

By the end of the course, participants will have an understanding of how to effectively carry out the major bioinformatic components of an ancient metagenomic project in an open and transparent manner. Attendees will be eligible for ECTS points (awarded by the JSMC Graduate School, Friedrich-Schiller University, Germany) or a certificate of completion (Max Planck - Harvard Research Center, MHAAM).

### SYLLABUS

#### Day 1

1:00 \* Lecture: Introduction to NGS data 2:00 \* Practical 1: BareBonesBash 1 3:00 \* Practical 2: BareBonesBash 2 4:00 \* Round table: Introductions

#### Day 2

1:00 \* Lecture: Introduction to ancient DNA 2:00 \* Practical 1: Bytesize git 3:00 \* Practical 2: ancient-MetagenomeDir 4:00 \* Practical: nf-core/eager 5:00 \* Round table: Project organisation

#### Day 3

1:00 \* Lecture: Introduction to metagenomics 2:00 \* Practical 1: Introduction to R and the tidyverse 3:00 \* Practical 2: Taxonomic profiling, OTU tables and visualisation 4:00 \* Round table: Taxonomic classifiers

#### Day 4

1:00 \* Lecture Introduction to microbial genomics 2:00 \* Practical 1: Genome mapping 3:00 \* Practical 2: Genome assembly 4:00 \* Roundtable: Databases

#### Day 5

1/2 \* Lecture Evolutionary biology 1/2 \* Practical 1: Phylogenomics 1/2 \* Practical 2: Functional genomics 1/2 \* Round table: Workshop review

ELIGIBILITY: The course is aimed at masters students and early-stage PhD students, to a maximum of 25 participants. Course instruction will take place online.

APPLICATIONS: Applications are open from April 29 to June 1 2022. To apply, please visit our website: <https://spaam-community.github.io/wss-summer-school/> For questions or more information, contact James Fellows Yates (james\_fellows\_yates@eva.mpg.de) or Christina Warinner (christina\_warinner@eva.mpg.de)

Best regards Christina and James

– James A. Fellows Yates

Microbiome Sciences Group, Dept. of Archaeogenetics  
Max Planck Institute for Evolutionary Anthropology

Dept. of Paleobiotechnology Leibniz Institute for Natural Product Research and Infection Biology Hans Knöll Institute

“James A. Fellows Yates”  
<james\_fellows\_yates@eva.mpg.de>

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## Online IntroDeepLearning Sep26-30

Dear all,

registration is now open for the 3rd edition of the Introduction to Deep Learning for biologists.

Dates: online, 26th-30th of September

The course is aimed at advanced students, researchers, and professionals interested in learning what deep learning is and how to develop a deep learning model for applications in biology. It will include information useful for both absolute beginners and more advanced users willing to delve into some aspects of the implementation of deep learning. We will start by introducing general concepts of deep learning presenting a functioning model and then we will progressively describe the main building blocks of a deep learning model and how the internal machinery works. Attendees are expected to have a background in biology and the research problems involving prediction, inference, and pattern discovery. There will be a mix of lectures and hands-on practical exercises using mainly Python, Jupyter Notebooks, and the Linux command line. Some basic understanding of Python programming and the Linux environment will

be advantageous but is not required.

Course website: ( <https://www.physalia-courses.org/courses-workshops/course67/> )

Full list of our courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops> )

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
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“info@physalia-courses.org” <info@physalia-courses.org>

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## Online LinearMixedModelsInR Sep26-30

Dear all,

registrations are now open for the Physalia course “LINEAR MIXED MODELS IN R”

Course website: ( <https://www.physalia-courses.org/courses-workshops/glmms-in-r/> )

Dates: Online, September 26th-30th In this course, you will learn to specify, interpret and validate linear and generalized linear mixed models. The key focus will be to produce a valid and defensible analysis of experimental or observational data in an applied research context in R, with a focus on the regression packages lme4 and glmmTMB.

Full list of our courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops> )

Should you have any questions, please do not hesitate to contact us at: info@physalia-courses.org

Best regards, Carlo

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courses.org>

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## Online lowcoverageWholeGenomeSe- quencing Oct10-13

ONLINE course “Population genomic inference from low-coverage whole-genome sequencing data”

When: 10-13 October 2022

Instructors: Dr. Nina Overgaard Therkildsen (Cornell University, US) Dr. Tyler Linderoth (University of Cambridge, UK), Dr. Arne Jacobs (University of Glasgow, UK) and Nicolas Lou (Cornell University, US)

Course website: ( <https://www.physalia-courses.org/-courses-workshops/course64/> )

In this course, we will explore workflows and the underlying rationale behind producing, processing, and analyzing low-coverage sequencing data for population genomic inference. Given that most species have insufficient reference data to allow reliable genotype imputation, we will focus on genotype likelihood-based methodology that can be applied to any system. We will primarily cover methods and algorithms implemented in the ANGSD software package and associated programs, providing best-practice guidelines and discussion of how participants can make maximal use of low-coverage whole genome re-sequencing data for their studies.

The course is aimed at researchers who might have previous experience with next generation sequencing (NGS) data (e.g. exome/RAD/pooled sequencing) and wish to explore the potential for using low-coverage whole-genome sequencing for their studies.

All hands-on exercises will be run in a Linux environment on remote servers. Statistical analyses and data visualization will be run in R.

Full list of our courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops> )

Should you have any questions, please feel free to contact us: [info@physalia-courses.org](mailto:info@physalia-courses.org)

Best regards,

Carlo

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## Online MetabarcodingMicrobialEcol Jun6-10 Lastcall

Dear all,

there are the last few seats available for the course METABARCODING IN MICROBIAL ECOLOGY.

Dates: Online, 6th-10th June

Course website: ( <https://www.physalia-courses.org/-courses-workshops/course30/> )

this course will provide a thorough introduction to the application of metabarcoding techniques in microbial ecology. The topics covered by the course range from bioinformatic processing of next-generation sequencing data to the most important approaches in multivariate statistics. Using a combination of theoretical lectures and hands-on exercises, the participants will learn the most important computational steps of a metabarcoding study from the processing of raw sequencing reads down to the final statistical evaluations. After completing the course, the participants should be able to understand the potential and limitations of metabarcoding techniques as well as to process their own datasets to answer the questions under investigation.

Full list of our courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops> )

Should you have any questions, please feel free to contact us: [info@physalia-courses.org](mailto:info@physalia-courses.org)

Best regards,

Carlo

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## Online RADSeq Jun6-9

The University of Connecticut's Computational Biology Core is offering a workshop on assaying genetic variation using restriction-associated DNA sequencing, or RAD-Seq.

The workshop will cover basic concepts and walk through a complete analysis on a high performance computing cluster. The analysis will start with raw reads and go through some very basic analyses of population genetic structure. The core learning goal is to familiarize attendees with the steps necessary to generate, filter and compare variant call sets using RAD-seq data, the tools available, common data formats and how to convert between them, and possible pitfalls they may encounter.

We'll use data collected from a landscape genetic study of arctic grayling, a marine fish, using the ddRAD method (Peterson et al. 2012). All code required to complete the full analysis will be provided in a public github repository, and sessions recordings will be available to all participants after the workshop.

The workshop will take place over 4 days for 3-3.5 hours each day.

Dates: June 6-9 2022 Time (ET): Day 1: 8:30am-12:00pm, Days 2-4 9.00am - 12.00pm Location: Online Cost: \$350/\$483USD for UConn affiliated/External attendees.

Workshop schedule:

Day 1: Introduction to Linux/HPC Day 2: Introduction to RADSeq, high throughput sequencing data, quality control, read mapping Day 3: Reference-based and de novo variant discovery approaches. Day 4: Manipulating, filtering, reformatting output files. Basic population genomic analyses.

Registration:

To register, please follow this link: <https://forms.gle/-daCLSmFtDhJQ7ndQA> Other upcoming virtual workshops: Variant detection with WGS - July 25-28 Differential expression analysis with RNA-seq, reference genome based - August 22-25 Genome assembly - September 26-29 Genome Annotation - October 24-27

Workshop FAQ:

Who should attend?

Anyone who wants to learn the fundamentals of RAD-seq analysis.

What are the prerequisites?

Prior bioinformatic experience is not required. We have dedicated the first day of the workshop to the basics of Linux and high performance computing.

What do I need?

You will need your own laptop to use, have a recent version of R/RStudio installed, and some other applications. We will send you details of software and installation instructions prior to the workshop.

Can I bring my own data?

We will provide experimental data for use during the workshop, as this helps to keep the workshop moving. There will be time, however, to discuss your own datasets and how you might work with them outside of the workshop.

How much does it cost?

The registration fee is \$350/\$483USD for UConn affiliated/External attendees.

How do I pay?

The fee is due at the time of registration. UConn affiliates can use KFS accounts. The only other means of payment we currently accept is credit card. Due to some complications we cannot accept international wire transfers at this time.

Where is the workshop?

It will be held on Zoom.

How do I apply?

All registration is "first-come, first-served." There is no application process. Sign up as soon as possible to ensure your place in the workshop.

Do you offer scholarships or tuition waivers?

Yes. For each workshop we offer waivers to up to two attendees without other funding sources. Preference will be given to students from primarily undergraduate institutions, from countries classified by the World Bank as low or middle-income, and those from underrepresented groups. Applicants for waivers may submit a one paragraph justification to [cbcsupport@uconn.edu](mailto:cbcsupport@uconn.edu).

Questions?

If you have any questions, please don't hesitate to contact us at [cbcsupport@uconn.edu](mailto:cbcsupport@uconn.edu)

Noah Reid [noah.reid@uconn.edu](mailto:noah.reid@uconn.edu)

Assistant Research Professor Institute for Systems Ge-



nomics University of Connecticut  
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## Online RADseqStacks Oct3-7

Dear all, registration is now open for the 3rd edition of the RADseq data analysis using Stacks course with Dr. Naiara Rodriguez-Ezpeleta (AZTI, Spain), Dr. Tereza Manousaki (Hellenic Centre for Marine Research, Greece) and Dr. Natalia Diaz Arce (AZTI, Spain). Dates: Online, 3th-7th October 2022 In this course, we will introduce the different approaches for obtaining reduced representation genome sequencing data and will specially focus on the data analysis using ( <http://catchenlab.life.illinois.edu/stacks/> ). We will cover all necessary steps to obtain genome variants from short read data that are informative for population genetics, phylogenetic and association studies.

If interested, please visit our website: ( <https://www.physalia-courses.org/courses-workshops/course16/> )

Full list of our Courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops> )

Should you have any questions, please feel free to contact us: [info@physalia-courses.org](mailto:info@physalia-courses.org)

Best regards,

Carlo

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“[info@physalia-courses.org](mailto:info@physalia-courses.org)” <[info@physalia-courses.org](mailto:info@physalia-courses.org)>

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## Online SeascapeGenomicsInR Nov31-Oct4

Dear all,

registrations are now open for the 3rd edition of the Physalia course on “Seascape Genomics”, which will take place ONLINE from October 31st to November 4th.

Instructors: Dr. Laura Benestan (CEFE-CNRS, FR) and Oliver Selmoni (EPFL, CH).

Course website: ( <https://www.physalia-courses.org/courses-workshops/course70/> )

In this course, students will learn the basics of this approach and train using state-of-the-art methods. Firstly, students will learn how to extract environmental data from publicly available databases and how to use it to characterize the seascape structure and conditions. For instance, students will learn how to use remote sensing data to describe seawater temperature oscillations or seawater movements. Next, the course will focus on genomic analyses: students will learn how to evaluate genetic structures in the marine environment and calculate and display connectivity between populations. The combination of environmental and genomic data will also lead to the study of local adaptation. Students will learn different methods to discover genetic/genomic signatures potentially involved in adaptation against specific environmental constraints. The course will also cover the critical task of the interpretation and validation of the results, particularly in an applied conservation and management context. Finally, the workshop will consider the crucial aspects and good habits to account for designing a seascape genomics experiment (e.g. sampling design) from a relevant scientific question.

Should you have any questions, please feel free to contact us at: [info@physalia-courses.org](mailto:info@physalia-courses.org)

All the best,

Carlo

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## Piancenza Italy WildlifeConservationGenomics Sep15-16

Dear Colleagues,

On behalf of the Organizing and Scientific Committees, I am happy to announce the International Workshop on the Integration of Genomic and Geographic Information System data for Wildlife Conservation WIGGIS (<https://wiggis.eu/>) organized by Life CLAW project

and to be held in Piacenza (Italy) on September 15-16, 2022.

Registration and abstract submission are open.

Thanks to the support of Life EU programme, the participation to the WIGGIS Workshop is free of charge. The registration includes coffee breaks, social dinner and one lunch. Maximum number of participants is 100.

Please, visit the Workshop website (<https://wiggis.eu/>) for detailed information.

Looking forward to meeting you in Piacenza,

Licia Colli

Dott.ssa Licia Colli Ricercatore Facoltà  $\frac{1}{2}$  di Scienze Agrarie, Alimentari e Ambientali / DIANA Dipartimento di Scienze Animali, della Nutrizione e degli Alimenti / BioDNA Centro di ricerca sulla Biodiversità  $\frac{1}{2}$  e sul DNA Antico [licia.colli@unicatt.it](mailto:licia.colli@unicatt.it) tel +39 0523 599 481 fax +39 0523 599 276 skype liquid-diamond

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"licia.colli@unicatt.it" <[licia.colli@unicatt.it](mailto:licia.colli@unicatt.it)>

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### SummerInstStatGenetics EarlybirdDeadline Jun3

The early-bird deadline for Summer Institute in Statistical Genetics is June 3. Over 200 participants have already registered for their choices of the 19 modules

being offered online during July 11-29, and some of the modules are nearly full. Complete information is available at <https://si.biostat.washington.edu> Bruce Weir, [bsweir@uw.edu](mailto:bsweir@uw.edu)

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### SwissAlps AncientDNAToStudyEvolution Aug28-Sep1

We are pleased to announce that we are organizing a new workshop on "Ancient DNA: A Time Machine to Study Evolution" in the Swiss Alps from August 28th to September 1st 2022.

The workshop will consist of two parts: 1) It will provide an introduction to the ancient DNA bioinformatic tool ATLAS (<https://bitbucket.org/wegmannlab/atlas/>) and on performing demographic inference with fastsimcoal2 (<http://cmpg.unibe.ch/software/fastsimcoal2/>). 2) It will involve students and invited speakers to discuss how ancient DNA can help to answer longstanding questions about evolutionary processes. All students will have an opportunity to present their work either through a short talk or a poster.

Confirmed speakers include Eline Lorenzen, Benjamin Peter, Joachim Burger, Serena Tuci and Daniel Bradley.

The workshop is supported by the CUSO. The program and registration is available at <https://bit.ly/39fwXGa> Beware that the workshop is limited to 30 people.

Daniel Wegmann <[phaentu@gmail.com](mailto:phaentu@gmail.com)>

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## Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). In addition, if it originates from 'blackballed' addresses it will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email [evoldir@evol.biology.McMaster.CA](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be send to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA) and processed later. In either case, please do not expect an instant response.

## Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L<sup>A</sup>T<sub>E</sub>X do not try to embed L<sup>A</sup>T<sub>E</sub>X or T<sub>E</sub>X in your message (or other formats) since my program will strip these from the message.