
E v o l D i r

April 1, 2021

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

Foreword

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

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

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



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Conferences

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IndianaU NCGASResSeminar Mar9

What do researchers who use NCGAS do? What are the biological questions they're interested in and what results come out of their genomic research? To find out, join us for our new webinar series, each presented by an NCGAS-affiliated Researcher. We'll also share recordings and tools for you to do similar analyses each month on our blog. These seminars will take place once a month, on the second Tuesday at 2PM (EST). We currently have speakers through August (see below).

For more information and to register (registration for each talk is required to receive the zoom link): <https://go.iu.edu/3Emt> March 9 P, 2.00PM. Petra Lenz, University of Hawai'i at Mānoa

“Environmental transcriptomics of seasonal dormancy in a sub-arctic copepod, a key crustacean zooplankter at the base of the metazoan food web.”

<http://www.pbrc.hawaii.edu/index.php/lenz-ph> April 13, 2.00PM. Jingwei Song, Virginia Institute of Marine Science

Comparative transcriptomics of spotted seatrout (*Cynoscion nebulosus*) populations to cold and heat stress

https://www.vims.edu/people/song_j/index.php May 11, 2.00PM. Jean-Francois Gout, Mississippi State University

A Genome-Wide View of Transcription Fidelity.

<https://sites.google.com/view/goutlab> June 08 , 2.00PM. Lydia Bright, SUNY New Paltz

Uncovering molecular determinants of *Holospira* infection in *Paramecium* cells

<https://www3.newpaltz.edu/directory/profile/lydiabright> July 13, 2.00PM. Layla R. Freeborn

“Red frog, green frog, blue frog: estimating phylogenetic relationships among closely related populations of *Oophaga pumilio* from Bocas del Toro, Panama”

Dr. Sheri Sanders Manager, Bioinformatic Analyst National Center for Genome Analysis Support (NCGAS)

NCGAS is a management unit of the Research Technologies division of UITS; NCGAS is affiliated with the Indiana University Pervasive Technology Institute.

“Sanders, Sheri” <ss93@iu.edu>

Online 2ndAsiaEvo Aug16-19

Title: Online.2ndAsiaEvoConference.Aug16-19

Dear all:

We are now calling for symposia for the upcoming 2nd AsiaEvo online conference to be hosted on August 16th-19th in Tokyo. Koichiro Tamura is the local chief organizer. Selection of symposium topics will be aimed at spanning the range of interests of the conference participants, including exciting new scientific developments to represent the geographic and gender diversity of organizers and invited speakers. The submission deadline for the proposals is Mar. 31st, 2021. Successful applications will be confirmed by the end of April. Please email us at asiaevo2@biol.se.tmu.ac.jp for any questions.

Each symposium will include 2 or 3 invited speakers and some contributed speakers. Symposium proposals should include names of 2-3 proposed invited speakers capable of delivering a talk of high quality and wide interest. At the time of proposal submission, the symposium organizer should have confirmed that the proposed invited speakers agreed to accept the invitation. The symposium organizers will also select contributed speakers from the abstracts submitted by registered delegates.

The final decision on the selection of symposia, invited and contributed talks will be made by Scientific Organizing Committee (SOC). Criteria will include quality of the proposals, breadth of interest to participants, and representation of organizers and speakers' diversity. To submit your proposal, please go to <https://evolgen.biol.se.tmu.ac.jp/asiaevo2/> Thank you.

Regards – Qi Zhou, PhD Professor Life Sciences Institute Zhejiang University <http://qizhoulab.net/> Qi Zhou <zhouqi1982@zju.edu.cn>

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Regards – Qi Zhou, PhD Professor Life Sciences Institute Zhejiang University <http://qizhoulab.net/> Qi Zhou <qi.zhou@univie.ac.at>

Online BiodiversityGenomics Apr21

Dear biodiversity enthusiasts,

We are pleased to invite you to the Senckenberg Biodiversity Genomics Symposium on 21. April 2021.

This one-day virtual event is co-organised by the LOEWE Centre for Translational Biodiversity Genomics (tbg.senckenberg.de/) at the Senckenberg Research Institute, and PacBio. Scientists from Europe and elsewhere will share their experiences in using PacBio long-read sequencing techniques to generate reference-quality genomes of taxonomically diverse organisms to address key questions in ecology and evolution.

The event includes: - Presentations with a focus on biodiversity - Live Q&A sessions - Poster presentations - On-demand tutorials for those new to PacBio

We have a great list of confirmed speakers, presenting genomic insights from a broad range of eukaryotic species.

The agenda will be online soon.

A registration is required, but is completely free: <https://events.pacb.com/senckenberg-biodiversity> We look forward to meeting you at the Symposium.

Carola Greve and Michael Hiller

Michael Hiller, PhD Professor of Comparative Genomics LOEWE Centre for Translational Biodiversity Genomics, Senckenberg Society for Nature Research & Goethe University, Frankfurt am Main, Germany

Michael Hiller <michael.hiller@senckenberg.de>

Online CIGENE Mar17

Dear EvolDir members,

We are pleased to announce the coming talk at the online CIGENE seminar by Anneliese Mason (University of Bonn) on 17th March 2021 at 12:00-12:50 (Oslo time). He will talk about: “Making new crop species”.

Abstract: By investigating how hybrid species form, we hope to work out how to utilise these natural evolutionary processes for human agricultural benefit, making new Brassica crop types for food, oil and biofuel. Hybridisation and genome doubling are processes which often result in increased vigour and ability to exploit different environmental niches in nature. Hence, if we can harness these processes to produce new hybrid species, such species may have a wider tolerance of environmental conditions such as heat, drought and disease, which would be beneficial to human agriculture.

For more information on CIGENE seminars, please visit: <https://cigene.no/cigene-seminar-series/> Anybody interested except for Zoombomber is welcome. Recording is not planned.

Best wishes,

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>

Online CIGENE Mar24

Dear EvolDir members,

We are pleased to announce the coming talk at the online CIGENE seminar by Kentaro Shimizu (University of Zurich) on 24th March 2021 at 12:00-12:50 (Oslo time). He will talk about: “Genome duplication affected patterns of selection in polyploid Arabidopsis and wheat species”.

Abstract: In 1970, Susumu Ohno proposed that genome duplication is an important source of novelty in vertebrates. Recent advances in polyploid genomics enabled population genomic studies of initial stages of genome duplication. Our data supported that parental adaptive traits were combined thanks to allopolyploidization in natural Arabidopsis and crop wheat allopolyploid species.

For more information on CIGENE seminars, please visit: <https://cigene.no/cigene-seminar-series/> Anybody interested except for Zoombomber is welcome. Recording is not planned.

Best wishes,

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.saitou@nmbu.no” <marie.saitou@nmbu.no>

Online EcuadorHerbariumTour Mar11-12

Dear all,

The recently created herbarium UTCEC at Universidad Técnica de Cotopaxi, in collaboration with Universidad Regional Amazónica Ikiam (both in Ecuador) and with the endorsement of the Society for Herbarium Curators (SHC), International Association for Plant Taxonomy (IAPT), Asociación Latinoamericana de Botánica (ALB), and Asociación Botánica Ecuatoriana (ABE), are organizing a two-day virtual seminar titled “Herbaria and their treasures/Herbarios y sus tesoros/Herbários e seus tesouros.”

Everyone is welcome and your help sharing this announcement is greatly appreciated.

This event will happen on the 11-12 March 2021, from 09:00-14:00 hours (Ecuador Time) and the details are below:

Zoom Meeting No: 953 2831

Password: 607090 Registration: <https://forms.gle/Fz6GQFufkEgtc17S7> Contact information: Alina Freire-Fierro (alina.freire@ikiam.edu.ec) and Javier Irazábal (roberto.irazabal@utc.edu.ec)

Program: Thursday/Jueves/Quinta Feira
March/Marzo/Março 11, 2021

Opening/Inauguración, 09:00-09:30 (Ecuador Time), 14:00-14:30 (GTM) Javier Irazábal M.S., Tesoros del herbario UTCEC (Latacunga, Ecuador), 09:30-10:00 (Ecuador Time), 14:30-15:00 (GTM) Alina Freire-Fierro, Ph.D. et al., Tesoros de los herbarios Ecuatorianos (Latacunga/Tena, Ecuador), 10:00-10:30 (Ecuador Time), 15:00-15:30 (GTM) Break, 10:30-11:00 (Ecuador Time), 15:30-16:00 (GTM) Barbara Thiers, Ph.D., Treasures from the Herbarium NY (New York, USA), 11:00-11:30 (Ecuador Time), 16:00-16:30 (GTM) Muthama Muasya, Ph.D., Treasures from the Herbarium BOL (Cape Town, South Africa), 11:30-12:00 (Ecuador Time), 16:30-17:00 (GTM) Yao-Wu Xing, Ph.D., Treasures from the Herbarium XTBG (Xishuangbanna, China), 12:00-12:30 (Ecuador Time), 17:00-17:30 (GTM)

Q/A-Preguntas/Respuestas, 12:30-13:30 (Ecuador Time), 17:30-18:30 (GTM)

Friday/Viernes/Sexta Feira, March/Marzo/Março 12th, 2021

Bente B. KlitgÅrd, Ph.D., Treasures from the Herbarium K (Kew, United Kingdom), 09:00-09:30 (Ecuador Time), 14:00-14:30 (GTM)

Brendan Lepschi, Ph.D., Treasures from the Herbarium CANB (Canberra, Australia), 09:30-10:00 (Ecuador Time), 14:30-15:00 (GTM)

Gerardo Salazar Chávez, Ph.D., Tesoros del Herbario MEXU (México, México), 10:00-10:30 (Ecuador Time), 15:00-15:30 (GTM)

Break, 10:30-11:00 (Ecuador Time), 15:30-16:00 (GTM)

Banessa Falcón Hidalgo, Ph.D.(c.) and Rosa Rankin, Ph.D., Tesoros del Herbario HAJB (La Habana, Cuba), 11:00-11:30 (Ecuador Time), 16:00-16:30 (GTM)

Maria Candida Mamede, Ph.D., Tesouros do Herbário SP (São Paulo, Brazil), 11:30-12:00 (Ecuador Time), 16:30-17:00 (GTM)

Q/A-Preguntas/Respuestas, 12:00-13:00 (Ecuador

Time), 17:00-18:00 (GTM) Closing/Clausura, 13:00-13:30 (Ecuador Time), 18:00-18:30 (GTM) Virtual networking, 13:30-14:30 (Ecuador Time), 18:30-19:30 (GTM)

Lic. M.em C., Alina Freire-Fierro, M.S., Ph.D. Profesora Titular de Botánica Agregado 3, Universidad Regional Amazónica Ikiam Curadora Asociada del Herbario UTCEC, Universidad Técnica de Cotopaxi Alina.freire@ikiam.edu.ec, Alina.freire@utc.edu.ec

Skype: alinaff; Twitter: affbotanica
www.neotropicos.net T: (+593) 99-775-6935
alina.freire@ikiam.edu.ec

Online EvoEcoSeminars Mar31-Apr14

Dear EvolDir,

Join us for next week's talk in our popular, weekly, online seminar series in Evolution and Ecology. As we approach the Easter period, we are delighted to announce the details of our next three exciting seminars—save the dates!

—

Wed 31 March

Prof. Troy Day

Dept. of Mathematics & Statistics and Dept. of Biology, Queen's University, Canada

“The evolutionary epidemiology of emerging infectious diseases”

—

Wed 7 April

Prof. Aneil Agrawal

Dept. of Ecology & Evolutionary Biology, University of Toronto, Canada

Title TBC

—

Wed 14 April

Prof. Tracey Chapman

School of Biological Sciences, University of East Anglia, UK

“Sexual selection, sexual conflict & evolutionary change”

When: 5PM BST/ 9AM PST , every Wednesday

Where: talks live-streamed to our YouTube channel <https://www.youtube.com/channel/UCMsYvoHLNVm4rbcTLj162zQ> , post your questions for our speakers via Slack

Publicity: upcoming talks promoted on Slack & Twitter @EvoEcoSeminars (<https://twitter.com/EvoEcoSeminars>)

How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-x154980/-shared_invite/zt-ev4fe0io-M7B~D6p74blV_ZRcDtmAcg
Please follow our Twitter feed and join the Slack group for details of future upcoming talks.

Hope that you can join us. Feel free to circulate to anyone who may be interested.

Many thanks,

Dr. Elizabeth Duxbury Dr. Andreas Sutter Dr. Iulia Darolti Dr. Wouter van der Bijl

Dr. Elizabeth Duxbury Senior Postdoctoral Research Associate Prof. Alexei Maklakov Group School of Biological Sciences University of East Anglia Norwich Research Park UK

“Elizabeth Duxbury (BIO - Staff)”
<E.Duxbury@uea.ac.uk>

Online Evolution2021 Jun21-25

Virtual Evolution 2021 - June 21 - 25, 2021 - Registration is Open!

<https://www.evolutionmeetings.org/> The Evolution conference is the joint annual meeting of the American Society of Naturalists < <http://www.amnat.org/> >*, the Society for the Study of Evolution < <http://www.evolutionsociety.org/> >*, and the Society of Systematic Biologists < <https://www.systbio.org/> >*. The meeting is one of the premier opportunities for sharing research on evolutionary biology each year.—For 2021, our conference will be virtual with live-streamed plenaries, scheduled faux-live concurrent sessions, on-demand talks, and topical networking events.

We are pleased to offer free meeting registration to 200 society members from 139 countries and territories around the world. Applicants must be members of ASN, SSB, or SSE. If you have joined SSE through

the Global Membership Assistance Program < <http://www.evolutionsociety.org/index.php?module=content&type=user&func=view&pid=8#gma> >*, you are eligible for free registration. Learn more and apply here < <https://www.evolutionmeetings.org/global-participation.html> >*

Events

Plenaries.: Each day will be highlighted by a live-streamed plenary. On Friday, the 25th, we will live stream award symposia and talks.

Faux-live talks.: Up to ~1,000 synchronous “faux-live” talks will be accepted. These pre-recorded talks will be played at a certain time and available to view after that time. These talks will be limited to 10 minutes. Each faux-live concurrent session—will include 9 faux-live talks played sequentially. During each talk, presenters will be present to answer questions via chat. Video discussion sessions for presenters and attendees will follow each faux-live session. See the Schedule Overview < <https://www.evolutionmeetings.org/overview.html> >— for more information.

On-demand talks.: Up to ~800 on-demand talks will be accepted. These pre-recorded talks will be available to view any time, much like browsing a set of posters. These talks will be limited to 6 minutes.

Networking and Discussion.: We will have numerous opportunities for networking/discussion:

* After each concurrent session the speakers and attendees will participate in discussion/networking Zoom sessions focused on the same topic. * Networking lounges will be available in the conference lobby. * An open Zoom room will be available in the lobby to mingle and meet with other attendees throughout the conference. Breakout rooms will be available for group conversations. * The virtual platform will allow attendees to—find other attendees with similar interests, arrange group meetings, and advertise conference-related activities. * You will be able to sign up to participate in faculty-student networking groups for coffee, lunch, or happy hour meetings.

Satellite Events.: The societies are planning a variety of workshops, panels, and social events. See the Workshops and Networking Events page < <https://www.evolutionmeetings.org/workshops-and-networking-events.html> > for more information.

– Mitch Cruzan (He/Him) Professor of Biology Portland State University PO Box 751 Portland, OR 97207 USA Web: <https://cruzanlab.weebly.com/> Evolutionary Biology - A Plant Perspective

/Mitchell B. Cruzan// Available through all

good bookshops, or direct from Oxford University Press < <https://global.oup.com/academic/product/-evolutionary-biology-9780190882679?cc=us&lang=en&#> >/

Mitchell Cruzan <cruzan@pdx.edu>

Online EvolutionAndMedicine Jul15-16

Abstract submission and registration are now open for the July 15-16 Sixth Annual Meeting of the International Society for Evolution, Medicine, and Public Health. <http://isemph.org> ISEMPH 2021 will be all online, making it possible for friends and colleagues from around the world to participate at nominal expense. Plenary speakers and interactive activities will be live, all other talks will be pre-recorded and available via our website on our YouTube channel, followed by moderated discussions with Q&A. Full information at <https://isemph.org/2021-Meeting> ->20% discount on ISEMPH membership and renewal fees using code "COVIDYEAR" until March 31. ->Discounted early meeting registration until April 30. ->Abstract submission closes April 30.

Confirmed Plenary speakers include:

Dr. Kizzmekia Corbett Vaccine Research Center, National Institute of Allergy and Infectious Diseases "SARS-CoV-2 mRNA Vaccine Development Enabled by Prototype Pathogen Preparedness"

Dr. Kath Maitland Surgery & Cancer, Imperial College London "The FEAST Trial: 10 Years On."

Dr. Beverly Strassmann Anthropology, The University of Michigan "Developmental Origins in Evolutionary Perspective: A 20-year Prospective Cohort Study of the Dogon of Mali"

Dr. Paul Turner Ecology and Evolutionary Biology, Yale University "Leveraging Evolutionary Trade-Offs and Phage Selection Pressure to Reduce Bacterial Pathogenicity in Patient Therapy"

ISEMPH 2021 emphasizes the multiple interfaces between evolutionary biology and human health in medicine, nursing, veterinary medicine, anthropology, evolutionary psychology, behavioral ecology and epidemiology. Students and clinicians at all stages of professional development are especially welcome.

Winners of the George C. Williams Prize and the Gilbert Omenn Prize will also give plenary presentations. The

\$5000 Williams prize goes to the best 2020 article published in the OUP journal Evolution, Medicine, and Public Health. Nominations are now open for the \$5000 Omenn Prize for the best 2020 article in any journal on a topic related to evolution, medicine, and public health. <https://isemph.org/Omenn-Prize> The ISEMPH2021 Program Committee is chaired by Michael Muehlenbein, PhD, MsPH, Professor and Chair in the Department of Anthropology at Baylor University.

The mission of the International Society for Evolution, Medicine, and Public Health's is to foster communication among scientists, students, clinicians and public health professionals who use evolutionary insights to improve medical research and practice, and information on human health and disease to advance evolutionary biology. Previous meetings have been at Arizona State University, Duke University, Groningen, Netherlands (with ESEB), Park City, Utah, and Zurich, Switzerland. The 2022 meeting will be in Lisbon, Portugal.

In addition to annual meetings, ISEMPH sponsors ->the Oxford University Press journal Evolution, Medicine, & Public Health, <https://academic.oup.com/-emph> ->The Evolution and Medicine Review, and <http://evmedreview.com> ->and <http://EvMedEd.org> . rmnesse@gmail.com

Online EvolutionEcol Mar17

Dear EvolDir,

Join us for next week's talk in our popular, weekly, online seminar series in Evolution and Ecology.

—
Wed 17 March

Dr. Pavitra Muralidhar

Center for Population Biology, University of California, Davies, USA

"Sex chromosomes and genetic conflict"

—
When: please note time change- 4PM GMT/9AM PST start just for this week (due to clocks change in Pacific region).

Where: talks live-streamed to our YouTube channel <https://www.youtube.com/channel/UCMsYvoHLNVm4rbcTLj162zQ> , post your questions for our speakers via Slack

Publicity: upcoming talks promoted on Slack & Twitter @EvoEcoSeminars (<https://twitter.com/EvoEcoSeminars>)

How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-xl54980/-shared_invite/zt-ev4fe0io-M7B~D6p74blV_ZRcDtmAcg
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Many thanks,

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— Dr. Elizabeth Duxbury

Senior Postdoctoral Research Associate Prof. Alexei Maklakov Group School of Biological Sciences University of East Anglia Norwich Research Park UK

“Elizabeth Duxbury (BIO - Staff)”
<E.Duxbury@uea.ac.uk>

Online EvolutionEcology Feb24

Dear EvolDir,

Join us for this week's talk in our popular, weekly, online seminar series in Evolution and Ecology.

—
Wed 3 March

Dr. Melissah Rowe

Dept. of Animal Ecology, Netherlands Institute of Ecology (NIOO-KNAW)

“Reproductive microbiomes and the functional evolution of avian ejaculates”

—
When: 5PM GMT / 9-10AM PST, Wednesdays.

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“Elizabeth Duxbury (BIO - Staff)”
<E.Duxbury@uea.ac.uk>

Online EvolutionEcology Mar10

Dear EvolDir,

Join us for next week's talk in our popular, weekly, online seminar series in Evolution and Ecology.

—
Wed 10 March

Prof. Li Zhao

The Rockefeller University, New York, USA

“The origin and evolution of new genes and phenotypes”

—
When: 5PM GMT / 9-10AM PST, Wednesdays.

Where: talks live-streamed to our YouTube channel <https://www.youtube.com/channel/UCMsYvoHLNVm4rbcTLj162zQ>, post your questions for our speakers via Slack

Publicity: upcoming talks promoted on Slack & Twitter @EvoEcoSeminars (<https://twitter.com/EvoEcoSeminars>)

How to join: our Slack 'Evolution and Ecology Seminars' here https://join.slack.com/t/evolutionecol-xl54980/-shared_invite/zt-ev4fe0io-M7B~D6p74blV_ZRcDtmAcg
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“Elizabeth Duxbury (BIO - Staff)”
<E.Duxbury@uea.ac.uk>

Online Herbaria Mar11-12

Dear all,

The recently created herbarium UTCEC at Universidad Técnica de Cotopaxi, in collaboration with Universidad Regional Amazónica Ikiam (both in Ecuador) and with the endorsement of the Society for Herbarium Curators (SHC), International Association for Plant Taxonomy (IAPT), Asociación Latinoamericana de Botánica (ALB), and Asociación Botánica Ecuatoriana (ABE), are organizing a two-day virtual seminar title “Herbaria and their treasures/Herbarios y sus tesoros/Herbários e seus tesouros.” Everyone is welcome and your help sharing this announcement is greatly appreciated. This event will happen on the 11-12 March 2021, from 09:00-14:00 hours (Ecuador Time) and the details are below:

Zoom Meeting No: 953 2831

Password: 607090 Registration: <https://forms.gle/Fz6GQFufkEgtc17S7> Contact information: Alina Freire-Fierro (alina.freire@ikiam.edu.ec) and Javier Irazábal (roberto.irazabal@utc.edu.ec)

Link to find out your local time: <https://www.thetimezoneconverter.com/> ~ ~ Lic. M.em C., Alina Freire-Fierro, M.S., Ph.D. Profesora Titular de Botánica Agregado 3, Universidad Regional Amazónica Ikiam Curadora Asociada del Herbario UTCEC, Universidad Técnica de Cotopaxi Alina.freire@ikiam.edu.ec, Alina.freire@utc.edu.ec ~ ~ Skype: alinaff; Twitter: affbotanica www.neotropicos.net T: (+593) 99-775-6935 ~ ~

Alina Gladys Freire Fierro <alina.freire@ikiam.edu.ec>

Online IntlSocEvolMedicine

I'm pleased to let you all know that registration and abstract submission are now open for the International Society for Evolutionary Medicine and public health (ISEMPH) annual meeting: <https://isemph.org/ISEMPH-2021> Given that the conference will be online, and the rates are very reasonable (especially for members and students), now is the ideal time to try out an ISEMPH meeting, if you've never attended one.

If you register to join us, I would also particularly encourage you to consider taking part in the Evolutionary Medicine and Public Health Grand Challenges < <https://isemph.org/Grand-Challenges-2021> >. The Grand Challenges events will offer an excellent networking opportunity, and will make the conference feel much more interactive than an online conference would usually be.

Best wishes, Gillian

Dr Gillian Pepper Newcastle University Henry Wellcome Building Framlington Place Newcastle upon Tyne NE2 4HH United Kingdom

Email: gillian.pepper@ncl.ac.uk Mobile: +44 (0) 7951 295 751 Website: <http://gillianpepper.com/> Gillian Pepper <Gillian.Pepper@newcastle.ac.uk>

Online MicrobiomeBioinformatics Jun7-11

Conference Announcement (registration now open):
Holistic Bioinformatics Approaches Used in Microbiome Research

The Bioinformatics Virtual Coordination Network (<https://biovcnet.github.io/>) is an online community of Early Career Researchers committed to reducing entry barriers into bioinformatics. In June 2021, we are hosting a virtual conference that will bring together a diverse group of Early Career Researchers as well as senior PIs from across the globe who are equally committed to reducing such entry barriers.

The goal of the conference is to provide a step-by-step

open access series of presentations that demonstrate state-of-the-art bioinformatics pipelines within microbiome research.

Registration is free for this week-long event, and all participants are invited to submit a virtual poster for our poster session. Graduate students, postdocs, and PIs are all encouraged to attend, with target attendance quotas from each career stage.

Virtual conference details, including invited *speakers list* and *registration* - <https://biovcnet.github.io/-pages/conference-2021/> 7-11 June 2021

The virtual conference will span 5 days, with 2-3 hours of activity each day.

Day 1-3: 2 Speaker presentations each day (7-9 June 2021)

Day 4: Speaker Q&A Panels (10 June 2021)

Day 5: Virtual attendee poster session (11 June 2021)

Expected attendee capacity. 150 attendees

Holistic Bioinformatics Approaches used in Microbiome Research is funded by the Code For Science & Society (CS&S). The BVCN was made possible by grant number GBMF8449 from the Gordon and Betty Moore Foundation.

Jake Weissman <jw4336@terpmail.umd.edu>

thus avoiding mutational meltdown (Muller's ratchet) and genomic decay.

Sexual reproduction is realised in an impressive array of different strategies. Still, asexual species are found on terminal branches in many unrelated clades throughout the eukaryotic tree of life. The availability of high quality phased genomes only now allows us, to study the genomic underpinnings of transitions in reproductive modes, to compare the long-term effects of sex and asexuality on genomes, and to analyse the functional mechanisms of the loss and even regain of sex.

In this two half-days symposium we will invite speakers working on genomic aspects of sex and asexuality in organisms across the eukaryotic tree of life and invite talks on - genomics and genomic models of the drivers of loss of sex/gain of sex - analyses of the consequences of loss of sex on the genomic level - genomic changes accompanying transitions in reproductive systems such as from unisexual or hermaphroditic to separate sexes, or from environmental sex determination to genetic sex determination.

We are looking forward to your participation and great talks and discussions.

All the very best,

Astrid Bohne and Philipp Schiffer

worm-lab <worm-lab@protonmail.ch>

Online SexAsexuality Jun16-17

Dear all!

With this email we would like to announce an ESEB online satellite meeting on "Genomic signatures and consequences of sex and asexuality" to be held on the 16th and 17th of June 2021, 13:00 to 17:00 CET (each day). We are delighted to already have been able to recruit two excellent keynote speakers and will send out a general invitation for registration and abstract submission in the coming weeks. In the meantime, please see the abstract below and save the date!

Abstract: Sex, including outcrossing with meiosis, is by far the most common form of reproduction in eukaryotes. However, under similar ecological and genetic conditions, an individual undergoing asexual reproduction without outcrossing, will generate more offspring (each of which is itself capable of generating offspring) than a sexual sibling. It is thought that this cost of sex is offset by the benefits conferred by the exchange of genetic material,

Online SMBE2021 CallForSymposia

SMBE2021 Call for Symposia - Deadline 2 April 2021

SMBE2021 Call for Symposia - Application Deadline 2 April 2021 -

Dear SMBE Members,

We're delighted to announce that the Society for Molecular Biology & Evolution is now accepting proposals for symposium topics for the 2021 Annual Meeting. SMBE 2021 is taking place virtually 4-8 July (3-7 July in the United States). The deadline for symposia applications is 2 April 2021 (23:59 GMT).

Please visit

<https://app.oxfordabstracts.com/events/2080/-symposia/create> 'V to access information and the submission portal.

Proposals will be reviewed by the committee with

around 20-30 topics selected for inclusion within the scientific programme.

Format for SMBE 2021: SMBE 2021 will run across three geographical hubs. We hope in this way to make the conference as accessible as possible across our global community. All presentations will be pre-recorded and discussion rooms will be available for all participants to interact live online with speakers. There will also be designated poster space and live interactive poster sessions.

Key dates

2 April 2021 (23:59 GMT) - Deadline for symposia applications

16 April 2021 'V Symposia selection process concludes

23 April 2021 'V Abstract submission system opens and selected symposia announced to Society

14 May 2021(23:59 GMT) - Abstract submission system closes

28 May 2021 'V Talks and posters finalized by SMBE reviewers and all presenters notified

Proposals should span the range of interests of SMBE members, including exciting new scientific developments, and should represent the geographic and gender diversity of our membership.

Symposium Proposal Guidelines

Please review the following guidelines before submitting a Symposium Proposal:

Individuals can only be listed as an organiser for one symposium proposal, although organisers can be listed as an invited speaker on another proposal

Each symposium will include one invited speaker plus a number of contributed speakers

All invited speakers included within a symposium should have verbally agreed to be involved before the proposal is submitted

An individual can only give one talk at the SMBE meeting, so in the event that a speaker is invited to two successful symposium applications the organisers should consider a back up

Symposium organisers should provide a description of the symposium (250 words max) that will be made public if selected.

The symposium organisers will also provide a description of how their proposal brings forward SMBE's objective of equity and diversity, as well as any additional information for the committee to make an informed review (250 words max).

The symposia proposals selected for inclusion within the SMBE 2021 scientific programme will be listed on the abstract submission portal (opens on 23 April 2021). Abstract submitters will be asked to select the symposia in which your abstract most closely fits.

Symposia organisers will be responsible for selecting contributed talks from the pool of abstracts submitted and will be required to work to the deadlines outlined by the conference organisers (dates given above).

Symposia organisers will be required to moderate their symposia and associated discussion sessions to ensure the conference is a safe and respectful environment for participants at all times. Moderator training will be made available to symposia organisers.

Please direct all questions regarding SMBE 2021 to

smbe@allenpress.com (please cc
smbe.contact@gmail.com).

smbe2021.org

SMBE 2021 Organising Committee

SMBE President Harmit Malik Division of Basic Sciences, Fred Hutchinson Cancer Research Center; Howard Hughes Medical Institute; Department of Genome Sciences, A1-162 Box 358080, Seattle, WA hsmalik@fhcrc.org

Committee Members Margarita Takou Xuan Zhuang Maud Tenaillon Vincent Castric Anne Genissel Emmanuelle Lerat Laure Segurel Bertrand Servin Laura Carrilero Aguado Xuming Zhou Weiwei Zhai Debayan Dey Lev Yampolsky

Official Liaison Officers Mary O'Connell Beth Shapiro

SMBE Administrator Lulu Stader

SMBE Business Office Manager Christopher Lapine

Society for Molecular Biology & Evolution
smbe@allenpress.com

Society for Molecular Biology & Evolution
<smbe@allenpress.com>

Online SMBE2021 CallForSymposia Reminder

SMBE2021 Call for Symposia - Deadline 2 April 2021, Reminder

Dear Colleagues,

Just a reminder that the Society for Molecular Biology & Evolution is still accepting proposals for symposium topics for the 2021 Annual Meeting. SMBE 2021 is taking place virtually 4-8 July (3-7 July in the United States). The deadline for symposium applications is 2 April 2021 (23:59 GMT).

Please visit

<https://app.oxfordabstracts.com/events/2080/-symposia/create> to access information and the submission portal.

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SMBE Administrator Lulu Stader

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Society for Molecular Biology & Evolution
 smbe@allenpress.com (please cc
 smbe.contact@gmail.com)

“Lulu Stader (SMBE admin)”
 <smbe.contact@gmail.com>

PorquerollesIsland France MCEB
Jun13-17

Dear all,

The 2021 edition of the MCEB conference will take place on June 13-17 in Porquerolles, France:

<https://mceb2021.sciencesconf.org/> We are aiming at having a “regular” conference, with all participants spending a week on the island. Yet, current restrictions limit the number of attendees to 60. Other restrictions (e.g., wearing masks, keeping physical distances between two persons to at least one meter, etc.) will likely apply too.

Submissions of posters and/or talks will open the 24th of March and close the 9th of April. Notification of acceptance or rejection will be sent by the 26th of April.

Registration to the conference will open the following day (the 27th of April). Registration fees (about 500 euros, refundable in case of cancellation of the event) will cover accommodation plus breakfast, diner and supper.

The main focus of this year’s edition will be on “Climate Changes and their Impacts on Evolution”, in particular the preservation of biodiversity, the conservation of species, the study of ecosystems and their dynamics, and the reconstruction of major past changes of climate and living conditions on Earth.

We will also welcome contributions dealing with mathematical and computational techniques that improved our understanding of the COVID-19 pandemic. The design and application of integrative approaches that incorporate genetic data along with other sources of information (e.g., geography) in order to decipher the processes governing the evolution of SARS-CoV-2, will be of particular interest.

The list of invited speakers for this year’s edition is given below:

- Bastien Boussau (Laboratoire de Biométrie et Biologie Evolutive, CNRS, Lyon, FR) - Lounes Chikhi (Instituto Gulbenkian, Lisboa and CNRS, Toulouse, FR) - Christophe Dessimoz (University of Lausanne, CH) - Simon Gravel (Mc Gill University, Montreal, CA) - Emma Hodcroft (ISPM, University of Bern in Switzerland) - Michel Milinkovitch (Université de Genève, CH) - Tandy Warnow (University of Illinois, USA)

Best regards,

The MCEB Organizing Committee

Stephane Guindon <stephane.guindon@lirmm.fr>

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AarhusU StatisticalGenetics

Dear all,

I am looking for applicants for a (funded) PhD at Aarhus Uni, Denmark. The focus is developing new methods in human statistical genetics (e.g tools for finding causal variants, predicting phenotypes and understanding genetic architecture). The PhD would be suitable for someone with a background in maths, statistics, engineering, computer science or genetics. The application deadline is 1st May.

For more details, see below and this link <https://phd.tech.au.dk/for-applicants/apply-here/may-2021/method-development-in-human-statistical-genetics/> . If you have any questions, please email doug@qgg.au.dk.

Thanks, Doug

####

Applications are invited for a PhD fellowship/scholarship at Graduate School of Technical Sciences, Aarhus University, Denmark, within the Department of Quantitative Genetics and Genomics (QGG) PhD programme. The position is available from 1 August 2021 or later.

Title: Method development in human statistical genetics

Research area and project description: The PhD will be supervised by Professor Doug Speed, and based at the Department of Quantitative Genetics and Genomics (QGG) at Aarhus University. Dr. Speed's research involves developing methods for better analysing data from genome-wide association studies, with a particular focus on improving our understanding of human complex traits (e.g., physical traits such as height and BMI, or common diseases such as schizophrenia and epilepsy). Dr. Speed has developed the software LDAK (www.ldak.org).

The aim of the PhD is to develop new methods with the following goals: to identify causal loci (i.e., find genetic variant that influence phenotypes); to construct prediction models (be able to predict an individuals phenotypes from their genetic information); or to understand genetic architecture (investigate the biological mechanisms underlying complex traits). These methods will then be applied to large-scale datasets (e.g., 100,000s of individuals from UK Biobank). Please see the LDAK website and the following three references for examples of previous methods:

- MultiBLUP: improved SNP-based prediction for complex traits (2015) PMID: 24963154
- 44 - Reevaluation of SNP heritability in complex human traits (2017) PMID: 28530675
- SumHer better estimates the SNP heritability of complex traits (2019) PMID: 30510236

Qualifications and specific competences: The applicant must have an Bachelors degree and a MSC degree (or similar). As the project involves applied statistics, the applicant should have strong knowledge of statistics (e.g., a degree in mathematics, statistics, genetics or closely-related subjects). The applicant should ideally have some coding experience (e.g., in R, Stata, Matlab, C, etc). For applicants originally trained in mathematics or statistics, it will be desirable to have had previous experience in genetics, but not necessary. The applicant must be fluent in English, both oral and in writing.

Place of employment and place of work: The PhD will be based in the QGG, which is a major center for research and education in quantitative genetics and quantitative genomics <https://qgg.au.dk/en/>. QGG is an international research center with about 70 employees and visiting researchers from over 15 nations. Its members perform research within human genetics, livestock and plant breeding. It has buildings in Foulum, Flakkebjerg and on the main campus in Aarhus center. The PhD candidate is expected to be at the Aarhus Campus.

Contacts: Applicants seeking further information are invited to contact doug@qgg.au.dk

“Speed, Doug” <doug.speed@ucl.ac.uk>

AberystwythU AfricanMarineEvolution

A Margaret Wooloff funded PhD opportunity is available in the group of Dr Niall McKeown at Aberystwyth University. The project title is “Understanding African marine forests and developing sustainable livelihoods for coastal communities”. This exciting and impactful research has been developed in collaboration with the University of Namibia and there is considerable flexibility in project direction.

Project Description: Kelp are large multicellular algae which often form extensive marine forests. These forests are among the most productive habitats on earth and shape diverse ecosystems that support socioeconomically important industries. Over the last 50 years climate change has driven substantial global declines of kelp. Although the west coast of Africa represents a climate change hotspot this region has been neglected in kelp research to date. This knowledge gap may have extreme negative environmental, social, and economic consequences for the local communities that already experience disproportionate levels of poverty, drought, and

abusive external appropriation of resources, culminating in compromised food security and human health.

The proposed research has been developed with the University of Namibia in response to these concerns. It will combine genetics, ecology, and synthesis of local knowledge to understand the diversity, productivity, and resilience of marine forest ecosystem functioning and services along the west coast of Africa. This will inform prediction of responses to climate change and contingency planning for existing kelp dependent industries (e.g. subsistence fisheries). It will also aid development of sustainable kelp harvesting and aquaculture activities which represent untapped livelihood/income opportunities for the local communities.

The research also comprises exploratory bioprocessing of alginates focused on identifying compounds with drought alleviation properties. Broadly, this multidisciplinary project in collaboration with African based partners aims to obtain and communicate a greater understanding of the region’s marine forests and serve as an engine to enable the local communities to fully utilise and benefit from their own natural resources.

Please contact Dr McKeown directly (email: njm2@aber.ac.uk) for more information about the project and the application process. Deadline is May 1st 2021.

Dr Niall J McKeown Institute of Biological, Environmental and Rural Sciences Edward Llwyd Building - Room 1.10 Aberystwyth University Penglais Aberystwyth Ceredigion SY23 3DA e-mail: njm2@aber.ac.uk phone: +44 (0)1970 622314

Y Brifysgol orau yn y DU am Ansawdd ei Dysgu a Phrofiad Myfyrwyr Best University in the UK for Teaching Quality and Student Experience (The Times and Sunday Times, Good University Guide 2021) Rydym yn croesawu gohebiaeth yn Gymraeg a Saesneg. Cewch ateb Cymraeg i bob gohebiaeth Gymraeg ac ateb Saesneg i bob gohebiaeth Saesneg. Ni fydd gohebu yn Gymraeg yn arwain at oedi.

We welcome correspondence in Welsh and English. Correspondence received in Welsh will be answered in Welsh and correspondence in English will be answered in English. Corresponding in Welsh will not involve any delay.

“Niall McKeown [njm2]” <njm2@aber.ac.uk>

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Rydym yn croesawu gohebiaeth yn Gymraeg a Saesneg. Cewch ateb Cymraeg i bob gohebiaeth Gymraeg ac ateb Saesneg i bob gohebiaeth Saesneg. Ni fydd gohebu yn Gymraeg yn arwain at oedi.

We welcome correspondence in Welsh and English. Correspondence received in Welsh will be answered in Welsh and correspondence in English will be answered in English. Corresponding in Welsh will not involve any delay.

“njm2@aber.ac.uk” <njm2@aber.ac.uk>

Antwerp EvolGenomics

===== Final call =====Apply before April 2nd 2021.

The Svoldal lab at the University of Antwerp, Belgium, is looking for PhD and Postdoc candidates to be part of an exciting funded project to study the rapid adaptive diversification of 100s of cichlid fish species.

In one of two available project you will either

(1) establish novel molecular and computational techniques to identify structural variants

or

(2) develop machine learning and population genomic approaches to model the evolutionary and adaptive history of these structural variants and understand their role in adaptive radiation.

A quantitative background (computational genomics, population genetics) is a plus, but also candidates with a different background interested in these topics are encouraged to apply.

The vacancy is open until filled. Applications will be evaluated from April 2nd. Starting date can be negotiated. Remote work possible.

Direct application link:

PhD:

<https://www.uantwerpen.be/en/jobs/vacancies/-academic-staff/?q=1433&descr=Doctoral-scholarship-holder-in-Evolutionary-computational-genomics> PhD fellowships come with competitive salary and are for 4 years conditional on positive evaluation after 1 year.

– Hannes Svardal Research Professor in Evolutionary, Ecological and Environmental Omics Department of Biology University of Antwerp

Campus Groenenborger, room U758
hannes.svardal@uantwerpen.be

Hannes.Svardal@uantwerpen.be

AustralianNatIU VenomEvolution

The diversity of venomous animals fascinates us both on a scientific and cultural level. “Is it venomous?” is an age-old question humans and other animals had to quickly answer to survive. Ecologically, venom is a game changer. It enables the acquisition of novel food sources and strikes fear into much larger potential predators. Surprisingly, the steps taking animal salivary glands to venom glands remain poorly understood. Recent work in my lab has shown that (a) reptilian and mammalian venoms evolved from the ancestral salivary gene regulatory network, and furthermore (b) key toxins evolved from homologous ancestral genes that underwent sequence and copy number changes in venomous organisms. I am looking for a Ph.D. student who will build on this work. The overall goal will be to examine whether the evolution of venom has modified the ancestral salivary gene regulatory network to accommodate the increased demand for protein synthesis and folding.

The first aim will be to take a comparative approach to test the hypothesis that parallel origins of venom led to parallel changes in gene regulatory networks. Venom glands originated as salivary glands, which have conserved gene regulatory networks, representing a consistent set of initial conditions for subsequent evolution. Remarkably, despite the sophistication of some venom glands, such as those of advanced snakes, much of the regulatory architecture has been preserved, albeit with some modifications, such as gene duplications in certain core members. We will use repeated origins in reptiles (lizards and snakes) and mammals (short-tailed and water shrews). This is an ideal system to address a key knowledge gap in evolutionary biology 'V how gene

regulatory networks evolve alongside phenotypes 'V because venom evolved at least twice in each group. At the same time, at a genetic level, venom is a simple phenotype consisting of a relatively small number of toxin genes, making their interactions with the rest of the network possible to trace. Characterising the extent of parallelism will reveal the role gene regulatory networks play in trait evolution, as well as deeper mechanistic insights into how phenotypic novelty arises.

This will be a fully funded Ph.D. student position at the Australian National University. Applicants are expected to have at least one first-author publication, or something equivalent like a masters thesis.

Having traveled all over the world, I will vouch for the fact that Canberra is a fantastic place to live in terms of quality of life and climate. Furthermore, the Research School of Biology, and particularly the Division of Ecology and Evolution, offers dynamic and intellectually stimulating environments, particularly for early career researchers.

Applications close 30 March, 2021

Please don't hesitate to contact me if you have any questions.

Sasha (Alexander) Mikheyev alexander.mikheyev@anu.edu.au

Associate Professor Research School of Biology Australian National University

Sasha Mikheyev <alexander.mikheyev@anu.edu.au>

Barcelona PredictingEvolution

1. Basic job and project description:

The position is the Autonomous University of Barcelona (UAB).

-The main project questions are:

Can we predict evolution? Or at least some aspects of it?

How should gene networks and cell interactions be organized to lead to complex phenotypes?

How is such organization achieved in evolution?

How does gene network organization affect how the phenotype evolves (e.g. evolvability)?

In our lab we think that there is a limited number of

ways in which gene and cell interactions can be organized to lead to robust and complex phenotypes. If that is the case, we should be able to predict evolution? Or at least some aspects of it under specific selection pressures?

We will use computational models of the genotype-phenotype map and computational models of evolution by natural selection to study such questions for the case of organismic complexity (e.g. anatomy). The genotype-phenotype maps models we develop are based on realistic gene network models of pattern formation and morphogenesis that lead to realistic 3D multicellular phenotypes.

The position is in Salazar-Ciudad's group and it entails obtaining a PhD from the Autonomous University of Barcelona (UAB).

2. Background of the project:

There is no consensus definition of complexity, yet it is evident that organisms are complex and explaining such complexity is one of the most fundamental questions of biology. Morphological complexity has not increased in the evolution of all lineages and, in general, it is unclear whether there is a general trend of increasing complexity in evolution. Yet, one may ask about the mechanisms by which such complexity has increased in the lineages where it has increased. How complexity increases during evolution is necessarily related to development: any evolutionary change in morphology is first a change in the development that produces such morphology.

It has been argued that, in spite of the remarkable morphological complexity of organisms, their development is achieved through a limited number of cell behaviors and types of cell interactions. These cell behaviors would be cell division, cell adhesion, cell death, cell growth, cell contraction, extracellular signal and matrix secretion, extracellular signal reception and cell differentiation. In addition to cell behaviors, development involves interactions between cells, either mechanical or through extracellular signalling.

The questions we want to approach in this study are: how should these interactions and cell behaviors be coordinated to produce complex and robust morphologies? The question is, then, whether there are some logical requirements that developmental mechanisms should fulfill in order to lead to complex robust morphologies. Are there, for example, some requirements at the level of gene network topology or at the level of cell behaviors and their coordination during development?

If, as suggested above, pattern transformations in development involve a limited set of cell behaviors and cell interactions, then any mathematical model imple-

menting those and intracellular gene networks should be able to reproduce, to a large extent, the range of pattern transformations possible in animal development. In this project we will use one such model, EmbryoMaker (Marin-Riera et al, 2015), to simulate a large number of possible developmental mechanisms and try to discover what, if anything, do the mechanisms leading to robust complex morphologies have in common.

3. Job description

The main tasks of the student include using and modifying existing models of embryonic development (e.g. EmbryoMaker) in order to simulate the development of complex morphologies. These models will be combined with models of evolution, in a population context with mutation, genetic drift and natural selection on morphology (see for example Salazar-Ciudad and Marin-Riera, 2013). The gene networks found to lead to the development of complex and robust phenotypes in evolution would be analyzed to extract general regularities, if any, these gene networks need to fulfill.

The main tasks, thus, consist in simulation, theorizing, data analysis, coding, literature searching, writing and presenting results in conferences. We seek candidates highly motivated for theoretical work and data analysis with a broad and deep understanding of the evolutionary theory and/or developmental biology and/or modeling.

4. Requirements:

- Candidates should have a University Degree and a Master's Degree in biology, or similar within the European Higher Education System (minimum 300 ECTS) or equivalent by September 2019.
- Scientific programming skills or a willingness to acquire them is required.
- The most important requirement is a strong interest and motivation on science and evolution. A capacity for creative and critical thinking is also required.

5. Salary and conditions:

- The salary would be the standard one graduate students in Spain.

— / —

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

Berlin 11 PlantConservation

We are looking for 11 PhD students within the grad school BioMove, located in the Berlin area, Germany.

<https://www.bio-move.org/> Apply here before May 14:

<https://bio-move.org/Ausschreibungstext.Biomove.pdf>

Dr. Kristin Scharnweber Docent Scientific Coordinator of Research Training Group BioMove <https://www.bio-move.org/> University of Potsdam Plant Ecology and Nature Conservation Am Mühlenberg 3 14476 Potsdam-Golm, Germany Email: scharnweber@uni-potsdam.de Phone: +49 (0)331 977 6254 <https://www.kscharnweber.com/> biomove-rtg@uni-potsdam.de

BielefeldU BlackGrouseGenomics

Due to a limited response, we have extended the deadline for the following position until April 30th 2021. We welcome applications for this exciting project!

PhD studentship: Genomics of sexual trait expression in black grouse. With Prof Joe Hoffman (Bielefeld University, Germany), Dr Carl Soulsbury (University of Lincoln, UK) and Prof Kees van Oers (Netherlands Institute of Ecology and Wageningen University, the Netherlands).

An outstanding opportunity is available for a PhD student to work on the evolutionary genomics of sexual trait expression in an iconic avian model system, the black grouse (*Lyrurus tetrix*). The position is available in Joe Hoffman's research group (www.thehoffmanlab.com) at the Department of Animal Behaviour at Bielefeld University and is fully funded for three years.

The PhD project Since Darwin first coined the term 'sexual selection' to explain the evolution of exaggerated male traits, we have come to understand the complex interrelationships among these traits, the information they encode and the life histories of the animals they are embedded into. Sexual selection is built on the idea that individual quality is signalled by the expression of these traits, yet a clear mechanistic understanding of the genetic architectures of sexual traits and the

mechanisms regulating sexual trait expression remains elusive.

We know that inbreeding is an important component of individual quality, and several studies have documented inbreeding depression for sexually-selected traits. Moreover, trait expression can be influenced by dynamic factors such as age and environmental variation, so epigenetic control mediated by body condition has been proposed as a means of regulating genotype-dependent sexual trait expression. Resolving long-standing evolutionary questions about mate choice and sexual selection therefore requires a fundamental understanding of the genetic and epigenetic basis of sexual traits.

This project will combine the genomic inference of inbreeding with genome-wide methylation analysis to investigate the genetic and epigenetic mechanisms affecting sexual trait expression and reproductive success in a classical lek model system, the black grouse. Genomic estimates of inbreeding will be used to quantify the impacts of consanguinity on multiple sexual traits and to evaluate the 'genetic capture' hypothesis, which argues that sexual traits are influenced by the cumulative effects of large numbers of loci distributed across the genome. Finally, we will build upon a recent pilot study linking heterozygosity to sexual trait expression via differential DNA methylation (Soulsbury et al. 2017) by using a genome-wide methylation assay, epi-GBS, to identify genome-wide epigenetic signatures associated with inbreeding and sexual trait expression.

Overall, this project will tackle an important knowledge gap by combining detailed data from multiple sexual traits over individual lifespans with genomic and epigenetic data in a classical lekking species. The PhD student will therefore have a fantastic opportunity to tackle sexual selection using a number of innovative and cutting-edge approaches.

Applicant's profile We seek a bright and highly motivated student who holds a good first degree and an M.Sc. or equivalent in a relevant topic (e.g. molecular ecology, population genomics, bioinformatics). The ideal candidate will have strong quantitative skills, including proficiency in working in R and writing custom scripts. Practical experience of working with next generation sequence data (e.g. RAD sequencing, SNP array or whole genome resequencing) would be advantageous, but full training will be provided. The candidate should also be able to work both independently and as part of a multidisciplinary team. A high standard of spoken and written English is required.

The working environment The PhD student will be based at the Department of Animal Behaviour at Bielefeld University, Germany (www.uni-bielefeld.de/biologie/

[vhf/index.html](#)). The department is the oldest of its kind in Germany and currently hosts seven principal investigators, nine postdocs and 15 PhD students. It offers a stimulating, supportive and highly international environment as well as an excellent research infrastructure. The working language of the Department is English.

Bielefeld is a city of 325,000 inhabitants with an attractive historical centre and easy access to the Teutoberger Wald for hiking and other outdoor pursuits. It is an affordable and pleasant city to live in and is well connected to most major European cities.

This project is lab based and is located at Bielefeld University, but the PhD will also spend some time at the University of Lincoln (<https://www.lincoln.ac.uk/home>) and at the Netherlands Institute

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CharlesU Prague LarchPhyloPaleoecology

PhD position at Department of Botany, Charles University, Prague, Czech Republic

We are opening a 4-year STARS PhD position on the “Origin and long-term survival of Central European populations of larch (*Larix decidua*): combining phylogeography, paleoecology and niche modeling approaches”.

The position starts 1st October 2021.

We are seeking a motivated student willing to work in a multidisciplinary team consisting of molecular ecologists, paleoecologists, forest scientists and historians. The aim of this project is exploring population genetic structure, current and past ecology of larch populations, with special emphasis on identifying lowland Holocene refugia, i.e. regions where larch has persisted continuously since the last glacial period. First, the integration of historical, archaeobotanical, paleoecological and climatic niche modeling approaches will help to distinguish potential refugia from obvious plantations. Second, selected populations will be screened using microsatellite DNA and mitochondrial/chloroplast sequencing (using NGS approach) and results interpreted together with already available data from the entire European distribution.

We expect - master’s degree in botany/ecology/evolution or related fields (M.Sc. or equivalent obtained before the position starts) - interest in molecular, paleoecological or niche modeling approaches - experience with statistical analysis of ecological and/or molecular data is an advantage (but not mandatory) - ability to conduct field research - good English communication skills (spoken and written)

We offer - project-funded PhD position for 4 years - fellowship of ca. 25,000 CZK net per month (note that living costs in the Czech Republic are significantly lower than in western Europe) - international working environment with many students from abroad and with English being the main communication language - work in an inspiring academic environment in the historical centre of the UNESCO heritage site of Prague

Please, apply through the STARS portal of the Faculty of Science, Charles University (<https://stars-natur.cz/-phd-positions/biology>) by March 11th 2021. For questions regarding the position requirements and the application submission process please contact Dr. Tomas Fer (tomas.fer@natur.cuni.cz).

Tomas Fer <tomas.fer@centrum.cz>

Denmark FishPopulationGenomics

The Population Genetics group at DTU Aqua is looking for a PhD student interested in developing their skills in genomics and fisheries management to participate on the BiodivERSA funded project: Biodiversity on the run: evolutionary and socio-economic consequences of shifting distribution ranges in commercially exploited marine fishes (GenClim). Deadline for application is April 5th 2021, 5pm (Central European Time).

This is collaborative project with ISPA-IU (Portugal), CCMAR (Portugal), Stellenbosch University (South Africa) and Kiel University (Germany). Funding is available for three years for a competitive PhD fellowship, laboratory costs and travel between partner institutions. You will be supervised by Prof Einar Eg Nielsen, Dr Romina Henriques and Prof Rita Castilho, and work in close proximity with Dr Mark Payne (DTU), Prof Joana Robalo (ISPA) and Prof Sophie von der Heyden (SU).

For more details and how to apply, please follow the link: <https://www.dtu.dk/english/About/JOB-and-CAREER/vacant-positions/job?id=c248f42b->

9036-43b1-b399-1f48291e65f7 Romina Henriques
<romhe@aqua.dtu.dk>

JagiellonianU HGT PhageEvolution

— PhD student in the area of bioinformatics of bacteria-phage interactions —

> General description We are inviting applications for a PhD student in the area of bioinformatics of bacteria-phage interactions. The successful candidate will join the Microbial Genomics Group at Malopolska Centre of Biotechnology, Jagiellonian University in Krakow (<https://mostowylab.com>). This is a 4-year National Science Foundation (ncn.gov.pl) funded position, available from October 2021, with the exact start date to be agreed on.

The successful candidate will work on bioinformatics and genomics of phages that infect opportunistic bacterial pathogens like *Klebsiella pneumoniae* and interact with their polysaccharide capsules. Bacterial polysaccharides are known to be highly diverse, both structurally and genetically, however evolutionary forces that drive that diversity are not fully understood (Mostowy & Holt 2018, Trends Microbiol). Hence, to better understand and quantify evolution of phages, we need tools that can inform us how evolutionary process, like mutation and horizontal gene transfer (HGT), shape phage diversity at different levels, from domains, to proteins, to modules and genomes.

As a successful candidate, you will work on a new generation of bioinformatic methods to study how HGT impacts bacterial genome. Specifically, you will combine state-of-the-art approaches in the field of microbial genomics (e.g., pan-genome view of microbial diversity) with those in phylogenomics (e.g., tree reconciliation methods) to reconstruct how phage diversity emerges at different levels and how it shapes evolution of bacterial genomes. You will design new bioinformatic methods for the phage biology community and apply them on large datasets consisting hundreds of thousands of genomes of both lytic and lysogenic phages. You will interact with other members of our rapidly growing group working on microbial genomics and work together as a team. You will work in collaboration with other top research groups: those with expertise in genomic epidemiology of *Klebsiella pneumoniae* (Kat Holt at Monash University in Australia), bacterial evolutionary genomics (Florent Lassalle at Wellcome Trust Sanger Institute) and struc-

tural bioinformatics (Stanisław Dunin-Horkawicz at University of Warsaw). Finally, your work will contribute to the fight against the problem of antibiotic resistance by helping us understand the adaptive potential of phages to bacterial pathogens and quantify underlying evolutionary forces that drive success or failure of phage therapy.

The successful candidate will be able to influence the direction of the project depending on his or her profile and strengths. They will have the opportunity learn multiple new skills, particularly in the areas of genome informatics and functional genomics, and develop international contacts, but will be expected to manifest an increasing degree of intellectual independence throughout the project.

> Specific requirements The successful candidate will:
- hold a MSc in a quantitative field like biology, chemistry, physics, mathematics, computer science or similar,
- manifest a high degree of enthusiasm for the advertised project,
- have a very good knowledge of at least one programming language (e.g., R, Python, C/C++, Java),
- have excellent oral and written communication skills in English,
- have strong presentation skills (ideally having presented on at least one international conference),
- enrol in the Biomedical Sciences Doctoral School programme at the Jagiellonian University in Krakow,
- enjoy support of and interaction with other group members.

The ideal candidate will also fulfil the following requirements: - demonstrate evidence of in-depth experience in designing bioinformatics methods or pipelines (e.g., via GitHub), - demonstrate evidence of having led and completed scientific projects in the area of computational biology, population genetics, phylogenetics, phage biology, microbiology or similar, - have a track record of presenting at research conferences and/or published research, - have an active interest in the area of genomics of bacteria-phage coevolution.

We offer: - opportunity to work on an ambitious and important scientific problem, hence contributing to the fight against antimicrobial resistance, - opportunity to collaborate with world-class scientific leaders at the leading scientific institutions, - a fun and interactive working environment closely linked to the bioinformatics community at Malopolska Centre of Biotechnology, - participation in collaborations and scientific meetings across the globe,

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JagiellonianU Krakow EvolutionaryBiology

We are seeking a motivated Masters student for a project: Biological Clocks in the Wild: the effects of artificial light at night on circadian rhythms of a migratory bird at the Institute of Environmental Sciences, Jagiellonian University (Poland)

What do we study: It is well established that biological rhythms are fundamental drivers of biochemistry, cell biology, physiology and behaviour. The regularity of behaviours is governed by endogenous clocks, which are adjusted and synchronised with environmental cues, primarily light. Rapidly expanding anthropopressure largely disrupts these cues. Yet, it is surprising how little we know about the effects of disorders in the functioning of the internal time-keepers in free-ranging animals. The project will aim at understanding the effects of disturbance in environmental cues, i.e. light exposure, on circadian clock of a wild migratory bird: collared flycatcher (*Ficedula albicollis*). We will employ an experimental setup introducing artificial light at night in nestboxes during breeding season, at different stages of development and quantify its effects on circadian clock, physiology and behaviour. As a result we will try to build a comprehensive understanding of shifts in circadian rhythms and their consequences in a natural population.

Job description: The MSc candidate will actively participate in fieldwork (collecting phenotypic, biological and environmental data), analytical and lab work. S/he will be interacting with the PI and other team members, collaborators in Poland and worldwide, and attend relevant workshops and conferences. It is expected that the candidate will learn a large ecological skill set that will allow him/her to infer the evolutionary ecology of disturbed photoperiods in wild flycatchers. Specifically, the thesis will focus on the behavioral part of the project and the tasks will involve:

* active participation in fieldwork across two breeding seasons (ca. 2-3 months each year) on the Swedish island of Gotland, * installation of cameras and light sources in randomly selected nestboxes, * recording, and then carefully viewing behavioral responses of birds in a dedicated software, * analysing the results in cooperation with other team members.

Salary: A National Science Centre stipend (2000 PLN/month, tax-free stipend) is available for 24 months.

Requirements:

1) Formal conditions:

* admission (or being already enrolled) to an MSc program at the Jagiellonian University (for example programs in English: https://studia.eko.uj.edu.pl/en_GB/-ecoevo, https://studia.eko.uj.edu.pl/en_GB/epm or programs in Polish)

2) Specific merit requirements for the project include:

* strong English language command, communication, organizational and collaboration skills; * experience with field work (preferably with birds) is considered advantageous; * bird ringing/handling experience, ethical permits to work with animals and driving license are a plus.

Informal enquiries: email to the principal investigator Joanna Sudyka (joanna.sudyka@uj.edu.pl) or the project manager Wioleta OleÅ (wioleta.oles@uj.edu.pl).

The formal application should be sent by 31.03.2021 to Wioleta OleÅ (wioleta.oles@uj.edu.pl) with the term "MSc position" as email subject line and include:

1) CV (maximum 2 pages) including information on relevant academic achievements, relevant experience and training and contact information for two referees;

2) cover letter (maximum 1 page), explaining how the applicant's background and research interests make them a suitable candidate for the position;

3) signed copy of a formal statement concerning the processing of personal data, available here: https://cawp.uj.edu.pl/en_GB/wynagrodzenia/stypendia (Wzór oÅwiadczenia o przetwarzaniu danych osobowych)

The documents must be in English or Polish.

The applications will be considered by a selection committee according to the regulations about scientific scholarships in research projects financed by the National Science Centre, Poland (https://www.ncn.gov.pl/sites/default/files/pliki/regulaminy/-ncn_scholarships_in_projects_en.pdf). If there will be lack of eligible applications, the enrollment will be extended or a new deadline will be announced.

Joanna Sudyka <joanna.sudyka@uj.edu.pl>

LinköpingU PhylogeneticsStatistics

At the Division of Statistics and Machine Learning, Department of Computer Science, Linköping University, Sweden we have opened a PhD student in Statistics position that is related to phylogenetics :

<https://liu.se/en/work-at-liu/vacancies?rmpage=-job&rmjob=15865&rmlang=UK> https://www.ida.liu.se/~krzba67/PhD_May2021.pdf Please feel free to spread the word and of course apply if you are interested!

Best wishes Krzysztof Bartoszek, PhD Docent, Senior Lecturer in Statistics Division of Statistics and Machine Learning Department of Computer and Information Science Linköping University krzysztof.bartoszek@liu.se +46 (0)13 28 18 85

Krzysztof Bartoszek <krzysztof.bartoszek@liu.se>

LundU LepidopteraPhylogenomics

I would like to advertise a position in Lepidoptera phylogenomics at Lund University, Lund, Sweden.

PhD position: Lepidoptera Phylogenomics

We are searching for a PhD candidate that will be part of a joint project with Dr Krzysztof Bartoszek at Linköping University funded by ELLIIT Call C, including collaboration with Prof Fredrik Ronquist (Swedish Museum of Natural History). The PhD candidate will use publicly available genomic resources on Lepidoptera (100 whole genomes and hundreds of transcriptomes) to develop and empirically test new statistical methods to investigate gene and species histories across deep evolutionary time (100 million years of evolution). A parallel PhD candidate will be hired in Linköping to develop the theoretical and statistical framework for the new methods, and the two PhD candidates will be working closely together. The proposed project is interdisciplinary, and will enable the prospective PhD candidate to acquire a wide range of skills in state-of-the-art phylogenetics, genomics, bioinformatics, as well as experience with theoretical and statistical models.

The PhD candidate will accordingly be trained by supervisors with complementary skills and interests. The primary supervisor will be Prof Niklas Wahlberg, with Dr Mikael Pontarp, Dr Jadranka Rota (all three Lund University), and Dr Krzysztof Bartoszek (Linköping University) as co-supervisors.

If you would like to apply, use the link below. The application deadline is May 8 with September 1, 2021 as start of employment.

<https://lu.varbi.com/en/what:job/jobID:387547/>

Thanks for your help.

Best wishes, Jadranka

Jadranka Rota, PhD Entomology Curator Room E-E331 Lund University Biological Museum Department of Biology Ecology building Sölvegatan 37

223 62 Lund, Sweden Phone: +46 46 222 84 57

www.choreutidae.net www.biology.lu.se/jadranka-rota

Jadranka Rota <jadranka.rota@biol.lu.se>

Montpellier AlpineButterflyEvolution

* PhD Studentship - Adaptation and speciation in Alpine butterflies - CEFE-CNRS Montpellier France *

A fully-funded 3-year PhD studentship is available at the CNRS Centre for Evolutionary and Functional Ecology (CEFE) in Montpellier, France, supervised by Mathieu Joron, on the modes of diversification of an alpine butterfly species complex along the altitudinal gradient.

Application deadline: 11 April 2021.

Starting date: between June and November 2021.

Announcement and application details (CNRS portal): <https://bit.ly/3ltsIbK> Information and enquiry: mathieu.joron@cefe.cnrs.fr, [<https://joron.cefe.cnrs.fr/> | <https://joron.cefe.cnrs.fr>], [<https://www.cefe.cnrs.fr/en/> | <https://www.cefe.cnrs.fr/en/>] Detailed announcement:

The proposed work is part of a collaborative project to investigate the modes of diversification of an alpine butterfly species complex along the altitudinal gradient. Our goal is to identify the mechanisms underlying the repeated evolution of reproductive barriers among closely-related species adapted to different altitudinal niches, but still interconnected by gene-flow. Co-investigators are Laurence Despres at University of Grenoble and

Claire Lemaitre at INRIA Rennes, and their associated teams.

The student will be in charge of characterising phenotypic variation for traits involved in reproductive isolation and in adaptation to altitude, in order to understand their role in the diversification of this complex. Chemical, morphological, physiological or life history traits can be assumed to play a role in this adaptive radiation, and may be investigated using a combination of experimental and analytical approaches. Another aim is to identify the genomic regions associated with variation at those traits to understand the genomic and genetic architecture of adaptation and speciation.

We are looking for a highly motivated student with great academic achievement, a clear interest and top-level education in evolutionary ecology and population genetics, independent thinking and experience with field ecology and/or experimental approaches. Independence and motivation are essential to successfully carry out challenging field and experimental work. The project allows for much flexibility in the questions tackled by the student, depending on her/his interest, skills, and ideas.

The studentship is funded by an ANR grant for collaborative research and the student will join a lively consortium of teams whose research combines experimental ecology, population genomics, and bioinformatics. The student will be based at CEFE in Montpellier, with summer field work in the Alps.

The CEFE is the largest ecology lab in France and a major institute for evolutionary ecology and genetics worldwide. Our group focuses on butterfly ecology and genomes to decipher how diversity is shaped by natural selection and other processes. Montpellier is a major hotspot for evolutionary and environmental research and has a vibrant scientific community with several hundred researchers in biological sciences and biodiversity, and highly praised graduate programmes. The University of Montpellier ranked 1st worldwide in the 2018 Shanghai ranking in Ecology. Montpellier lies near the Mediterranean region in the South of France and enjoys pleasant weather, fantastic nature and great cultural and city life.

Starting date should be as soon as possible but no later than the end of 2021. Net salary is around 20.5K€/year, including social benefits and public health insurance.

Application deadline: 11 April 2021

Applications should be done through the CNRS portal. Link : <https://bit.ly/3ltsIbK>. Applicants should upload (1) an application letter explaining their motivation and achievements and including a paragraph

on the preferred questions or approaches they would like to focus on during the project, and (2) a full CV, including academic transcripts and contact details of two references.

Informal enquiry : Mathieu Joron (Mathieu.joron@cefe.cnrs.fr). Website : <https://-joron.cefe.cnrs.fr> – Centre d'Ecologie Fonctionnelle et Evolutive (CEFE) CNRS, 1919 route de Mende, 34293 Montpellier 5, France <https://joron.cefe.cnrs.fr> +33 (0)4-67-61-32-03.

Mathieu JORON <mathieu.joron@cefe.cnrs.fr>

MuensterU MicrobePlantEvolution

The Institute for Evolution and Biodiversity at the University of Münster, Germany, invites applications for a

Doctoral Research Position Wissenschaftliche/r Mitarbeiter/in (Salary level TV-L E13, 65%)

in the Plant Adaptation-in-Action group, headed by Prof. Shuqing Xu (<https://www.uni-muenster.de/-Evolution/plantadapt/people/shuqingxu.shtml>)

The successful candidate may start as soon as possible, preferably before July 2021. The salary will be provided for three years.

In this DFG funded project, the candidate will work closely together with Dr. Antonino Malacrin² and other members in the Plant Adaptation-in-Action group to study how microbes affect plant evolution using an experimental evolution approach.

During the course of the project, the candidate will learn new scientific skills and methods, gain didactical proficiencies and additionally will get experience in project planning and management. The position serves the purpose to acquire a PhD degree and to facilitate a successful career development. The candidate will also join the Münster Graduate School of Evolution (MGSE, <https://www.uni-muenster.de/Evolution/mgse/>), which offers a stimulating studying environment and opportunities to get in touch with excellent researchers in the fields of biology, medicine, geosciences, mathematics, and philosophy.

Requirements: We are looking for a highly motivated researcher of any nationality with the equivalent of a MSc degree in biology or related fields. The successful candidate is expected to design, conduct and analyse

both field and lab experiments, with a high degree of independence. A strong background in plant-microbe interactions is required. Applicants must demonstrate their experience and knowledge in working with plants and microbes, as well as skills in data analysis and statistics. Experience with field work, plant-herbivore interactions, evolutionary biology and analytical chemistry are advantageous. Our group consists of people of various nationalities and teamwork is essential for all projects in the group. Therefore, excellent communication skills, as well as proficiency in spoken and written English are expected. Good knowledge in German is a plus.

The University of Münster is an equal opportunity employer and is committed to increasing the proportion of women academics. Consequently, we actively encourage applications by women. Female candidates with equivalent qualifications and academic achievements will be preferentially considered within the framework of the legal possibilities. The University of Münster is committed to employing more staff with disabilities. Candidates with recognized severe disabilities who have equivalent qualifications are given preference in hiring decisions, although some restrictions related to specific project-related tasks may apply.

Applications must be in English and include: 1. a motivation letter stating the research interests with reference to the stated requirements in no more than 2 pages, 2. a detailed CV including academic and extracurricular achievements, as well as details of all research experience, 3. abstracts of both the BSc and MSc thesis, and 4. contact details of at least two referees.

Applicants should send their documents in one single PDF file to Dr. Antonino Malacrino² (antonino.malacrino@gmail.com) with title of "PhD position - Your name". The application review will commence on 15th April 2021. The position will remain open until filled.

Antonino Malacrino² <antonino.malacrino@gmail.com>
Antonino Malacrino² <antonino.malacrino@gmail.com>

NHM UOslo EvolutionaryGenomics

For the following PhD (Jobbnorge ID: 201587), please apply at <https://www.jobbnorge.no/en/available-jobs/-job/201587/phd-research-fellowship-in-evolutionary-genomics> The deadline for applications is 23.03.2021.

Natural History Museum PhD Research Fellow in Evolutionary Genomics

Job description: Applications are invited for a 3 year position as a PhD Research Fellow in Evolutionary Genomics at the Natural History Museum, University of Oslo. The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the PhD program at the Faculty of Mathematics and Natural Sciences. Appointment to a research fellowship is conditional upon admission to the Faculty's research training program.

Starting date as soon as possible.

More about the position: The position is placed in the ?Sex and Evolution Research Group? (SERG). The research group is broadly interested in understanding evolutionary processes such as speciation, hybridization, diversification and adaptation with a particular focus on the role of sex and sexual conflict, and the evolution of male gametes. These processes are studied at different levels of organization, like genes, genomes, gametes, individuals, populations and species.

This PhD fellow will be working in a team investigating the diversity of sperm cells in birds. There is tremendous variability in sperm phenotypes, particularly with respect to overall size, shape and relative size of various components. The team seeks to understand this diversity in an evolutionary context using comparative, phylogenetic methods, and the selective forces shaping the variation in and among populations.

The PhD fellow will work specifically on genes involved in spermatogenesis in selected species of passerine birds, and reveal how these genes are organized in the genome and how they are expressed in testicular tissue. We are therefore looking for a highly motivated PhD student with a strong interest in evolutionary questions and with a curiosity for the genetics of phenotypic variation. The successful candidate must have strong computational and analytical skills.

The research group has access to large museum collections in ornithology, including a DNA bank of more than 60 000 tissue samples, and a unique collection of formalin-preserved sperm cells from more than 500 species with an associated database of sperm morphology measurements. We have accumulated genomic resources including whole genomes, transcriptomes, and proteomes from a variety of species, but there will be further field sampling of targeted species in Norway and abroad, through a network of collaborating scientists. The museum has access to relevant research infrastructures, such as a DNA laboratory, computer-assisted sperm analysis (CASA), microscopes with imaging soft-

ware, and electron microscopes.

Qualification requirements: -Applicants must hold a Master's degree or equivalent in biology or related disciplines like bioinformatics. -Good communication skills (including written and spoken English) -Experience in relevant wet laboratory practices, such as DNA/RNA extraction -Experience in the application of genomics and bioinformatics to address evolutionary questions -Computational skills including experience with UNIX and programming (e.g. in Python or R)

Preferred experience (experience with one or more of these would be beneficial):

-Quantitative PCR -Library preparation for NextGen Sequencing -RNAseq analysis -Genome/transcriptome de novo assembly -Sequence evolution analysis (e.g. multiple sequence alignment, dN/dS analysis) -Histology/microscopy/cell disassociation/cell staining

We offer: -Salary NOK 482 200 ? 526 000 per year depending on qualification and seniority as PhD Research Fellow (position code 1017)

Challenging research questions and a friendly working environment -A beautiful campus located in the Botanical Gardens, which is close to the city center of Oslo, but also not far from the fjord and the woodlands surrounding the city -Full funding of the project research-related activities, including field work, lab work and presentation of results at international conferences -Membership in the Norwegian Public Service Pension Fund -Attractive welfare benefits

How to apply: The application must include: -Application letter -CV (summarizing education, positions and academic work, scientific publications and other relevant experience) -Copies of educational certificates -List of publications and academic work that the applicant wishes to be considered by the evaluating committee -A one-page statement explaining how a PhD in the actual research field will fit into the applicant's career plan -Names and contact details of 2-3 references (name, affiliation,

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NHM UOslo Evolutionary Genomics ExtDeadline

For the following PhD (Jobbnorge ID: 201587), please apply at <https://www.jobbnorge.no/en/available-jobs/-job/201587/phd-research-fellowship-in-evolutionary-genomics> The deadline for applications has been extended to 06.04.2021.

Natural History Museum PhD Research Fellow in Evolutionary Genomics

Job description: Applications are invited for a 3 year position as a PhD Research Fellow in Evolutionary Genomics at the Natural History Museum, University of Oslo. The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the PhD program at the Faculty of Mathematics and Natural Sciences. Appointment to a research fellowship is conditional upon admission to the Faculty's research training program.

Starting date as soon as possible.

More about the position: The position is placed in the "Sex and Evolution Research Group" (SERG). The research group is broadly interested in understanding evolutionary processes such as speciation, hybridization, diversification and adaptation with a particular focus on the role of sex and sexual conflict, and the evolution of male gametes. These processes are studied at different levels of organization, like genes, genomes, gametes, individuals, populations and species.

This PhD fellow will be working in a team investigating the diversity of sperm cells in birds. There is tremendous variability in sperm phenotypes, particularly with respect to overall size, shape and relative size of various components. The team seeks to understand this diversity in an evolutionary context using comparative, phylogenetic methods, and the selective forces shaping the variation in and among populations.

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Qualification requirements: - Applicants must hold a Master's degree or equivalent in biology or related disciplines like bioinformatics. - Good communication skills (including written and spoken English) - Experience in relevant wet laboratory practices, such as DNA/RNA extraction - Experience in the application of genomics and bioinformatics to address evolutionary questions - Computational skills including experience with UNIX and programming (e.g. in Python or R)

Preferred experience (experience with one or more of these would be beneficial): - Quantitative PCR - Library preparation for NextGen Sequencing - RNAseq analysis - Genome/transcriptome de novo assembly - Sequence evolution analysis (e.g. multiple sequence alignment, dN/dS analysis) - Histology/microscopy/cell disassociation/cell staining

We offer: - Salary NOK 482 200 526 000 per year depending on qualification and seniority as PhD Research Fellow (position code 1017) - Challenging research questions and a friendly working environment - A beautiful campus located in the Botanical Gardens, which is close to the city center of Oslo, but also not far from the fjord and the woodlands surrounding the city - Full funding of the project research-related activities, including field work, lab work and presentation of results at international conferences - Membership in the Norwegian Public Service Pension Fund - Attractive welfare benefits

How to apply: The application must include: - Application letter - CV (summarizing education, positions and academic work, scientific publications and other relevant experience) - Copies of educational certificates - List of publications and academic work that the applicant wishes to be considered by the evaluating committee - A one-page statement explaining how a PhD in the actual research field will fit into the applicant's career plan - Names and contact details of 2-3 references (name,

affiliation,

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NorthernArizonaU 2 TreeGenomics

Graduate Research Assistantships in Tree Genomics

Two MS graduate positions are available to join the Forest Genomics Lab at NAU. The positions include a monthly stipend, full tuition and health benefits for 2 years.

Position 1: The student will use genomic tools to study postglacial migration and phylogeographic history in two North American conifers. This position involves molecular lab work and data analyses.

Position 2: The student will use genomic tools to study levels of genetic diversity and the potential for adaptation in isolated populations of the endangered species whitebark pine. This position involves molecular lab work, data analyses, and might also include field work.

Minimum qualifications:

* Bachelor's degree in Genetics, Forest Sciences, Biology, Ecology, Plant Sciences, Evolutionary Biology, Bioinformatics or related fields of study. * Have taken at least one course in Genetics. * Familiarity with R, Perl or Python * Start date: August 1st, 2021 (Fall admission) or January 1st, 2022 (Spring admission). * Molecular lab experience.

How to apply: Please send a 1-page statement of interest, CV, unofficial copy of transcripts, and TOEFL scores (international students), and the names and contact information of 3 references by March 15th, 2021. If found to be a good match for the position, you will be encouraged to apply to the graduate program at NAU. Please note that NAU has the following admission requirements: GPA equal or higher than 3.0 and TOEFL = 213 (computer-based) or 80 (internet-based).

Contact Information: Dr. De La Torre, Amanda.de-la-torre@nau.edu Lab <https://treegenomicslab.com>
Amanda De La Torre <Amanda.de-la-Torre@nau.edu>

NRS McGillU FishBiodiversity

TWITTER FEED:

Arctic marine systems are warming and incurring biodiversity loss at 3x and 5x the global averages. We need to know more about species there before they disappear. Arctic marine fish ecology and evolution jobs in McGill's NRS. PhD students, Postdocs and Labtech positions available. See <https://denisroy.weebly.com/>; <http://mckinneylab.weebly.com> /opportunities, and EvolDir Jobs and Graduate positions - for more details.

Ad:

WHERE: Department of Natural Resource Sciences, McGill University

WHAT: Grad student (PhD),

Start date: Fall 2021

Members in the Department of Natural Resource Sciences at McGill University are seeking highly motivated applicants for graduate student and research technician positions for the FISHSENS project for Fall 2021. Most marine fishes in Canada's Arctic are not well enough known to assess how they will be affected by climate change, information which is urgently needed to reduce Arctic biodiversity loss and protect northern cultural and food systems.

FISHSENS will combine genomics data with dietary and movement assessments to develop tools needed by federal and Inuit co-management partners to establish Arctic marine fish monitoring strategies and assess their sensitivity to climate change. Recruited candidates will develop projects combining laboratory and data analysis approaches and will collaborate with Canadian academic, government, and Inuit organizations in Nunavut and the Inuvialuit Settlement Region in the Northwest Territories.

McGill University is committed to diversity and equity and welcomes applications from Indigenous persons, women, persons with disabilities, ethnic minorities, persons of minority sexual orientation or gender identity, visible minorities, and others who may contribute to diversification. For more information on support, funding, and community for Indigenous students at McGill:

<https://www.mcgill.ca/undergraduate-admissions/-indigenous-students>; <https://www.mcgill.ca/fph/>
McGill University is Canada's premiere university for

research excellence and teaching, is one of the top 50 universities worldwide, and was recently named the International Sustainability Institution of the Year. The Faculty of Agricultural and Environmental Sciences is located at McGill's Macdonald Campus, just 30 km from vibrant downtown Montreal, providing students with both urban culture and recreational opportunities.

Graduate students at Mac campus are $\hat{A} \frac{1}{4}$ of the student body and the campus houses 8 graduate programs and 100+ faculty members. See here for more information: <https://denisroy.weebly.com/>; <http://mckinneylab.weebly.com> ; <http://mcgill.ca>; <http://mcgill.ca/nrs> Ideal candidates will have a strong work ethic, enthusiasm for the research, independent and team-work skills, and a suitable academic training in a relevant discipline: natural resources, ecology, evolution, genetics, bioinformatics, environmental chemistry, environmental science, or a closely related field, and experience in at least one of the following:

- DNA extractions, library preparations, quality screening, PCR, extraction robots, gel docs, and associated instruments - Stable isotopes or fatty acids extraction and analysis (GC-FID, IRMS) - Statistical analysis of biological or environmental data (e.g., in R), bioinformatics tools (e.g., VCFtools, genome assemblies, and annotation) - Fieldwork, fish identifications, working in Inuit communities and organizations

Potential graduate students will have to apply to the Department of Natural Resource Sciences at McGill, which has strict admission standards (minimum GPA of 3.0/4.0, or 3.2/4.0 in the last two years). Transcripts, letters of support, CV, and a strong personal statement are part of the application. Deadlines for fall 2021 admission are May 31st for Canadian applicants and March 15th for international applicants.

Annual graduate student stipends will be provided, with opportunities for supplementation through applications for scholarships and teaching assistantships.

Please send a cover letter indicating your research experience and goals, a CV, and, unofficial transcripts. For genomics/bioinformatics positions, send application materials to Dr. Denis Roy, Assistant Professor, at denis.roy5@mcgill.ca. For dietary/chemical tracers positions, send application materials to Dr. Melissa McKinney, Assistant Professor, and Canada Research Chair, at melissa.mckinney@mcgill.ca. Please ensure to write "FISHSENS positions" in the subject line. Deadline is March 13th, or until minimum positions are filled. We encourage applications from First Peoples and Canadian students.

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ence and Management Penn State University email: keagy@psu.edu <jxk6051@psu.edu> web: <https://www.personal.psu.edu/jxk6051/> “keagy@psu.edu” <keagy@psu.edu>

PennsylvaniaStateU LandscapeGenomics

We are seeking an individual to pursue a Ph.D. in fish landscape genomics at The Pennsylvania State University. The student will take the lead in two projects: 1) a riverscape genetics project characterizing the population connectivity and invasion dynamics of flathead catfish, and 2) a landscape transcriptomics project connecting brook trout gill transcriptomes to landscape variables such as water temperature. Several large genomic datasets will be available at the start and there will be opportunities to participate in further field collections of tissue samples, work on DNA and RNA extractions, develop better methods for analyzing the data, and develop experiments to validate the transcriptomic results.

The student will be co-advised by Dr. Ty Wagner and Dr. Jason Keagy and be expected to contribute to an inclusive and equitable lab group.

Qualifications Competitive candidates will be highly motivated to both work with fish and analyze large genomic datasets. They will possess a B.S. and/or M.S. in Biology, Ecology, Wildlife and Fisheries, Zoology, Natural Resources, or related field. Individuals with a degree in Bioinformatics, Computer Science, or similar with a strong interest in wildlife biology would also be extremely competitive. Experience with R and bioinformatics and/or computer programming is preferred, but not essential. However, because much of the research will involve bioinformatic analyses of large genomic datasets, candidates will need to demonstrate strong interest and desire to learn about this topic. We particularly welcome applications from under-represented groups in wildlife and fisheries management and ecology. To apply: Send a single PDF that includes a brief cover letter outlining experience and research interests, curriculum vitae, unofficial university transcripts (a list of relevant coursework and grades is acceptable), and contact information for two references to Dr. Jason Keagy at keagy@psu.edu. Applications will be accepted until April 19th.

Jason Keagy Assistant Research Professor of Wildlife Behavioral Ecology Department of Ecosystem Sci-

PotsdamU EvolutionElectricFish

PhD position on Evolution and Behaviour of Weakly Electric fish at Potsdam University

A 3-year PhD position (TVEL 13/2) is available at the Unit of Evolutionary Biology/Systematic Zoology at the University of Potsdam, starting June 1st 2021.

The Unit of Evolutionary Biology/Systematic Zoology has a strong focus on population genetic and speciation research, involving various taxonomic groups and a suite of molecular, morphological, and behavioural approaches (see <https://www.uni-potsdam.de/en/ibb-evolutionsbiologie/index> for recent work).

The successful applicant will work on the speciation and adaptive radiation of electric fish, combining electrophysiological and behavioural studies. The project may involve field work in the tropics.

Recent publications on the topic include:

* Amen R, Nagel R, Hedt M, Kirschbaum F, Tiedemann R (2020) Morphological differentiation in African weakly electric fish (genus *Campylomormyrus*) relates to substrate preferences. *Evolutionary Ecology* /*34*, 427-437. * Nagel R, Kirschbaum F, Hofmann V, Engelmann J, Tiedemann R (2018) Electric pulse characteristics can enable species recognition in African weakly electric fish species. *Scientific Reports* /*8*, 10799. * Nagel R, Kirschbaum F, Engelmann J, Hofmann V, Pawelzik F, Tiedemann R (2018) Male-mediated species recognition among African weakly electric fishes. *Royal Society Open Science* /*5*, 170443.

The position includes a teaching duty of 2 hours/week in zoology/evolutionary biology for undergraduates.

Applicants must hold a university degree (Master of Science in biology or a related discipline). Familiarity with electrophysiology and/or behavioral methods (including multivariate statistics) is preferable.

The University of Potsdam is an equal opportunity employer. If equally qualified, disabled applicants will be preferably considered. The University of Potsdam aims at increasing the number of female researchers and encourages qualified females to apply.

Potsdam is a beautiful city in close vicinity to the German capital of Berlin. Potsdam University takes an effort to assist its members in family-related issues and has repeatedly been awarded the total e-quality award.

Please send your application by email (in a single pdf) before 10th of April 2021 to: Prof. Dr. Ralph Tiedemann, University of Potsdam, Institute of Biochemistry and Biology, Evolutionary Biology/Systematic Zoology, Email: tiedeman@uni-potsdam.de

“Prof. Dr. Ralph Tiedemann” <tiedeman@uni-potsdam.de>

QueenMaryU London EvolutionaryTheory

I am lecturer from Queen Mary University of London, working on evolutionary theory. I am looking for a PhD student to work on our project funded by EU commission, applying stochastic modeling, dynamical systems in cancer evolution.

Here is our job link

<https://webapps2.is.qmul.ac.uk/jobs/-job.action?jobID=5459> Dr. Weini Huang (Modelling individual interactions in species coevolution, cancer evolution)

Lecturer in Mathematical Biology Deputy Director of PGR Studies School of Mathematical Sciences Queen Mary University of London

London, UK

Weini Huang <weini.huang@qmul.ac.uk>

RuhrU SpeciesRecognition

PhD position - The genomic basis of host specificity as tool for species recognition and delimitations in Ustilaginales - a parasite group with high gene flow

The department Evolution of Plants and Fungi at the Ruhr-University Bochum (Germany) is offering one PhD position for a period of three years

We are seeking a highly motivated candidate with an interest in the evolution, ecology, and species diversity

of fungal plant parasites to join our group at the Ruhr-University Bochum for Evolution of Plants and Fungi (Begerow lab).

Our research focuses on fungal biodiversity, especially on the evolution of smut fungi (Ustilaginomycotina/Microbotryales) and fungal community diversity. Within this project we want to understand the evolution of fungal effectors in natural populations of species in the genus Anthracoidea, a group of parasites on sedges (*Carex*). Specifically, we are using whole genome sequencing and ddRADseq/Hyb-Seq to study the correlation of effectors and host specificity at different taxonomic levels, from species to population level. The results of this work will be incorporated into a systematic framework to understand the impact of host species on parasite species delimitations.

The applicant is expected to have a highly qualified Master of Science degree or equivalent in Biology, preferentially Botany or Mycology, with a strong interest in fungal plant parasite evolution. Suitable candidates have experience in one or more of the following areas: phylogenetics/phylogenomics and/or population genomics, preparation and analyses of high-throughput DNA sequencing data, systematic understanding in fungal parasites.

The Ruhr-University Bochum is an equal opportunity employer and particularly encourages application of candidates from underrepresented groups in this discipline. The remuneration is based on TV-L 13 (65%).

The position is open from April 2021. Application deadline is 28 March, but open until the position is filled. Candidates should submit their application as a PDF in English (including CV, one-sided motivation letter, professional references) to Dominik Begerow (dominik.begerow@rub.de) and Martin Kemler (martin.kemler@rub.de). If you have any questions please contact one of the PIs.

Martin Kemler <martin.kemler@ruhr-uni-bochum.de>

SouthDakotaStateU PlantInvasions

Two funded Masters (or one PhD) graduate research assistant position(s) are available (Aug 2021) in the Latvis Lab of the Department of Natural Resource Management for students interested in population genetics, bioinformatics, phylogenetics, or invasion biology. These graduate positions are part of a large, collaborative network: the Consortium for Plant Invasion Genomics (<https://www.invasiongenomics.com>), funded by the National Science Foundation (OIA 1920858).

Students in the Latvis Lab will investigate the biological invasion of *Salsola tragus* (prickly Russian thistle) into North America by combining population genomic data, herbarium records, and inference of ploidy. There will also be numerous opportunities to contribute to other collaborative projects, development of teaching/mentoring skills, workshop/conference attendance, and outreach. We emphasize broad training for professional success. Successful applicants will have a strong background in evolutionary biology, ecology, or bioinformatics. A willingness to learn new techniques is required. The graduate assistantships include a competitive stipend and tuition waiver.

The Department of Natural Resource Management at South Dakota State University combines Range, Wildlife, Fisheries, and Ecology within the College of Agriculture, Food & Environmental Sciences. The department is committed to quality mentoring and professional development for their students. SDSU is the Land Grant University for the state and has approximately 13,000 students. SDSU is located in Brookings, SD, approximately one hour north of Sioux Falls and four hours west of the Twin Cities and offers a low cost-of-living in a small college-town atmosphere.

To apply, send a CV; a letter describing your experience, research interests, and career goals; and contact information for three professional references to Maribeth Latvis (Maribeth.Latvis@sdstate.edu). Check out the Latvis Lab here: <https://maribethlatvis.wixsite.com/plantsyst> Maribeth.Latvis@sdstate.edu

SouthernIllinoisU PlantEvolution

The Evolutionary Ecology of Venus'Â looking glass: breeding system evolution, cryptic species, and climate change.

Plant Biology Program, College of Science, Southern Illinois University, Carbondale, IL.

The Weber Lab is actively recruiting MS and PhD students to work on a wide range of research questions in the plant genus *Triodanis* (and/or the sister genus *Legousia*). These small annual plants exhibit fascinating variation in breeding systems, intriguing biogeographical patterns, and established phenological responses to climate change. We are seeking students with interests in any aspect of the current research program. Projects would be developed with input from the student, but listed below are a couple of potential topics for graduate research:

1. What are the consequences for climate change on breeding system evolution and/or plasticity? Species in the native North American genus *Triodanis* exhibit a mixed mating system, with some flowers specialized for obligate self-fertilization. This breeding system varies among populations, and this variation is associated with environmental variation. With an extensive herbarium record, access to hundreds of field sites, and a tractable growth protocol 'V this system is well suited for examining the consequences of changing climate on plant breeding systems. As well, we can estimate the genetic and phenotypic consequences of changing climate with growth chamber, and molecular techniques.
2. To what extent is phenological behavior driven by plasticity and/or evolutionary history? Several species in the genus *Triodanis* exhibit shifts towards earlier flowering associated with earlier and warmer springs. Relatively few studies have examined patterns of phenological sensitivity or phenological niche at the genus (or broader) levels. We have extensive and detailed data of phenological patterns for both *Triodanis* and the sister genus, *Legousia*. Combined with climate data, this provides immense opportunity to examine the relative contributions of plasticity and genetics on phenological behavior. In addition, this system is highly tractable for investigating the consequences of shifts in phenology for overall impacts on plant life history (i.e., does earlier flowering increase the flowering window, or does it lead to earlier senescence?).

For more information about the Weber lab visit: <https://www.jenniferweber.org/> and the Plant Biology Graduate Program at SIUC <https://plantbiology.siu.edu/graduate/> Carbondale is in southern Illinois, providing a close link to many forested areas and lakes. The regional landscapes ranges from bottomlands to uplands with rolling hills, bluffs, and rugged topography. This is a great place for hiking, camping, kayaking, rock climbing, and biking, just to name a few activities. In addition, several larger cities are a relatively short drive away including St. Louis (~2h), Nashville (~3h), and Memphis (~3h). Chicago is also reachable via a train station right from Carbondale (~5h train ride).

Interested students are encouraged to contact Dr. Weber by April 3, 2021 (jennifer.weber@siu.edu). Competitive funding options and summer funding are available. Preferred start dates are Fall 2021/Spring 2022.

Jennifer J Weber, PhD (She/Her/Hers) Assistant Professor in Plant Biology Southern Illinois University, Carbondale <https://www.jenniferweber.org/> “Weber, Jennifer J” <jennifer.weber@siu.edu>

TU Munich

Molecular Evolution Wild Tomato

PhD. Student in Molecular evolution of pathogen defence in wild tomato species.

We are interested in understanding the diversity of pathogen resistance within wild plant species. Therefore we study different populations from a diverse and geographically differentiated tomato species, *Solanum chilense*. We have shown that populations show different levels of defence against a range of pathogens and have identified patterns of differential selection for defence-associated genes. However, the implications of these findings on a molecular level remain unknown.

We are looking for an enthusiastic PhD student to investigate the underlying molecular mechanisms and the effects on plant defence mechanisms in an evolutionary context, using a combination of genomics, transcriptomics and metabolomics.

The applicant must have a very good MSc in biology, biochemistry or bioinformatics, with a strong theoretic background. Knowledge and practical experience in molecular plant sciences and/or bioinformatics are required. English skills, both written and spoken, are essential.

The project will be carried out in the group of Dr. Remco Stam at the Chair of Phytopathology (Prof. Dr. Ralph Häckelhoven). The chair hosts several research groups studying molecular biology of plant pathogens and is well equipped to study defence responses on different levels. The project is integrated into the SFB924 “Molecular mechanisms regulating yield and yield stability in plants” and benefits from many collaborations and direct access to state of the art technology at the Bavarian Centre for Mass Spectrometry and the sequencing facilities on the TUM Life Science campus in Freising-Weihenstephan.

TUM has been pursuing the strategic goal of substantially increasing the diversity of its staff. As an equal opportunity and affirmative action employer, TUM explicitly encourages nominations of and applications from women as well as from all others who would bring additional diversity dimensions to the university’s research and teaching strategies. Preference will be given to disabled candidates with equal qualifications. International candidates are highly encouraged to apply.

The salary is according to German income level TV-L E13.

Please send your comprehensive application including a letter of motivation (1 page), your CV, certificates, list of publications, and names of 2 potential referees as a single pdf file by email to: remco.stam@tum.de Informal inquiries can be made on the same address.

The position is to be filled in from 17 April 2021. Working from home could initially be possible.

Non-EU nationals can apply, but should be willing to move to Germany by the starting date.

Reviewing applications will start immediately, until a suitable candidate has been found.

Website of the lab: www.remcostam.com Informal enquiries are highly encouraged.

Remco Stam <stam@wzw.tum.de>

UAntwerp EvolutionaryGenomics

The Svardal lab at the University of Antwerp, Belgium, is looking for PhD and Postdoc candidates to be part of an exciting funded project to study the rapid adaptive diversification of 100s of cichlid fish species.

In one of two available project you will either

(1) establish novel molecular and computational techniques to identify structural variants

or

(2) develop machine learning and population genomic approaches to model the evolutionary and adaptive history of these structural variants and understand their role in adaptive radiation.

A quantitative background (computational genomics, population genetics) is a plus, but also candidates with a different background interested in these topics are encouraged to apply.

The vacancy is open until filled. Starting date can be negotiated. Remote work possible.

Direct application link:

PhD:

<https://www.uantwerpen.be/en/jobs/vacancies/-academic-staff/?q=1433&descr=Doctoral-scholarship-holder-in-Evolutionary-computational-genomics> PhD fellowships come with competitive salary and are for 4 years conditional on positive evaluation after 1 year.

Hannes Svardal Research Professor in Evolutionary, Ecological and Environmental Omics Department of Biology University of Antwerp

Campus Groenenborger, room U758
hannes.svardal@uantwerpen.be

Hannes Svardal <Hannes.Svardal@uantwerpen.be>

UCopenhagen FungusPopulationGenomics

The Applied Evolutionary Ecology group at Department of Plant and Environmental Sciences, University

of Copenhagen, Denmark is looking for a PhD student interested in developing their skills in comparative/population genomics and plant pathogenic fungal research. The position is part of the Carlsberg Foundation funded project: From plants to animals - Understanding inter-kingdom host-shifts of fungal pathogens. Deadline for application is April 11th, 2021.

The project is a collaboration between researchers at University of Copenhagen (UCPH), University of Sao Paulo (USP), and the Max Planck Institute for Evolutionary Biology (MPI-EB). Funding is available for three years for a competitive PhD fellowship, laboratory costs and travel. The supervisors will be Henrik De Fine Licht and Birgit Jensen (UCPH) and the project will be carried out in close collaboration with Professor Italo Delalibera Jr. (USP) and Professor Eva Stukenbrock (MPI-EB).

For more details and how to apply, please follow the link: <https://employment.ku.dk/phd/?show=153677> Henrik H. De Fine Licht HHDDeFineLicht@plen.ku.dk

Henrik Hjarvard de Fine Licht
<hhdefinelight@plen.ku.dk>

UFrankfurt EvolutionaryBiology

Frankfurt.EvolutionaryBiology

The Junior Research Group Global Change Ecology (Dr. Jonas Jourdan) at the Institute of Ecology, Evolution and Diversity of the Goethe University Frankfurt am Main, is seeking one Research Assistant (f/m/d) (PhD student) (E13 TV-GU, 65%-parttime) within the framework of the research project "Convergent characteristics of cryptic species along environmental gradients" funded by the German Research Foundation (DFG). The position is limited to a period of 3 years, starting on July 1st, 2021.

Project Rationale: The emergence of genetic methods has led to the discovery of an increasing number of species that previously could not be distinguished from one another on the basis of morphological characteristics. The family Gammaridae (Crustacea, Amphipoda) is a prime example of a group that has recently seen a high degree of genetic diversity uncovered. Some of these genetic lineages have expanded their range in recent times, while others continue to have very small distributions. However, the reasons for this, as well as general ecological differences among these so-called

cryptic species, are poorly understood to date. The PhD position includes a unique combination of field work in the Balkans, experimental work and laboratory work, combining evolutionary biology with aspects of ecology and ecotoxicology. The overall goal of this interdisciplinary project is to investigate the question of ecological differentiation of closely related cryptic species under varying environmental conditions using the species complex *Gammarus roeselii* as an example.

Your profile: The successful candidate holds a degree (M.Sc.) in a relevant field (e.g., biology, ecology, water science, molecular biology, environmental sciences or applied mathematics/computer science) and has a sound knowledge in molecular genetic methods (e.g., DNA barcoding, metabarcoding) and experimental work. Ideally, the candidate has the necessary practical skills to conduct multivariate statistical analysis of ecological data (preferably in R). Publication experience in scientific journals is an advantage. Furthermore, a class B driver's license, a high ability to work under pressure, very good organizational and communication skills are required. Excellent English skills, oral as well as written are required. German language skills are helpful but not mandatory.

We offer a creative, appreciative working environment with a high degree of personal responsibility in a young and motivated team. You will benefit from a research network of national and international cooperation partners and can take advantage of further qualification opportunities through the Goethe Research Academy for Early Career Researchers (GRADE).

Please send your application electronically with the usual documents, as well as a letter of motivation (in English language, max. 1 page), contact details of two referees to support your application, as a single pdf document to Dr. Jonas Jourdan, Institute of Ecology, Evolution and Diversity, Goethe University of Frankfurt, e-mail: jourdan@bio.uni-frankfurt.de. Closing date for application is March 31st, 2021. Please contact Dr. Jonas Jourdan (jourdan@bio.uni-frankfurt.de) for further information.

More information at: <https://sites.google.com/view/-jonasjourdan/research/cryptic-species> – Dr. Jonas Jourdan

Department Aquatic Ecotoxicology, Faculty Biological Sciences Goethe University Frankfurt Biologicum | room 2.320 | Max-von-Laue-Str. 13

60438 Frankfurt am Main | Germany

Tel +49 (0)69 798 42149 E-Mail: jourdan@bio.uni-frankfurt.de <http://www.ecotox.uni-frankfurt.de> Jonas Jourdan <jourdan@bio.uni-frankfurt.de>

UHalle Germany PathogenSpilloverBees

We have an open PhD position to contribute to an exciting new project (ComBee) on interactions between bee species, their parasites and land use in the group of Robert Paxton at the University of Halle, Germany (https://www.zoologie.uni-halle.de/-allgemeine_zoologie/). The goals of the project are to explore how apiculture and agricultural practices, including organic farming and floral field margins, impact the health of honey bee and wild bee populations. The research includes field experiments in association with the team of Catrin Westphal at the University of Göttingen, Germany (<https://uni-goettingen.de/de/-601841.html>), as well as molecular genetic studies on bees and their viral pathogens. Interest in host-parasite relationships, population genetics, virology and molecular genetic skills in the lab are desired.

The PhD salary is on the standard national (German) scale and the position is for 3 years, with a start date as soon as possible. Halle (Saale) is an historical city located 150 km SW of Berlin, with many like-minded academic institutes in the vicinity (e.g. UFZ, iDiv). For further information, contact Robert Paxton, E-Mail: robert.paxton@zoologie.uni-halle.de

Applications should be submitted by April 7, 2021, cite registration number 5-3009/21-D and include a cover letter explaining your interests in the PhD position and contact details of three academic referees.

Related publications:

<http://dx.doi.org/10.1038/nature12977> <http://dx.doi.org/10.1111/1365-2656.12345>

Robert Paxton <robert.paxton@zoologie.uni-halle.de>

UInnsbruck HeatwaveAdaptation

University Assistant, PhD Position

(20 hours per week, will be increased to 30 hours per week once the dissertation agreement has been signed)
University of Innsbruck, Research Department for Limnology, Mondsee, Austria, duration 4 years

Position: In this position, you will experimentally examine the evolutionary ecology of the responses of the freshwater snail *Lymnaea stagnalis* to changing environmental conditions under climate change. The specific goals are to reveal (1) how selection imposed by heat-waves operates on snail phenotypes and (2) how snails evolve over generations when periodically challenged by high temperature. The project is linked to other work in the research group of aquatic evolutionary ecology (led by Prof. Seppaelae) that focuses on the evolutionary adaptation of organisms to environmental change and natural enemies.

Qualifications:

Master degree in Biology Experience in laboratory and experimental work Experience in statistical analyses Communicative personality and ability to work in a team Flexibility Please attach a CV and a written idea to your dissertation project (max. 5 pages; only full applications will be considered)

Location: The position is based at the Research Department for Limnology at the University of Innsbruck, Austria. Several research groups at the institute focus on evolutionary ecology and the consequences of climate change in aquatic systems. The institute is located on the edge of the Alps in a small town of Mondsee (Upper Austria). The nearest city is Salzburg, which offers history, culture and entertainment in a convenient distance from Mondsee.

Job profile:

The full, legally binding call for application (in german) can be found at

https://lfuonline.uibk.ac.at/public/-karriereportal.details?asg_id_in=11798&lang=1 (Code BIO-11798). We are looking forward to receiving your online application by 6th April 2021.

For questions or more information concerning research, please contact Prof. Otto Seppaelae: otto.seppaelae@uibk.ac.at Travel costs cannot be re-

imbursed.

Salary:

The minimum monthly gross salary for this position amounts to Euro 1.486,00 for 20 hours per week (14 times). For the employment of 30 hours per week the salary is accordingly higher (Euro 2.229,00, 14 times). Furthermore, the university has numerous attractive offers.

Universit??t Innsbruck

Forschungsinstitut f??r Limnologie, Mondsee Sonja Burggraf Institutssekretariat Mondseestrasse 9, A-5310 Mondsee Telefon +43 512 507-50201

E-Mail sonja.burggraf@uibk.ac.at, office-ilim@uibk.ac.at

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

UInnsbruck SnailEvolution

University Assistant ??? PhD Position

(20 hours per week, will be increased to 30 hours per week once the dissertation agreement has been signed)
University of Innsbruck, Research Department for Limnology, Mondsee, Austria, duration 4 years

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Qualifications:

Master??s degree in Biology Experience in laboratory and experimental work Experience in statistical analyses Communicative personality and ability to work in a team Flexibility Please attach a CV and a written idea to your dissertation project (max. 5 pages; only full applications will be considered)

Location: The position is based at the Research Department for Limnology at the University of Innsbruck, Austria. Several research groups at the institute focus on evolutionary ecology and the consequences of climate

change in aquatic systems. The institute is located on the edge of the Alps in a small town of Mondsee (Upper Austria). The nearest city is Salzburg, which offers history, culture and entertainment in a convenient distance from Mondsee.

Job profile:

The full, legally binding call for application (in German) can be found at https://lfuonline.uibk.ac.at/public/-karriereportal.details?asg_id.in=11798&lang=1 (Code BIO-11798). We are looking forward to receiving your online application by 23rd of March 2021.

For questions or more information concerning research, please contact Prof. Otto Sepp: otto.sepp@uibk.ac.at Travel costs cannot be reimbursed.

Salary:

The minimum monthly gross salary for this position amounts to ??? 1.486,00 for 20 hours per week (14 times). For the employment of 30 hours per week the salary is accordingly higher (??? 2.229,00, 14 times). Furthermore, the university has numerous attractive offers.

Thank you and kind regards,

Universität Innsbruck

Forschungsinstitut für Limnologie, Mondsee
Burggraf 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>

UKentucky InsectEvolutionGenomics

PhD position in insect evolution & genomics

I am seeking a highly motivated PhD student to join my research group at University of Kentucky. Work in my lab focuses on insect evolution, speciation, integrative taxonomy, and molecular systematics using genomic approaches. The exact research project topic for this potential student is somewhat flexible, but will ideally focus on the genomic architecture of speciation and hybridization in North American swallowtail butterflies. Other potential projects include investigating ways that machine learning can be used to facilitate species delimitation, evaluating ecological drivers of di-

versification in buck moths, and developing molecular diagnostic tools for species identification and pathway analysis in invasive insect pests. I am also open to ideas and encourage potential applicants to contact me directly to discuss their interests and suitability. For more information, see www.julianrdupuis.com. The Department of Entomology at University of Kentucky offers excellent graduate training in diverse areas of insect biology. The Entomology graduate program is ranked in the top 10 nationally and is consistently rated as one of the most productive programs at the University of Kentucky, measured by the total number of student publications and presentations. Students from our department go on to have successful careers in a variety of sectors, including academia, industry, government science, and extension, to name a few.

I am looking for a student with a strong background in biology, entomology, or ecology and evolution (BSc or equivalent, MSc preferred). Experience with field research, molecular biology/genomics, and bioinformatics is preferred, as well as demonstrated research experience through completion of a MSc or undergraduate research. This position includes a competitive stipend, tuition waiver, and health coverage.

Interested applicants should submit 1) a cover letter detailing research experience, interests, and career goals, 2) a CV and unofficial transcript, and 3) name and contact information for three references to julian.dupuis@uky.edu. The successful applicant will be required to apply to the University of Kentucky Graduate School, although application to the graduate school can come a later time. See <https://entomology.ca.uky.edu/-academics/graduate> for more information on how to apply.

– Julian R. Dupuis, Ph.D. Assistant Professor Department of Entomology University of Kentucky (859) 562-2544 julianrdupuis.com

“Dupuis, Julian R.” <Julian.Dupuis@uky.edu>

UKonstanz DaphniaPopulationGenetics

PhD project - Effect of nutrients on population genetic diversity and host microbiomes of *Daphnia* metaorganisms

The water flea *Daphnia* is a popular model system to study evolution, ecology, and development. *Daphnia*

are globally widespread in freshwaters, have short generation times, and clonal lineages can be maintained in the laboratory, which facilitates experimental evolution and laboratory assays of genes and traits that drive evolution over time. Here we are employing an existing mesocosm setup to study the effects of nutrient availability and community composition on population genetics and host microbiomes of *Daphnia pulex* and *Daphnia magna* to better understand the dynamics of abiotic and biotic factors on species success and survival (in collaboration with Jelena Pantel, <https://www.aup.edu/profile/jpantel>). Briefly, selected genotypes of both *Daphnia* species are exposed in combination and alone to increased/decreased nutrient levels to assess how community composition affect patterns of genotype diversity and the microbiome within and between species. Importantly, this is a multigeneration experiment where selection effects from one generation to the next can be tracked. Further, the opportunity for manipulative experiments is provided (e.g., provisioning of selected microbes to assess probiotic effects, effect of additional stressor, etc.). The project aims to measure genotype/allele frequencies using whole genome pool sequencing, assess microbiome dynamics through marker gene sequencing, and to collect a suite of physiological parameters to assess how external factors shape species survival/dynamics. The project is a collaborative effort between the Becks, Meyer, and Woolstra labs, integrated in the doctoral program of University of Konstanz and the Research Training Group R3 (www.rtg-resilience.uni-konstanz.de). The DFG Research Training Group R3 Resilience of Lake Ecosystems at the University of Konstanz studies the response, resilience, reversibility of aquatic ecosystems to changing abiotic and biotic conditions using Lake Constance.

Requirements:

MSc degree in Molecular Biology, Genetics/Genomics, Microbiology, Limnology, or a related discipline.

Interest in Ecology, Evolution, Genomics, Metaorganisms.

Experience in molecular work and bioinformatics analysis is a plus.

High proficiency in spoken and written English is expected.

Last final exam (Master Degree or equivalent) must have taken place no longer than six years ago

Applicants must not have resided in Germany for more than 15 months prior to the nomination.

Application:

To apply, send the following documents as a single PDF

file to applicationRTGR3@uni-konstanz.de until 31th March 2021.

Cover letter, including statement of motivation (1 page)

Curriculum vitae (including list of publications)

Certificates of education

2 letters of recommendation from faculty using the form found at <https://www.daad.de/medien/deutschland/-stipendien/formulare/recommendation.pdf> (can be handed in at a later timepoint)

Further details:

Details on the DAAD Graduate School Scholarship Program, the application procedure and eligibility criteria: <https://www.daad.de/go/en/stipa57034100> Starting date: as soon as possible, latest by second quarter of 2021

– Prof. Dr. Lutz Becks Limnological Institute University of Konstanz Mainaustraße 252 78464 Konstanz / Egg Germany Mail: lutz.becks@uni-konstanz.de Phone: 07531 88 2828

"lutz.becks@uni-konstanz.de" <lutz.becks@uni-konstanz.de>

UMaine PlantEvolutionEcology

PhD position – Evolution of Plant Function/Phylogenetics – University of Maine, USA

A PhD position is available in the Plant Evolutionary Ecology group < <http://www.meireleslab.org/> > at the University of Maine, fully funded through a combination of research and teaching assistantships. Our group focuses on linking phylogenies and genetic data with functional trait and physiological data to understand the distribution of plant diversity and the evolution of plant function.

A central part of our research program has been to leverage leaf-level spectral and airborne data to assess plant traits and ecophysiological attributes. The PhD student will have the opportunity to become part of our ASCEND Biology Integration Institute < <https://www.spectralbiology.org/> > and interact with an enthusiastic group of students and faculty at UMaine's School of Biology and Ecology.

Your Profile:

The candidate must be enthusiastic about plant evolu-

tion and ecology, have excellent communication skills (including academic writing), a strong background in quantitative thinking, experience programming in R or Python, and willingness to work in the field and in the lab.

Contact:

For more information, please contact Dr. Jose Eduardo Meireles < <https://sbe.umaine.edu/meireles/> > (jose.meireles@maine.edu).

Applicants should send Dr. Meireles a ****single PDF**** document that includes (1) a cover letter summarizing their interests and relevant experience, (2) their CV, (3) copies of undergraduate and masters transcripts, and (4) contact information of two references. ****The application deadline is March 29th.****

José Eduardo Meireles <jemeireles@gmail.com>

UParma BaboonPopulationGenomics

Graduate Position: University of Parma, PhD in Baboon Population Genomics

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

The project aims at investigating the evolutionary history of baboon populations using available and newly generated genomic data comprising high and low coverage whole genome sequences and faecal/salivary metagenomic data. Given the nature of the project applicants will be expected to have previous experience in the handling of genomic data within a population genomic context (including reads mapping and variants calling) and use of high-performance computational clusters.

The call for applicants is expected to open in Spring 2021 and the PhD will begin in Autumn 2021. Interested candidates fulfilling the indicate criteria are strongly advised to contact Prof. Capelli to discuss the project (email: cristian.capelli@unipr.it)

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

doctoral programs offered by the SCVSA department.

The SCVSA department has been recognised Department of Excellence (2018-2022) by the Italian Ministry of Education, University and Research (MUR), receiving 9 million euro of dedicated funding.

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

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

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

Cristian CAPELLI <cristian.capelli@unipr.it>

UPittsburgh EvolutionaryBiology

The Department of Biological Sciences at the University of Pittsburgh has post-baccalaureate fellowships available for the 2021-2022 school year. The Hot Metal Bridge Program (HMBP) at the University of Pittsburgh is a post-baccalaureate program designed to help talented students from groups traditionally underrepresented in their academic disciplines, including first-

generation graduate students and those from disadvantaged socio-economic backgrounds, to bridge the gap between an undergraduate degree and a graduate training program. Participants are provided with a fellowship for two semesters, covering both tuition and stipend. Students in the program integrate into our broad-based biology department (<http://www.biology.pitt.edu/>), performing two independent research rotations in either Ecology and Evolution (E&E) or Molecular, Cellular and Developmental Biology (MCDB) and take classes with first-year PhD students. We provide a mentoring committee of three faculty to each student in the program to facilitate their professional development and applications to graduate school throughout the year. Our HMBP students have successfully matriculated into competitive graduate programs across the country.

The due date for applications is *April 2, 2021*. More details on the program can be found here:

<http://www.diversity.as.pitt.edu/hot-metal-bridge-program> Please don't hesitate to contact Cori Richards-Zawacki (cori.zawacki@pitt.edu) with any questions you may have!

Cori Zawacki <cori.zawacki@pitt.edu>

UppsalaU 2 AnimalEvolution

Dear all,

Two PhD positions in Animal Ecology are available within the project ReCod (<https://balticwaters2030.org/project/recod-utsattning-av-smatorsk-i-ostersjon>), a collaborative project between Uppsala University and BalticWaters2030. The positions are placed at Campus Gotland in Visby. See below and at <https://www.uu.se/en/about-uu/join-us/-details/?positionId=378813> for more information.

Please distribute this message to potential candidates.

Thanks and best regards, Anssi

Anssi Laurila Animal Ecology/ Department of Ecology and Genetics Evolutionary Biology Center Uppsala University Norbyvägen 18D 75236 Uppsala Sweden

Uppsala University is a comprehensive research-intensive university with a strong international standing. Our ultimate goal is to conduct education and research of the highest quality and relevance to make a long-term difference in society. Our most important assets are all the individuals whose curiosity and dedication make

Uppsala University one of Sweden's most exciting workplaces. Uppsala University has over 45,000 students, more than 7,000 employees and a turnover of around SEK 7 billion.

Department of Ecology and Genetics is looking for two enthusiastic PhD students to work within project ReCod in Program of Animal Ecology. The Department of Ecology and Genetics is an international environment with research spanning from evolutionary ecology and genetics to ecosystem studies. For more information, see www.ieg.uu.se. The positions are located at Campus Gotland in Visby, and field and laboratory work is conducted at Research Station Ar in northern Gotland. Campus Gotland is an integrated part of Uppsala University. You will have the opportunity to take advantage of the courses organized by the new graduate school in sustainable development. For more information, see www.campusgotland.uu.se. Project description: Cod is one of the most important fish species in the Baltic Sea, but the Baltic cod population has collapsed during the last decade. One of the main reasons for the population collapse is high mortality at egg stage. Project ReCod, a collaboration between Uppsala University and BalticWaters2030 (www.balticwaters2030.org), aims to develop the methodology to push the cod population through the vulnerable egg stage by releasing hatchery-reared yolk-sac larvae at carefully selected sites. This will be done by producing large number of yolk-sac larvae under optimal conditions in the hatchery. The ultimate goal is to strengthen and rebuild populations of the top fish predator in the Baltic sea. The project is led by Prof Anssi Laurila (scientific leader) and Prof Gunilla Rosenqvist (head of Research station Ar) in collaboration with the project leader from BalticWaters2030.

Position 1: Rebuilding the Baltic cod populations by large-scale release of yolk-sac larvae. The thesis focuses on the methodology of producing, raising and releasing cod eggs and larvae as well as on the success of the releases. You will conduct exploratory fishing and environmental surveys at the release sites to assess factors affecting the establishment success. You will also conduct experimental studies to assess factor affecting establishment success.

Position 2: Phenotypic and genetic variation in early life history of the Baltic cod. The thesis focuses on the role of environmental variation in the performance of cod eggs and larvae and its potential on increasing survival through these stages. Another topic is phenotypic and genetic variation within the eastern population of the Baltic cod. You will use laboratory and field experiments to disentangle how environment and genetics affect survival and performance of early life stages in cod.

duties: You will work together with several persons to develop a well-adapted methodology for rearing and releasing cod larvae. These will be combined with detailed studies on cod biology to find a well-functioning methodology to rebuild cod populations. You will also participate in teaching at undergraduate level.

Requirements: A master degree (or equivalent) in ecology, marine biology, fisheries biology or a relevant field. We are looking for enthusiastic, highly motivated and independent candidates who must be able to express themselves fluently in spoken and written English. Driving license is required for work in Research station Ar.

Additional qualifications: Good knowledge on statistics (programming in R), experience on aquatic field work and on fish or other aquatic organisms is advantageous.

Application: The application should include 1) a letter of intent describing yourself, your research interests, motivation of why you

— / —

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>

UTartu Estonia LepidopteraPhylogeny

PhD position: phylogenetic studies on Lepidoptera in an ecological context

We are looking for a PhD student to perform part of a larger, lab wide project entitled: “Comparative studies on insects: a focus on body size” financed by Estonian Research Council (2020-2024) and carried out at Estonia’s leading research centre: the University of Tartu (<https://www.ut.ee/en>). The lab wide project focuses on reconstructing moth phylogenies based on DNA sequences and performing various analyses of trait evolution on the basis of these novel phylogenies. The PhD thesis work advertised here will concentrate on several sub-tasks, such as acquisition of nucleotide data from a number of moth species either by anchored hybrid enrichment technology and/or more traditional Sanger sequencing, and constructing phylogenies using both maximum likelihood and Bayesian phylogenetic inference. In addition, depending on the interests of the student, there will be possibilities to take part

in more ecology-oriented subprojects, primarily those on phylogenetic comparative analyses of life history traits. The work will be supervised by Dr. Erki Áunap and Prof. Toomas Tammaru (<http://www.ut.ee/~tammarut>). The group has a solid background in evolutionary ecology of insects, phylogenetic analyses and taxonomy of Lepidoptera, as well as collaboration ties with various universities across Europe. PhD studies in Estonia last for 4 years and publishing research papers is a requirement; PhD students receive competitive scholarships allowing them to work on their thesis full time (alongside taking some relevant classes). A successful candidate will have an excellent academic record, experience with phylogenetic analyses and interest in evolutionary biology. Some experience and/or genuine interest in the taxonomy/evolution/ecology of insects is an advantage. The candidate should have their master’s degree by August 01, 2021; the enrolment as a PhD student will be from September 01, 2021. If you are considering applying, please e-mail Toomas Tammaru (toomas.tammaru@ut.ee) before the end of March 31 (any time zone). Open to applicants from all nations.

Toomas Tammaru <toomas.tammaru@ut.ee>

UTasmania SexDeterminationEvolution

Graduate position: Genomics of Sex Determination in a viviparous reptile with genotypic and temperature-dependent sex determination

Project theme:

Sex-determination controls the most significant variation within animals- the division into males and females. While the different systems of sex-determination involving genetic or environmental control are relatively well understood, transitions between these systems remain enigmatic in evolutionary biology. This project aims to address this gap by revealing the genomic changes required to transition between modes, using one of only two known lizard species exhibiting both genetic and temperature control of sex. This knowledge will have important implications for species conservation, facilitating predictions of highly biased sex ratios under climate change, plus potential commercial applications for species where the production of one sex is favoured.

A PhD position is available to contribute to this research. This student will conduct advanced genomic research on species of Australian lizards to decipher the

changes accompanying transitions between genetic and temperature-dependent sex determination.

This collaborative research project is funded by an Australian Research Council Discovery Project grant awarded to the University of Tasmania (Assoc Profs Chris Burridge and Erik Wapstra), the University of Canberra (Prof Tariq Ezaz), and the University of Austria (Prof Oleg Simakov). This PhD project will be based at the University of Tasmania, but there is potential for a remote start given current travel restrictions to Australia. The project involves a variety of Next-Generation Sequencing (NGS) and bioinformatics, including assembly, annotation, and comparative mapping.

The Ideal Candidate

The ideal candidate is expected to have knowledge in genomics (e.g. NGS technology and bioinformatics). Knowledge of chromosome biology and sex determination is also desirable. The candidate will be self-motivated and well-organised, with a demonstrated capacity to learn and apply the broad skill set necessary for the successful completion of a research project. The successful candidate will be able to work alongside a wide variety of people in multi-function and multicultural laboratories. The successful candidate will also have a strong commitment to excellence in research and scholarship.

Scholarships

Financial support for domestic and international students is available for a high achieving student through a University of Tasmania scholarship (applications received continuously, but earlier applications have greater chance of success). These scholarships are highly competitive. To be competitive, candidates should have a Masters or first-class Honours degree or equivalent in a relevant area and other evidence of research potential (such as publications and relevant work experience). The scholarship and project are for 3.5 years. More information on the scholarships and admission process can be found at <https://www.utas.edu.au/research/degrees> Eligibility

The University of Tasmania scholarships are open to all nationalities. However, overseas candidates that have not written a thesis in English, or for whom English is not their first language, must secure an IELTS score of 7.0 and have no individual score falling below 6.5 to satisfy our English language requirements. More information and equivalent scores under different schemes (e.g. TOEFL) can be found at <https://www.utas.edu.au/research/degrees/what-is-a-research-degree> How to Apply

Interested applicants should submit a CV, a copy of their academic transcript, a sample of your written scientific work, and a cover letter outlining their research interests to chris.burridge@utas.edu.au

Chris Burridge | Associate Professor, Molecular Ecology & Evolution

School of Natural Sciences | University of Tasmania | Private Bag 55 | Hobart | Tasmania 7001 | Australia

Room 320a Life Sciences Building | Ph +61 3 6226 7653 | Fax +61 3 6226 2698 |

https://rmdb.research.utas.edu.au/public/rmdb/-q/indiv_detail_warp_trans/3975#research-tab-5

<http://scholar.google.com.au/citations?user=4cYH8ZYAAAAJ&hl=en> evogentas.org

Christopher Burridge <chris.burridge@utas.edu.au>

UTennessee Knoxville ClimateAdaptation

The Blum Lab in the Department of Ecology & Evolutionary Biology (EEB) at the University of Tennessee, Knoxville (UTK), is seeking PhD students to join research endeavors focusing on eco-evolutionary dynamics related to global change. Students will have opportunities to contribute to ongoing pursuits leveraging highly persistent soil-stored seed banks in Chesapeake Bay marshes to reconstruct century-long records of eco-evolutionary responses to climate change and corollaries thereof (e.g., sea level rise). Students also will have opportunities to become involved in a newly funded “Bridging Ecology and Evolution” project that will assess whether and how rapid evolution of an ecologically dominant plant to global change influences carbon cycling in Chesapeake Bay marshes. Joining one or both pursuit(s) will present opportunities to collaborate with partners at the University of Notre Dame, the Smithsonian Environmental Research Center, Bryn Mawr College, and other leading institutions.

Prospective students should have a mix of primary interests related to evolutionary biology, quantitative genetics, population genetics and genomics, transcriptomics, and epigenetics. Interests should also extend to plant physiology and functional traits, plant-microbe associations, coastal ecology, global change ecology, soil biogeochemistry as well as ecosystem processes related to carbon and nutrient cycling.

Students will be provided a competitive stipend as well as support for tuition and health insurance through a graduate research and/or teaching assistantship. Support is available for students to begin in the Fall semester of 2021 or Spring semester of 2022. Further information about the UTK EEB department can be found at eeb.utk.edu. Further information about work being undertaken in the Blum Lab can be found at eeb.utk.edu/people/michael-j-blum/.

Applicants must have an undergraduate degree from an accredited institution in ecology, evolutionary biology, genetics, botany, plant sciences or a related discipline so long as relevant coursework has been completed. Preference will be given to candidates with a MS degree and with relevant work experience. Candidates should email a letter of interest, curriculum vitae, unofficial transcripts, and contact information for three references as a single pdf to Dr. Michael Blum (mblum@utk.edu) by 1 May 2021.

The University of Tennessee is an EEO/AA/Title VI/Title IX/Section 504/ADA/ADEA institution in the provision of its education and employment programs and services. All qualified applicants will receive equal consideration for employment and admission without regard to race, color, national origin, religion, sex, pregnancy, marital status, sexual orientation, gender identity, age, physical or mental disability, genetic information, veteran status, and parental status.

Please contact Dr. Michael Blum (mblum@utk.edu) for further details about this opportunity.

“mblum@utk.edu” <mblum@utk.edu>

Versailles FruitFlies

To Evolutionary Biologists,

Please consider the following funded Ph.D. opportunity, Autumn 2021-2024, to be forwarded to any potential candidates.

Ph.D. title: Molecular and functional evolution of olfactory-guided attractive behavior in Tephritidae fruit flies

Ph.D. topic: Fruit flies of the family Tephritidae are the main pests of fruit and vegetable crops. Many species are highly invasive and spread outside their region of origin where they reduce or displace native populations. The oriental fruit fly (*Bactrocera dorsalis*), the melon

fruit fly (*Zeugodacus cucurbitae*) and the Mediterranean fruit fly (*Ceratitis capitata*) are among the most emblematic species of this family. Agroecological management of these pests integrates the use of attractants, including food lures (which are not very specific and have low attraction power) and male attractants. The latter are pheromonal precursors that provide a reproductive advantage to the males that consume them. The attractiveness of these compounds is variable among Tephritidae species. The main objective of this thesis is to identify and characterize the main receptors of male attractants of several species of tephritids, opening the way to the search for new agonists that will be potential attractants. The Research will be subdivided into two secondary objectives: (a) studying the neural coding of attraction behavior and (b) testing hypotheses for the evolution of insect olfactory systems.

Name of the scientific managers: Emmanuelle Jacquin-Joly, DR, INRAE Vincent Jacob, PhD, CIRAD

Working environment: The applicant will alternately integrate two laboratories that will co-supervise the thesis. (1) At the Sensory Ecology department of UMR iEES-Paris (<https://iees-paris.fr/departements/ecologie-sensorielle/>), INRAE Versailles campus, France, the applicant will have access to *Drosophila* genetic manipulation, electrophysiological equipment, and expertise in molecular phylogeny of insect odorant receptors (2) At UMR PVBMT (CIRAD - Université de la Réunion), Saint-Pierre, Ile de la Réunion, the applicant will dispose of eight Tephritidae species of agronomic interest routinely reared, as well as electrophysiological and behavioral testing equipment.

Application: Applicants should send a CV + motivation+ two letters of reference to Emmanuelle Jacquin-Joly : emmanuelle.joly@inrae.fr and Vincent Jacob : vincent.jacob@cirad.fr before June the 1st 2021

Candidate skills: We are looking for a candidate highly motivated to study insect behavior and its physiological and molecular mechanisms. The student will have the opportunity to carry out part of his/her thesis on a tropical island, Reunion Island, so adaptability is essential. Preference will be given to candidates with experience in insect behavior, electrophysiology or molecular phylogeny. Programming skills will be appreciated.

Vincent JACOB <vincent.jacob@cirad.fr>

Vienna PopulationGenetics

Call for PhD students in Population Genetics is open: apply by May 16, 2021 Start date: Sept 2021 (or earlier)

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

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

Topics include:

- Evolution from de novo mutations - influence of elevated mutation rates.
- Evolution of sex-specific neuronal signaling.
- Genome evolution in columbines.
- Inference of selection signatures from time-series data.
- Long-term dynamics of local *Drosophila* populations.
- Molecular genetics of epigenetics.
- Seed ecology.
- Structural variation and genome evolution.
- Tempera-

ture adaptation in *Drosophila*: phenotypic adaptation.
 - The sources of diversity shaping adaptive radiation.
 - Understanding polygenic adaptation.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by May 16, 2021 will be considered. Two letters of recommendation need to be sent directly by the referees.

Depending on the project, PhD degrees will be awarded either in genetics, mathematics or statistics. PhD students will receive a monthly salary based on currently 2.237,60 before tax according to the regulations of the Austrian Science Fund (FWF).

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator

www.popgen-vienna.at <https://twitter.com/PopGenViennaPhD>
 c/o Institut für Populationsgenetik
 Veterinärmedizinische Universität Wien (Vetmeduni
 Vienna) Veterinärplatz 1, 1210 Wien

Current home office contact via Skype: julia.hosp Office: +43 1 25077 4338 (currently unavailable)

<http://www.vetmeduni.ac.at/en/population-genetics/>
<https://twitter.com/PopGenVienna> Julia Hosp
 <Julia.Hosp@vetmeduni.ac.at>

Jobs

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Amherst MA LabTech EvolutionTickDiseases

MedZu Inc is a public benefits corporation that conducts crowd-sourced tick-borne disease surveillance via a vis its private testing service for human-biting ticks (TickReport). This service provides subscribers with the earliest risk assessment for tick-borne disease. In aggregate, these data have provided valuable insights to the ecology and evolution of tick-borne diseases including Lyme disease ((Sci Rep 10:10289; J. Med Entomol. <https://doi.org/10.1093/jme/tjaa140>; Emerging infectious diseases, 26(4), 648-657; Emerg. Inf. Dis. June 24(6):1143-144; Vectorborne Zoo. Dis. 19: 106-114 <http://doi.org/10.1089/vbz.2018.2323>).

MedZu analyzes over 20,000 tick and other arthropod samples per year via qPCR pathogen analysis. In the busiest season of the year, we conduct DNA/RNA extraction and/or qPCR analysis of over 1,000 samples per week. We are seeking two candidates who will each specialize in either extraction or qPCR analysis and will cross-train with the other to provide coverage and support as needed.

MedZu is committed to professional growth and sustainable careers; successful lab members will find many opportunities for additional responsibilities and advancement. Slower seasons (roughly 6 months per year) will provide opportunities for training, research, and advancement.

Responsibilities:

- Follow Standard Operating Procedure (SOP) to conduct DNA/RNA extraction of ticks and related materials and maintain the highest standards of quality control.
- Conduct molecular diagnostics (primarily

qPCR, and conventional PCR, sequencing, and genotyping as needed in cooperation with technical advisors).

- Report results to clients and agencies and support maintenance/curation of database.
- Coordinate with accessioning division to ensure efficient processing of samples according to QA/QC standards and protocols.
- Participate in routine lab cleaning and upkeep (glassware, instrument service, ordering, etc.). Anticipate needs and order laboratory stocks. Qualifications:

- Molecular biology experience outside of coursework. Highly-qualified candidates will quantify in their application their past experience with DNA/RNA extraction and/or qPCR analysis of large numbers of samples. Be prepared to describe the type and volume of samples you have worked with in the past.
- At least one year of experience in a laboratory.
- An Associate's degree with a major in biology or a related field (e.g., Microbiology, Environmental Science, Biochemistry, Public Health) or an equivalent combination of education and training.
- Ability to problem-solve in a team setting and with minimal supervision
- Flexibility in responding to inconsistent workload and non-uniform samples
- Willingness to accept instruction
- Good organizational skills
- Familiarity with spreadsheets and/or database software

Note: Training in specific techniques to work with ticks and pathogens will be provided. It is expected that the incumbent will contribute to honing and improving efficiencies of these methods over time.

\$44,000.00 - \$54,000.00 per year— Benefits: 401(k), 401(k) matching, Dental insurance, Disability insurance, Flexible schedule, Health insurance, Paid time off, Retirement plan, Vision insurance Supplemental Pay: Bonus pay, Commission pay MedZu Inc 29C Cottage St,— Amherst, MA 01002 smrich@tickreport.com 413.559.0193

“Dr. Stephen Rich” <smrich@tickreport.com>

AstraZeneca Bioinformatician

Are you a quantitatively-minded scientist looking to apply bioinformatics and machine learning to design the next generation of therapeutics? Do you wish to join a growing team where you will have the possibility to further exploit our drug discovery platforms? If yes, we have the position for you at AstraZeneca in Cambridge!

We are currently looking for a Senior Bioinformatician to join us at AstraZeneca in Cambridge, UK as part of the Data Sciences and Quantitative Biology team in biopharma R&D:

<https://careers.astrazeneca.com/job/cambridge/-senior-bioinformatician-data-sciences-and-quantitative-biology/7684/18216461> Deadline for applications *23rd March*!

Best wishes, Sergio

Sergio Martinez Cuesta <sermarcue@gmail.com>

Bolzano Italy BarkbeetleMycobiomeMaxPlanck Poznan EvolutionaryBiology

Job:Max_Planck_NCN_ExcellenceDCPoznan.GroupLeader
Faculty of Biology AMU Poznan welcomes applications in the area of evolutionary and/or environmental biology for Leaders of Max-Planck-Gesellschaft (MPG) and National Science Centre Poland (NCN) Dioscuri Centres of Scientific Excellence in Poland,. Applicants will be asked to provide a concept for the DC they plan to establish, which includes an innovative research programme as well as an outline for the DC's structural development. DCs are expected to conduct top-class internationally competitive and innovative research, in collaboration with partners from German universities or research institutions. Each DC will be funded with up to 300,000 p.a., initially for five years. This amount will be part of a larger package involving supplementary funds, infrastructure, scientific equipment, and a long-term perspective for the leader of the DC at the respective Host Institution (to be arranged indi-

vidually between selected candidates and their Host Institutions). This will put the DCs in a position to attract additional funding from NCN and other Polish and European/international sources. See <https://ncn.gov.pl/dioscuri/dioscuri4/call-announcement> for more details. Please contact Prof. Jacek Radwan jradwan@amu.edu.pl for initial enquiries on establishing DC at FB AMU. < <http://evobio.home.amu.edu.pl/> >

Jacek Radwan <jacek.radwan@amu.edu.pl>

ClemsonU PDFs Jobs HumanGenomics

Center of Biomedical Research Excellence (COBRE) in Human Genetics Clemson University and the Greenwood Genetic Center

The Clemson University Center for Human Genetics and the Greenwood Genetic Center have been awarded a five year Phase I COBRE in Human Genetics grant to understand the genetic, genomic, and epigenetic mechanisms by which molecular genetic variation affects transcriptional and other molecular networks in health and disease. Several positions are available immediately.

The Research Core is seeking a Molecular Genetics Technician and a Programmer. Contact Dr. Trudy Mackay (tmackay@clemson.edu) for details.

Project 1 (CRISPR Screening in Cultured Human Cells) is seeking a Research Technician. Contact Dr. Andrei Alexandrov (andreaia@clemson.edu) for details.

Project 2 (Mechanisms of Disease Pathogenesis in Congenital Disorders of Glycosylation) is seeking a Postdoctoral Fellow. Contact Dr. Heather Flanagan Steet (heatherfs@ggc.org) for details.

Project 3 (Transposable Elements, Genome Architecture and Gene Regulation) is seeking a Computational Scientist and a Postdoctoral Fellow. Contact Dr. Miriam Konkel (mkonkel@clemson.edu) for details.

Project 4 (Genomic Prediction of Human Disease) is seeking a Postdoctoral Fellow. Contact Dr. Fabio Morgante (fabiom@clemson.edu) for details.

TRUDY F. C. MACKAY, PhD, FRS

SELF FAMILY ENDOWED CHAIR OF HUMAN GENETICS

DIRECTOR, CENTER FOR HUMAN GENETICS

PROFESSOR OF GENETICS AND BIOCHEMISTRY

Center for Human Genetics
 Clemson University
 110 Self Regional Hall
 114 Gregor Mendel Circle
 Greenwood, SC 29646
 w 864-889-0522
 c 919-604-6531
 tmackay@clemson.edu

Center of Biomedical Research Excellence (COBRE) in Human Genetics Clemson University and the Greenwood Genetic Center

The Clemson University Center for Human Genetics and the Greenwood Genetic Center have been awarded a five year Phase I COBRE in Human Genetics grant to understand the genetic, genomic, and epigenetic mechanisms by which molecular genetic variation affects transcriptional and other molecular networks in health and disease. The Research Core of the COBRE in Human Genetics is seeking a Molecular Genetics Technician to support the genomics research of Research and Pilot Project Leaders and their laboratories. Ideally, the successful applicant will have previous molecular biology and genomics experience, including (but not limited to) basic molecular biology and next generation sample and library preparation for Illumina short read and Pacific Biosciences long read sequencing. Salary will be commensurate with credentials and experience.

Enquiries should be addressed to Dr. Trudy F. C. Mackay, Self Family Endowed Professor and Director of the Center for Human Genetics, Clemson University, Self Regional Hall, 114 Gregor Mendel Circle, Greenwood, SC 29646 (tmackay@clemson.edu). Applications must include a cover letter explaining the qualifications for this position and the names of three references. The position is available immediately. Clemson University is an equal opportunity employer.

To apply, go to jobs.clemson.edu and apply for job ID 105538.

TRUDY F. C. MACKAY, PhD, FRS

SELF FAMILY ENDOWED CHAIR OF HUMAN GENETICS

DIRECTOR, CENTER FOR HUMAN GENETICS

PROFESSOR OF GENETICS AND BIOCHEMISTRY

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Center of Biomedical Research Excellence (COBRE) in Human Genetics Clemson University and the Greenwood Genetic Center

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Enquiries should be addressed to Dr. Trudy F. C. Mackay, Self Family Endowed Professor and Director of the Center for Human Genetics, Clemson University, Self Regional Hall, 114 Gregor Mendel Circle, Greenwood, SC 29646 (tmackay@clemson.edu). Applications must include a cover letter explaining the qualifications for this position and the names of three references. The position is available immediately. Clemson University is an equal opportunity employer.

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Cleveland Museum Nat History 2 Environmental Change

Two positions at the Cleveland Museum of Natural History

The first position is our Assistant Curator of Environment. See description below:

Cleveland Museum of Natural History JOB ANNOUNCEMENT Assistant Curator of Environment

Summary: The Cleveland Museum of Natural History is seeking a highly-motivated scientist capable of developing a modern, relevant research program in a Museum focused on connecting people with the natural world. The Museum seeks a strong communicator that can inspire, connect, and engage with a broad audience on the importance and relevance of science and nature.

The successful candidate will develop a research program in the area of environmental change that utilizes both the Museum's extensive preserved collections and its holdings of 66 natural area preserves totaling nearly 12,000 acres distributed across Northern Ohio. Building a research program that addresses relevant environmental questions with an interdisciplinary approach that pulls from the expertise of other curators and regional partners is targeted. A systems approach using botanical specimens as a basis to address changes in biodiversity, ecosystem structure, species distribution, freshwater quality, climate, or other is desired. Understanding the impact these preserves have the region's environmental health, the change we are seeing within these pristine habitats, and the methods of stewardship that ensure their future are all areas of interest for the Museum. The successful candidate will oversee the Museum's herbarium, which holds more than 85,000 specimens in a modern facility with a computerized database. The Museum's zoological collections would also be available for research and include more than 500,000 specimens of invertebrates and vertebrates representing both regional and global taxa. Other resources pertinent to the development of an impactful, relevant research program on the environment includes collaboration with the staff responsible for the stewardship and restoration of the preserves, a diversity of curatorial and collections staff, and a focus on integrating human health and impact into the Museum's research and education programs.

The curatorial staff at the CMNH are expected to develop research programs, in their appointed area, that integrate with Museum strategy and vision, collaborate across the Museum and the region, incorporate student training, incorporate public outreach, support public programs, enhance institutional collections, and attract external funding. A strong commitment to connecting people with nature through science and natural history is desired. The CMNH maintains an affiliation agreement with Case Western Reserve University for curator adjunct appointments, within the Department of Biology, that enables both teaching and graduate student advisement. Curators at the CMNH also provide oversight and direction of the collections through collaboration and interaction with the collections management staff. The CMNH is strongly committed to diversity, equity, and inclusion, particularly in its candidate selection and hiring process.

Essential Duties and Responsibilities (Must be able to perform the essential functions of this position with or without reasonable accommodation.) . Establish and build a research program that integrates with Museum strategy, programs, and community engagement. . Function as a science communicator in support of the Museum's mission and strategy to inspire, connect, and engage with a broad audience on the importance and relevance of science and nature. . Work with cross-institutional teams to provide scientific content, ensure scientific accuracy, and plan high quality experiences that serve the largest possible number of participants from diverse backgrounds. . Serve as content provider on project teams, guiding the collaborative development and implementation of scientific content for exhibitions, education programs, and other programmatic projects. . Seek and secure funding to support research activities. . Publish research in disciplinary journals, books, reports, and general interest pieces. . Enhance use, digitization, and quality of CMNH collections. . Train graduate students through service on graduate committees or graduate qualifying committees. . Oversee research assistant staff members as well as volunteers, students, and other specialized staff involved in research activities. . Responsible for tracking research activity, progress, and impact for institutional use. . Work with collections management staff to approve loans, collections acquisitions, deaccessions, and major collections changes within the collections of appointment. . Responsible for providing advisement and assistance for the

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mcmaster.ca/~brian/evoldir.html

ColoradoC 1yr Visitor AnimalEvolution

The Department of Organismal Biology and Ecology at Colorado College announces a one-year, non-tenure track Assistant Professor position in Animal Biology and Ecology to begin in August 2021. A review of completed applicant files will begin immediately and continue until the position is filled.

Responsibilities for this Animal Biology & Ecology position entail teaching six courses, including introductory zoology/animal biology, ecology, either an upper-level or non-majors course in the candidate's area of specialty, and directing student research. The ability to integrate subfields of physiology, behavior, experimental design, ecology, and evolutionary biology and a familiarity with Rocky Mountain or Southwestern ecosystems are highly desirable. We seek an individual with demonstrated potential for excellence in undergraduate teaching, which includes fostering inclusive learning environments where all students can thrive. Apply electronically to: <https://employment.coloradocollege.edu/postings/4642> Colorado College is a private, undergraduate, highly selective liberal arts institution enrolling approximately 2000 students. The college uses the Block Plan calendar in which students take one class at a time, allowing for significant field and lab experiences. The Organismal Biology and Ecology (OBE) Department at Colorado College studies the structure and function of organisms in an ecological and evolutionary context. OBE research foci include botany, animal and plant ecology, comparative physiology, conservation biology, and molecular ecology. The department strives to perform cutting-edge research and include all students in these opportunities.

PhD (or near completion) and teaching experience required. Applications will include the following: 1) a description of relevant professional background, 2) three statements (a. teaching philosophy, b. diversity/inclusion/antiracism commitment, and c. research interests), 3) curriculum vitae with email address, and 4) three letters of recommendation. Information about Colorado College and OBE can be found at our web site: <https://www.coloradocollege.edu/academics/dept/obe/>. Inquiries about the position may be sent to the OBE chairperson, Dr. Shane Heschel at sheschel@coloradocollege.edu.

Colorado College welcomes members of all groups and reaffirms its commitment not to discriminate on the basis of race, color, national origin, gender, age, religion, gender identity or expression, disability, or sexual orientation in its educational programs, activities, and employment practices. Colorado College is committed to increasing the diversity of the college community and to becoming an antiracist institution. OBE believes the College grows stronger by recruiting and retaining a diverse faculty committed to building an inclusive community. Candidates who can contribute to that goal are particularly encouraged to apply.

sheschel@coloradocollege.edu

Denmark Bioinformatician

We have a new position for a bioinformatician / computational biologist with interest in bioinformatics and clinical microbiology. <https://candidate.hr-manager.net/-ApplicationInit.aspx?cid=198&ProjectId=-214671&DepartmentId=6871&MediaId=5&uiculture=-da&s> Thomas Vognbjerg Sydenham, MD, PhD. Dept of Clinical Microbiology Odense University Hospital Denmark

Venlig hilsen

Thomas Vognbjerg Sydenham Afdelingsl??ge, ph.d.
Thomas.Sydenham@rsyd.dk- www.ouh.dk Tlf. +45 6541 4798

Klinisk Mikrobiologisk Afdeling

Odense Universitetshospital og Svendborg Sygehus J. B. Winsl??ws Vej 21, 2. sal, 5000 Odense C

Thomas Vognbjerg Sydenham
<Thomas.Sydenham@rsyd.dk>

FieldMuseum Chicago CollectionsManager

Full Time

Field Museum is hiring a Collections Manager to manage its world-class Herpetology collections. The Collections Manager reports to the Head of Zoological collections and will manage day-to-day activities in the Herpetology

collection including management of staff. The Collections Manager will work jointly with curators to set long and short-term priorities for the Herpetology collections and will also interact with other collections areas, research scientists, exhibition developers, and education staff. The Collections Manager will have opportunities to pursue research for up to a maximum of 20% of their work time and seek funding for collections improvements and specimen-based research projects. The successful candidate will be evaluated on the ability to promote, study, build, care for, and ensure accessibility to the great wealth of specimens in the collection.

Field Museum houses one of the world's largest collections of zoological specimens. The 306,000-specimen Amphibian and Reptile Collection are comprised of over 286,688 catalog entries.

The collection is a major research resource for the national and international scientific communities. Containing unique material of special historical and ecological significance, the collection is world-class in size as well as taxonomic and geographic scope. The bulk of the collection (98%) is stored in 70% ethanol and contained in over 30,000 jars and 97 steel tanks. The skeletal collection contains over 7,600 skeletons and 1,700 cleared and stained preparations. There are also over 20,000 specimens with genetic resources stored in our cryogenic facility.

Applications must include Cover Letter and a CV to be considered. The review of applications will begin on April 12th, 2021.

To be considered, application materials must be submitted via email to FieldHerpsCM@fieldmuseum.org

Duties and Responsibilities

digitization tasks including imaging specimens, georeferencing, species inventory, and development and evaluation of workflows and standards to ensure best practices

new material into the collection, preparing, sorting, identifying, and cataloging specimens

and reporting metrics of collection use and growth

the herpetology collection budget

an active loan program and on-site use of the collection by researchers

in the museum's public programming and promoting the mission of the museum and its fundraising goals

the museum's commitment to increasing diversity, access, and inclusion across its programs

, mentorship, and supervision of staff, interns, and volunteers in the collection

Qualifications

in Biology (with an emphasis in Herpetology) with at least 3 year's collections experience; Ph.D. (with an emphasis in herpetology) desirable. A well-versed background in Herpetology is required, including familiarity with other Herpetology collections and research;

of taxonomic principles and Herpetology collection management;

organizational skills necessary to keep collection accessible;

experience with collection databases, imaging systems, and data aggregators is required, as well as a strong history of managing digitization projects;

knowledge of international and domestic regulations for the shipment of specimens and requirements for packing loans;

history of building and managing a diverse team of staff, interns, and volunteers.

The Field Museum is committed to equity, diversity, and inclusion. We strive to create a working environment that is free of sexual, racial, and ethnic discrimination, and one that promotes human dignity and mutual respect among all staff. As such, it is the policy of the Field Museum to hire without regard to race, religion, color, national origin, age, sex, sexual orientation, disability, or veteran status.

The Field Museum strives to ensure that our career website and recruiting process are accessible to all. If you are unable or limited in your ability to use or access our online application, or if you require a reasonable accommodation in completing this application, interviewing, completing any pre-employment testing, or otherwise participating in the employee selection process, please direct your inquiries to toaccessibility@fieldmuseum.org.

<https://careers.hireology.com/fieldmuseum/525376/-description> –

Adam W. Ferguson, Ph.D. Negaunee Collection Manager of Mammals, Field Museum 1400 S. Lake Shore Dr. Chicago, IL 60605 fieldmuseum.org 312.665.7749

The Field Museum resides on the ancestral homelands of the Three Fires Confederacy: Ojibwe, Odawa, and Potawatomi. The area was also a site of trade, gathering and healing for more than a dozen other Native tribes. Illinois is currently home to more than 100,000 tribal members. My

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mcmaster.ca/~brian/evoldir.html

Frankfurt ResAssoc 1yr Biodiversity

Job announcement ref. #01-21012

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. The head office of Senckenberg is Frankfurt am Main together with the Senckenberg Research Institute and Natural History Museum Frankfurt.

To support the DFG-funded Specialised Information Service Biodiversity Research (BIOfid, www.biofid.de) at our location in Frankfurt am Main or optionally in Görlitz we are looking for a

Research Associate (m/f/d)

(full time)

at the earliest possible date.

We are an interdisciplinary team of natural scientists, text technologists and librarians developing new text mining tools for semantic indexing of 19th and 20th century Central European biodiversity literature (mainly in German language). Existing data on the systematics and ecology of various organisms, which have been difficult to access until now, can thus be mobilised and used by scientists for further studies. In our second project phase, we focus on ecosystem services in the sense of plant-pollinator interactions and soil invertebrates.

Your tasks

Extension, standardisation and structuring of existing vocabularies and thesauri on morphological and functional traits of soil fauna based on the data warehouse Edaphobase and in collaboration with an international team
Support for the ontology development on species traits of soil fauna and its linkage to taxonomic ontologies
Evaluation and consolidation of text mining technologies
Analysing and publishing project-related data
Project presentations at national and international conferences
Participation in the organisation of workshops for user groups
Reporting to the DFG and the scientific advisory board

Your profile

Successfully completed university studies (ideally a doctoral degree) in biology, bio(diversity)informatics or a related field
Good knowledge of terminologies and nomenclatures in biology, especially morphology, systematics and traits of soil fauna
Basic understanding of zoological-ecological interactions and functions
Knowledge of basic data standards for biodiversity data
Fluency in English both spoken and written
Excellent abilities in team work and communication as well as self-reliant service- and target-oriented operation

Advantageous are

German language skills
Software skills for the development of ontologies (e.g. Protégé)
Experiences with database queries

What is awaiting you?

An attractive and challenging position in a research institution of international standing
The opportunity to gain experience in the above-mentioned fields of research as well as the chance to participate in an international network with scientists in interdisciplinary fields
Flexible working hours - mobile working - leave of absence due to family reasons - parent-child-office (certified by the audit berufundfamilie) - annual special payment - company pension scheme - Senckenberg badge for free entry in the Senckenberg museums - leave of 30 days/year - discounted job ticket (for the Rhine-Main area)

Salary and benefits are according to a full-time public service position in Germany (TV-H E13). The contract should start as soon as possible and will initially be limited to one year (with option of extension).

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 or optionally in Görlitz, Germany.

You would like to apply?

Please send your complete and meaningful application documents (letter of motivation, CV, educational and professional certificates and credentials, as well as professional references), mentioning the reference of this job announcement (ref. #01-21012) and if possible your preferred place of work (Frankfurt or Görlitz) before April 7th, 2021 by e-mail (attachment in a single pdf document) to recruiting@senckenberg.de or apply directly on our homepage using the online application form.

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

For more subject-specific information, please contact Dr. Christine Driller, christine.driller@senckenberg.de

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

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

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Harvard ResAssoc MalariaGenomics

The Neafsey Lab at the Harvard T.H. Chan School of Public Health is seeking a Research Associate to contribute to our research program in the evolutionary genomics of malaria (<https://sites.sph.harvard.edu/~neafsey-lab/>). The successful candidate will develop a personal research program as well as manage experimental laboratory processes, including high throughput DNA extraction and multiplexed PCR assays to perform targeted Illumina sequencing. Our lab generates and analyzes large genomic datasets from malaria parasites and vector mosquitoes to understand mechanisms of disease evolution, transmission, population dynamics, drug resistance, immune evasion, and host/vector/pathogen interactions. The successful candidate will join a diverse group with expertise that spans molecular epidemiology, computational biology, and evolutionary genomics.

Candidates are required to have a Ph.D. in biology/molecular biology/molecular parasitology or equiv-

alent, as well as at least three years of postdoctoral experience. Strong molecular biology laboratory skills are essential, previous experience with in vitro culture and manipulation of Plasmodium or other eukaryotic parasites strongly desired. Experience supervising research assistants, negotiating with vendors, managing project/protocol budgets, and administering lab safety protocols strongly desired.

Candidates should demonstrate a track record of consistent publication, have strong organizational, written, and oral communication skills, and should be able to work both independently and as part of a team. Spanish language proficiency is a plus.

Please contact Professor Neafsey by email: neafsey@hsph.harvard.edu with CV, letter of interest, and names of three references.

We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability status, protected veteran status, gender identity, sexual orientation, pregnancy and pregnancy-related conditions or any other characteristic protected by law.

Daniel Neafsey <neafsey@broadinstitute.org>

INVE Aquaculture Molecular Biotechnology Scientist

Job: Scientist position in molecular biology and translational sciences in shrimp and fish (the job is preferably based in Thailand; alternatively in Belgium)

INVE Aquaculture seeks to recruit a highly skilled and motivated scientist to join its growing innovation team of Advanced Nutrition in aquaculture. The successful applicant will closely collaborate and support research and development, oversees translational activities and contribute to advancing our growing portfolio of innovative programs.

The successful candidate will have a PhD or MSc with at least five years of relevant experience in molecular biology, with a deep understanding of the dynamics of host/pathogen interactions. S/he will have competence in novel assay development, is highly familiar with the latest technological advances in the field, and ideally has experience in computational biology and programming in R, MySQL and Perl or python.

Main Duties And Responsibilities - Finding, exploring and understanding molecular mechanisms underlying microbial diseases of fish and Shrimp, and the interactions between pathogens and their fish/shrimp host, and translating this into input for disease prevention in fish and shrimp

Qualifications and experience - Advanced level of Knowledge in Molecular Biotechnology, or - Bioscience Engineering, Biochemistry and Biotechnology, Veterinary Sciences with a speciality in Molecular Biotechnology, or Applied Bioinformatics - At least five years of demonstrated experience in research or development projects (preferentially in collaboration with industry), with a focus on pathogenic diseases in aquatic animals - Knowledge of virology is an advantage - Good Knowledge of English (writing/speaking) is required

Location: Preferably is based in Thailand (Bangkok). Alternatively in Belgium (Dendermonde). Willing to travel frequently.

We offer a challenging job in a dynamic sector and in a growing company with a compatible salary package in-line with your experience. Interested applicants can forward their CV and a cover letter to Mr. Marc De Feyter, HR Director, at HRM@inveaquaculture.com.

For online vacancy details, please visit: <https://www.inveaquaculture.com/careers/> (scientist position)

p.deschryver@inveaquaculture.com

LeibnizInst Hamburg 1BiodivInf 1Coll Man

Two positions are announced below:

1: Leibniz Institute for Analysis of Biodiversity Change (LIB) is seeking a Collection Manager (m/f/d) in Hamburg.

Leibniz Institute for Analysis of Biodiversity Change (LIB) will be established as an integration of Centre of Natural History of University of Hamburg (CeNak), Hamburg into Zoological Research Museum Alexander Koenig - Leibniz Institute for Animal Biodiversity (ZFMK), Bonn, as such LIB will be a foundation under public law and research museum of Leibniz Association. LIB will contribute to biodiversity research with its extensive collections and in research fields of taxonomy, morphology and molecular science, will contribute to conservation of global biodiversity, to documenting

and analyzing evolutionary and ecological biodiversity change and engage in science transfer activities on biodiversity change and its potential causes.

The Collection Manager (m/f/d) will play a central role in the implementation of high standards of curation, accessibility, digitization and protection of collections at LIB in Hamburg, in collaboration with curators and technical staff of the collections and the biodiversity informatics group at LIB.

We expect the candidate to * hold a university degree in biology, at least at the MSc level, * have working experience with scientific collections, preferably collection management (e.g., loan services, maintenance, pest control), * be familiar with pertinent legislations (such as the Nagoya Protocol, CITES) to support curators in the permitting process, * have practical experience with collection databases, * implement with the curators standards for documentation and security of the collections, * collect, curate, document, provide, and archive collection-related data and statistics (e.g. for reports, inquiries, and webpages), * engage in existing and participate in developing future concepts of digitization and collecting strategies, * participate and represent the collections in international and national digitization initiatives and collection networks, * help manage infrastructural collection development, * have excellent social, communication and organizational skills and the ability to work in teams as well as independently, * be fluent in English and preferably versed in a broad range of office, productivity, and database software applications.

The candidate will work at LIB Centre for Taxonomy and Morphology, Hamburg and contribute to the ongoing development of LIB as a globally leading institute for the study of biodiversity change.

The successful candidate is expected to interact intensely with LIB collection managers in Bonn, with curators, and directorate. The candidate will take part in self-administration and outreach activities. Working language is English, German language skills should be acquired on long term.

Leibniz Association is committed to diversity and equal opportunities. LIB is certified as a family-friendly institution. We aim to increase the proportion of women in areas, where women are under-represented and to promote their careers in particular. We therefore strongly encourage women with relevant qualifications to apply.

Applications will be handled in accordance with the Landesgleichstellungsgesetz NRW (State Equality Act). Applications from suitable individuals with a certified serious disability and those of equal status are particularly welcome. Salary corresponds to grade TV-L E 13

in the German Public Service Scheme.

We offer a highly motivating environment and ability to work independently. Salary and benefits are according to a public service position in Germany (TV-L E 13). ZFMK advocates gender equality. Women are therefore strongly encouraged to apply. The contract will start as soon as possible, earliest on July 1st 2021 and will initially be restricted to three years. A permanent position will be subject to personal performance reviewed by a commission.

Applications in English, accompanied by supporting documentation (CV, certificates) should be submitted no later than April 11th 2021 only digitally to Katharina Ostermann: www.leibniz-zfmk.de/en/-job-portal For further information about ZFMK and CeNak please see: <https://www.leibniz-zfmk.de> and <https://www.cenak.uni-hamburg.de>

2: Leibniz Institute for Analysis of Biodiversity Change (LIB) is looking for a Biodiversity Informatics Scientist (m/f/d) in Hamburg.

Leibniz Institute for Analysis of Biodiversity Change (LIB) will be established as an integration of Centre of Natural History of University



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LeibnizInst Hamburg 6 Curators

Leibniz Institute for Analysis of Biodiversity Change (LIB) seeks to fill the position of a Curator (m/f/d) for Crustacea in Hamburg.

Leibniz Institute for Analysis of Biodiversity Change (LIB) will be established as an integration of Centre of Natural History of University of Hamburg (CeNak), Hamburg into Zoological Research Museum Alexander Koenig ' Leibniz Institute for Animal Biodiversity (ZFMK), Bonn, as such LIB will be a foundation under public law and research museum of Leibniz Association. LIB will contribute to biodiversity research with its extensive collections and in research fields of taxonomy, morphology and molecular science, will contribute to conservation of global biodiversity, to documenting and analyzing evolutionary and ecological biodiversity

change and engage in science transfer activities on biodiversity change and its potential causes.

LIB is looking for a scientist for a tenure track position of a

Curator Crustacea (m/f/d)

in Hamburg starting July 1st 2021, representing research at an internationally competitive level, who will develop the field as a bridge between systematic and evolutionary research, and research on drivers of biodiversity change.

We expect the candidate to:

§hold a PhD in zoology or related areas, preferred with focus on Crustacea,

§have experience in the curation of scientific collections,

§be a designated expert in the taxonomy and biology of Crustacea,

§have a strong publication record with a focus on evolution, taxonomy and systematics of crustaceans,

§acquire substantial third-party funding,

§support the scientific community in this field as well as their societies,

§promote LIB-internal teamwork and external collaborations,

§have a vision of future work in the field, and promote novel ideas for collection-based research.

The candidate will work in Centre for Taxonomy and Morphology and contribute to the ongoing development of LIB as a globally leading institute for the study of biodiversity change. As curator, the candidate will take responsibility for substantial crustacean collections housed by LIB in Hamburg. This includes collection care, service to the scientific community, development of the collection, digitization activities, and collection-based research, with special emphasis on taxonomy.

LIB provides research labs for molecular and morphological work, from imaging to genomics. The successful candidate is expected to work on a sound theoretical basis, to build up an independent research group, to apply an array of appropriate modern methods, to integrate into existing and future in-house collaboration, to contribute to teaching at the university, and to take part in self-administration and outreach activities. Working language is English, German language skills should be acquired on long term. Leibniz Association is committed to diversity and equal opportunities. LIB is certified as a family-friendly institution. We aim to increase the proportion of women in areas, where women are under-represented and to promote their careers in par-

ticular. We therefore strongly encourage women with relevant qualifications to apply. Applications will be handled in accordance with the Landesgleichstellungsgesetz NRW (State Equality Act). Applications from suitable individuals with a certified serious disability and those of equal status are particularly welcome. We offer a highly motivating environment and ability to work independently. Salary and benefits are according to a public service position in Germany (TV-L E 13). An upgrade of salary and benefits to TV-L E 14, is possible and will be subject of the tenure evaluation. The ZFMK advocates gender equality. Women are therefore strongly encouraged to apply. The contract will start as soon as possible, earliest on July 1st 2021 and will initially be restricted to three years. A tenured position will be subject to personal performance reviewed by a commission. Applications in English, accompanied by supporting documentation (CV, certificates, lists of publications and funding) and a concept for collection-based research in Crustacea section of LIB should be submitted no later than April 11th 2021 only digitally to Sandra Middelhoff: www.leibniz-zfmk.de/en/job-portal For further information about ZFMK and CeNak please see: <https://www.leibniz-zfmk.de> and <https://www.cenak.uni-hamburg.de>

– Zoologisches Forschungsmuseum Alexander Koenig - Leibniz-Institut für Biodiversität der Tiere - Adenauerallee 160, 53113 Bonn, Germany www.zfmk.de
Stiftung des öffentlichen Rechts; Direktor: Prof. Dr. Bernhard Misof Sitz: Bonn

Leibniz Institute for Analysis of Biodiversity Change (LIB) seeks to fill a Curator (m/f/d) for Lepidoptera in Hamburg

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LundU FieldAssist BlackbirdEvolution

Full-time paid field assistant position to work on blackbirds in Lund

at the Biology Department, Lund University (Sweden)

What do we study: We use a population of free-living blackbirds (*Turdus merula*) to investigate the physiological mechanisms of partial migration, with a focus on the immune system. At present we have just under 200 colour-ringed birds in Lund that we monitor using radio telemetry and field observations. We use these data in combination with measurements taken from blood samples to assess whether immune function is a cause or consequence of partial migration.

Job description: The field assistant will work alongside other team members to observe and recapture colour-ringed blackbirds in/around Lund. Capture methods will include mist-nets and snap traps. The field assistant will be responsible for making observations of colour-ringed blackbirds in the field, helping to set up and monitor mist nets and/or snap traps, extracting and processing birds and recording data.

Requirements: He/she must be confident with setting up mist nets and handling/extracting a range of small passerine species unsupervised. Experience with colour ringing and taking more detailed biometric measurements (e.g., tarsus length, moult score), as well as radio telemetry is desirable but not essential. Ideally, the candidate would be available full-time for a period of 3 months between April and July. Proficiency in English language (spoken and written) and the ability to ride a bike are essential.

How to apply: All enquiries and applications should be sent directly to Dr Rosie Lennon (rosie.lennon@biol.lu.se). Applications (in English) should be sent no later than Wednesday the 24th March 2021 with the term 'Field assistant' as email subject line and should include:

- 1) CV (maximum 2 pages) with information on relevant experience and training;
- 2) a brief cover letter (maximum 1 page) explaining how the applicant's background makes them a suitable candidate for the position.

Selected candidates will be invited to an online interview.

Kind regards, Rosie Lennon

Rosie J Lennon Postdoctoral Researcher Biology Department (Ecology Building) Lund University

ResearchGate: <https://www.researchgate.net/profile/Rosie-Lennon> Latest publication: <https://doi.org/10.1016/j.scitotenv.2020.140493> Rosie Lennon
<rosie.lennon@biol.lu.se>

MichiganStateU Tech SwitchgrassEvolution

The Lowry Lab in the Plant Biology Department at Michigan State University is currently looking for a field technician to conduct research on the physiology and genetics of evolutionary adaptations in the bioenergy crop switchgrass. The successful applicant will work with a team of other technicians, undergraduate students, and postdocs. Applicants should send their resume/CV and contact information for at least two references to David Lowry at dlowry@msu.edu. The starting wage will be \$17 per hour. The successful applicant will be located at the Kellogg Biological Station in western Michigan. This position is available now and will continue through December 1st. More information about research in the Lowry Lab can be found at: <http://davidbryantlowry.wordpress.com/> David B. Lowry Associate Professor Plant Biology Department Michigan State University Plant Biology Laboratories Room 268 517-432-4882 <http://davidbryantlowry.wordpress.com/> David Lowry <dlowry@msu.edu>

NCBI 2 Bioinformatics

Computercraft seeks a highly skilled and self-motivated bioinformatics curator to join the Sequence Read Archive (SRA) group at the National Center for Biotechnology Information (NCBI), part of the National Library of Medicine (NLM) at the National Institutes of Health (NIH). The successful candidate will receive, process, and solicit genetic sequencing datasets from scientific projects and investigators. Other job responsibilities include creating complete and accurate SRA records, analyzing sequence data and metadata to address questions about the content, and helping administer and maintain the database.

The SRA, the largest publicly available repository of high-throughput sequencing data, stores raw sequencing data and alignment information to enhance reproducibility and facilitate new discoveries through data analysis. It is located under the Primary Data Archives at NCBI, which includes GenBank. To learn more about the

SRA database, go to <https://www.ncbi.nlm.nih.gov/sra/>. The successful candidate will work together with experts from NCBI to create and enhance a suite of databases and cutting-edge tools available to researchers worldwide. The position will initially focus on viral and microbial metadata curation associated with coronavirus submissions, offering an opportunity to support the national COVID-19 pandemic response.

This is a full-time position working on site at the NIH Campus in Bethesda, Maryland, but the new hire will initially telework. Currently, all Computercraft employees at NIH are teleworking full time to prevent the spread of coronavirus. Employees will return to onsite work as soon as it is deemed safe to do so.

To apply for this position or learn about other Computercraft job opportunities, please visit the Careers section of our website: <https://computercraft-usa.com/>. Computercraft offers a competitive salary, an excellent benefits package, and the opportunity for a positive work-life balance with a standard 40-hour work week and the chance to work alongside a team of highly accomplished professionals.

Computercraft is an equal opportunity employer.

Joan Yu <jyu@computercraft-usa.com>

Computercraft is seeking data wranglers to contribute to an exciting new initiative of the National Center for Biotechnology Information (NCBI), part of the National Library of Medicine at the National Institutes of Health (NIH), to expand tools and resources for working with genomic data. NCBI is planning a major modernization of its resources, their user interfaces, and their underlying infrastructure to support the rapidly growing collections of sequence and other data on species across the tree of life. By rearchitecting these resources, NCBI aims to improve the user experience for researchers doing a wide range of work, reach more users, support more research organisms, and ultimately drive biomedical discoveries that have the potential to improve human health.

Data wranglers with collective expertise in a variety of eukaryotic organismal backgrounds will primarily perform analyses on new and refined tools to assess quality, and ensure the tools meet the needs of users. The data wranglers will serve a central role between users and the development team, understanding the perspective of users and ensuring NCBI develops the interfaces and exchange of content users need with a high level of data quality.

This is a full-time position working on site at NCBI, NIH, in Bethesda, Maryland, but the new hire will ini-

tially telework. Currently, all Computercraft employees at NIH are teleworking full time to prevent the spread of coronavirus. Employees will return to onsite work as soon as it is deemed safe to do so.

To apply for this position or learn about other Computercraft job opportunities, please visit the Careers section of our website: <https://www.computercraft-usa.com/>. Computercraft offers a competitive salary, an excellent benefits package, and the opportunity for a positive work-life balance with a standard 40-hour work week and the chance to work alongside a team of highly accomplished professionals.

Computercraft is an equal opportunity employer.

Joan Yu <jyu@computercraft-usa.com>

Netherlands 4 Biodiversity

Two senior researchers and two post-doctoral fellows at Naturalis Biodiversity Center (Netherlands)

<https://www.naturalis.nl/en/vacatures/two-senior-researchers-and-two-post-doctoral-fellows> The closing date for applications is April 19, 2021.

Naturalis Biodiversity Center in Leiden is the Dutch national research institute for biodiversity and systematics. With our collection of 42 million specimens (one of the world's largest), and our state-of-the-art research facilities we offer the (inter)national research infrastructure for species, identification and monitoring. We closely collaborate with many Dutch universities, research institutes, industry and government. We host over 120 researchers including 13 academia embedded professors and 40 PhD students.

More information: <https://www.naturalis.nl/en/science/researchers-and-specialists> We are seeking *four ambitious, enthusiastic, innovative scientists* to strengthen our research capacity and multidisciplinary lines of research. We provide a vibrant environment organised in 9 research groups, and provide access to state-of-the-art laboratory facilities and the 42 million natural history objects in our collection. At Naturalis you will get the opportunity to develop your research career, to collaborate with inspiring colleagues and to teach at Dutch universities.

As a (senior) researcher, you are challenged to develop your leadership skills and to set up your own line of research. You will be expected to acquire project fund-

ing for new research, participate in outreach activities and mentor new researchers. After a successful first year evaluation, the contract will be extended. After a maximum of 4 years, the contract will be converted into permanent employment.

For postdocs this is an opportunity to pioneer your own research line within the context of one or more research groups. Postdocs are expected to spend part of their time on the acquisition of research funding.

Information on how to apply: <https://www.naturalis.nl/en/vacatures/two-senior-researchers-and-two-post-doctoral-fellows> Feel free to contact Maaïke van de Kamp-Romijn if you have any questions about the positions. maaïke.vandekamp-romijn@naturalis.nl

If interested in studying marine evolution, contact Katja Peijnenburg. Katja.Peijnenburg@naturalis.nl

Katja Peijnenburg <katja.peijnenburg@naturalis.nl>

OregonStateU 1yr TeachingEvolution

Subject: OSU Integrative Biology Job Opportunity

The Department of Integrative Biology invites applications for a full-time (1.0 FTE), 12-month, fixed term Instructor position in Genetics and Development, to begin June 2021. Reappointment is at the discretion of the Department Head. We seek applications from individuals who utilize innovative approaches to providing inclusive online and in person instruction. Preference will be given to candidates with demonstrated success in development and delivery of courses in genetics and animal development. We particularly encourage applications from individuals who belong to underrepresented groups in science. To review the full posting and apply, go to <http://oregonstate.edu/jobs>. Apply to posting #98854. For full consideration, please apply by March 26th, 2021. Contact Tara Bevandich at Tara.Bevandich@science.oregonstate.edu or 541-737-5336 with questions. OSU is an AA/EOE.

"Blouin, Michael" <Michael.Blouin@oregonstate.edu>

Paris EcolEvolutionaryBiology

Professor of Ecology in the Biology Department of ENS (Ecole Normale Supérieure) and team leader in the Ecology and Evolutionary Biology Section of the Institute of Biology of ENS (IBENS), Paris, France

The Biology Department of the Ecole Normale Supérieure (ENS) is recruiting a Professor of Ecology, to join the Ecology and Evolutionary Biology Section of the Institute of Biology of ENS (IBENS). An ENS-CNRS-INSERM unit, IBENS is over 300 people, organized in 30 teams that are pursuing cutting-edge research agendas in life sciences. The Institute prides itself in strong interdisciplinary research across genetics, functional genomics, cellular and developmental biology, neurosciences, ecology and evolutionary biology.

With her/his team, the successful candidate will develop an innovative and ambitious research program, focused on the ecology of communities and/or ecosystems. Themes may relate for example to the mechanisms of origin and maintenance of biodiversity, the relation between diversity, function and resilience, and the functional and structural responses of communities and ecosystems to global changes.

Approaches combining experimentation or data mining with mathematical or computational modeling will be most appreciated. Experimental research can be planned to use infrastructures and resources available at the Ecotron IleDeFrance platform (UMS 3194 CNRS-ENS) and/or be developed in conjunction with academic programs on global biodiversity that IBENS and PSL University are involved in (for example /Tara Oceans/). The diversity of IBENS teams also offers research opportunities at the interface of ecology and environmental genomics and/or evolutionary biology. International networking, a potential for connections with other IBENS teams, and active training of doctoral students will also be strong assets.

The candidates' educational project will meet the Ecole Normale Supérieure (ENS) and the Paris Sciences & Lettres University (PSL)'s objectives: train elite students to research by offering high-level teaching that is directly related to IBENS laboratories' research activities. The successful candidate will be actively involved in the educational, organizational and managerial components of training programs of ENS Department of Biology in Ecology and Evolutionary Biology (upper-division

Undergraduate, Master's of Life Sciences) and PSL University Graduate Program in Earth and Biodiversity Sciences.

The successful candidate will teach courses (in English) in the field of community and ecosystems ecology. She/he must have strong expertise and a record of outstanding teaching experience in these fields.

Applications must be submitted before March 30th, 2021, 4PM Paris time (CET = GMT+1) via the online platform of the French Ministry of Higher Education, Research and Innovation at

www.galaxie.enseignementsup-recherche.gouv.fr/-ensup/cand_postes.GALAXIE.htm#1EC Please contact IBENS Director Dr. Pierre Paoletti for information or help with the application process, if needed.

The Department of Biology at ENS wishes to promote diversity in its academic team and welcomes all applicants.

Contact: Dr. Pierre Paoletti (he/his) pierre.paoletti[AT]bio.ens.psl.eu

Regis Ferriere <ferriere@biologie.ens.fr>

SangerInst DataScientist

Looking for a data scientist to join my group at the Wellcome Sanger Institute and work on large scale sequencing data from malaria mosquitoes in Africa as well as from a broad range of flying insect species in the UK.

Job advert is here: <https://jobs.sanger.ac.uk/vacancy/-senior-data-analyst-438835.html> This role would suit a creative and innovative individual with significant previous data science experience and a deep understanding of sequencing data analysis.

You should have an advanced degree in statistics, bioinformatics, computer science, computational biology, genomics, population genetics, or other relevant area of quantitative analysis - OR - equivalent experience with a focus on computing.

Any questions, please get in touch. mara@sanger.ac.uk

Thank you, Mara Lawniczak

The Wellcome Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215

Euston Road, London, NW1 2BE.

Mara Lawniczak <mara@sanger.ac.uk>

Stuttgart Biodiversity Monitoring

As part of the “Integrative Taxonomy” initiative of the state of Baden-Württemberg, a competence center for biodiversity and integrative taxonomy (KomBioTa) is being established at the University of Hohenheim in cooperation with the Stuttgart Museum of Natural History.

The University of Hohenheim’s (UHOH) Faculty of Natural Sciences invites applications for the position of a

Full Professor (W3) of Biodiversity Monitoring

at the Institute of Biology to be filled as soon as possible.

At the Stuttgart Museum of Natural History (SMNS) the position of the

Director of the Biodiversity Monitoring Department

is to be filled.

The joint appointment by the UHOH and the SMNS will be made according to the Jährlich model. Appointment to the University involves an immediate leave of absence to perform duties at SMNS, where the tasks will predominantly be carried out.

The SMNS is one of the most important natural history research museums in Germany and cooperates closely with the UHOH in research and academic teaching. The UHOH’s Institute of Biology excels in high-level basic research in organismic biology, among other areas. Together, the two institutions provide an active and strong research environment for studies in systematics, biodiversity, and evolution.

We are seeking a highly motivated scientist (m/f/d) with excellent teamwork skills and proven research achievements in the field of biodiversity monitoring at a high international level. Willingness to engage in a combination of field monitoring and analyze the collection data is expected. Sound knowledge of ecology, statistics, and taxonomy is required, ideally combined with expertise in molecular biology. The successful candidate should be able to teach both in German and English on topics of biodiversity research, methods of monitoring, and aspects of organismic biology at UHOH.

The tasks of the newly established Biodiversity Monitor-

ing Department will include the expansion and further development of the molecular biology laboratory as the SMNS’s central biodiversity research facility. In addition, it is expected that the professor will bring in new ideas for interdepartmental networking and profile raising of research activities at SMNS and closely cooperate with related disciplines at UHOH. A central task is to contribute to establishing the Competence Center for Biodiversity and Integrative Taxonomy at UHOH.

Requirements for your application are a habilitation or equivalent scientific achievements including proven experience in university teaching, in acquiring and managing third-party funded projects as well as corresponding publication achievements.

The advertised position is tenured. If appointed as full professor for the first time, the University of Hohenheim reserves its right to probationary employment. With equal qualifications, preference will be given to candidates with disabilities.

The UHOH and SMNS seek to increase the proportion of women in research and teaching and therefore strongly encourage female scientists to apply.

Please attach the following documents to your application: a cover letter, a statement of your future research interests, a curriculum vitae, transcripts of records and degree certificates, a list of publications, a list of third-party funded projects, a teaching record, information on teaching evaluations as well as three key publications.

<https://naturkundemuseum-bw.de/en/jobs> “Warth, Peter” <peter.warth@smns-bw.de>

Surrey England 2 Evolutionary Statistician

Location: Guildford, Surrey

Salary: £35,000-£45,000 per annum, depending on experience Start: Immediately Duration: Permanent

Applications are invited for an Ecological Statistician to join an expanding science-based start-up. The successful candidate will work closely with the members of the Data and wider Science teams to implement robust statistical approaches for optimising sampling design and interpreting patterns of community diversity derived from sequence-based biodiversity data.

Applicants should have significant experience of ecological statistics, including occupancy modelling, power analysis, and inference of the drivers of change in alpha and beta diversity from community datasets. Experience of such analyses with metabarcoding data would be an advantage.

The successful applicant will be comfortable working independently and as part of a wider team. They will be a proactive problem-solver with a high level of attention to detail and an ability to work on multiple projects at once. This role reports to the Head of Data and will be responsible for ensuring that analyses are statistically robust.

This is an ideal role for an early-career researcher with a PhD in the field of statistics and/or quantitative analysis of DNA-based biomonitoring data who is looking to work in an applied setting to enable better decision-making for nature using these tools.

NatureMetrics is a high growth start-up company leading the revolution in molecular biodiversity monitoring, enabling environmental managers to measure and monitor biodiversity with DNA-based tools. NatureMetrics has grown rapidly over the last five years and validated our technology in multiple industry sectors and regions of the world. We now have an exciting scale up plan backed by ambitious and supportive investors. We are a team of bright, enthusiastic individuals who are excited to be breaking new ground and disrupting the world of biodiversity monitoring. We take great pride in our work and are seeking new team members who will do the same.

The full specification can be found below. To apply please email careers@naturemetrics.co.uk including a CV and covering letter, and state that you are applying for the Ecological Statistician role. There is no fixed deadline for applications and the position will be held open until we find the right candidate.

Roles & responsibilities

General

Work with the Data, Science, and Business Development teams to design optimal sampling strategies for complex projects, balancing project aims, requirements, and constraints.

Devise statistical analysis pipelines for DNA-based community datasets, enabling clients to gain deeper insights into their data.

Lead the data analysis component of large projects, including hypothesis testing, occupancy correction, inference of drivers of alpha and beta diversity patterns, and comparisons between conventional and DNA-based

data where appropriate.

Learn and incorporate new and appropriate methods from the statistics and ecology literature into company analysis pipelines.

Ensure that the analyses undertaken by the company are statistically robust and answer the client's questions.

Contribute to scientific publications and reports.

Contribute to the preparation of grant applications and tenders where relevant.

Documentation

Maintain version-controlled, fully annotated scripts following NatureMetrics style guides.

Write guides/explainers for statistical pipelines suitable for different audiences.

Prepare and contribute to reports and applications where relevant.

Reporting

This role reports to the Head of Data.

Communication

Attend regular update meetings with the wider team.

Update wider company, management or board on progress as required.

Work collaboratively with the Data and Science teams.

Person Specification

Education & qualifications

You will have a PhD in statistics or an ecological discipline with a strong quantitative and statistical focus. Postdoctoral experience would be an advantage.

Specialist knowledge, skills & experience

Experience of independent analysis of community and/or high-dimensional datasets is required.

A strong background in experimental design is required.

Strong R and/or Python coding is essential, with good working knowledge of relevant packages.

Experience in one or more of occupancy modelling, power analysis, time-series analysis, and the use of multivariate statistics in community ecology is required.

Experience in the application of statistical models to metabarcoding data would be an advantage.

Experience in the field of Environmental Impact Assessment would be an advantage.

Interpersonal & communication skills

?? Organised & meticulous with effective communication skills.???

— / —

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SwissOrnithologicalInst HeadMigrationResearch

The Swiss Ornithological Institute in Sempach is a private foundation for the study and conservation of birds. Renowned in Switzerland and internationally, the institute unites basic research, applied research and implementation of conservation measures under the same roof. Due to the upcoming retirement of the current jobholder, we are looking for a

Head of the department of Bird Migration Research (80-100%)

starting on 1 December 2021 or by arrangement.

In this position, you will be responsible for directing and advancing research on bird migration. You will be supported by a team of currently 14 researchers.

Your tasks include - leading and organizing the department for bird migration research - coordinating research activities - conducting, publishing and directing scientific projects of your own - fundraising - supervising student theses - contributing to the development of the institute - promoting internal and external collaboration and fostering a professional network

What we are looking for Internationally respected in your discipline, you are passionate about research in bird migration and have a broad international network. You are an innovative and creative person interested in new ideas and methods and always seeking to advance your professional field. As an integrative researcher, you enjoy conceptual work, constructive and open communication, guiding your team members and supporting their development.

Requirements You have a doctoral degree in biology as well as several years of experience in carrying out own research. Experience leading large teams and major projects is essential, as is knowledge of ornithology. You

regularly publish in high-ranking journals and are an experienced fundraiser and supervisor of academic theses. You speak one of Switzerland's national languages and have a very good command of English. Other requirements include team skills, excellent interpersonal skills and a detail-oriented and independent working style.

We offer a varied position in an inspiring work environment, flexible working hours to facilitate the balance between family and work, and excellent social security benefits. The place of work is Sempach.

For questions about the position, please contact Dr Gilberto Pasinelli (gilberto.pasinelli@vogelwarte.ch). The Swiss Ornithological Institute is committed to increasing the representation of women in leadership roles and research and specifically encourages applications from qualified women.

We look forward to receiving your online application by 9 April 2021: <https://www.vogelwarte.ch/en/-vogelwarte/getting-involved/job-vacancies/> Pasinelli Gilberto <gilberto.pasinelli@vogelwarte.ch>

SyracuseU Bioinformatician

Assistant Professor 'V Bioinformatics The Department of Biology at Syracuse University seeks applicants for a tenure-track position in Bioinformatics at the Assistant Professor level. Candidates should have demonstrated bioinformatics and computational biology research experience that complements existing departmental strengths in Genetics, Genomics and Epigenetics; Cell, Molecular and Developmental Biology; Evolution and Animal Behavior; Neuroscience and Ecology and Plant Biology. Candidates must have expertise in the application of bioinformatics techniques and should be interested in the development of novel statistical and algorithmic approaches, potentially including Machine Learning, Artificial Intelligence, Data Analytics and Optimization Algorithms. The candidate is expected to develop a vigorous externally funded research program and participate in graduate and undergraduate teaching and mentoring in the areas of his or her expertise. Candidates must have a PhD in a relevant area of biology and an outstanding record of research experience at the postdoctoral level.

This recruitment is part of the ambitious Invest Syracuse Big Data Initiative in the broad area of Genomics, Bioinformatics, Data Sciences and Analytics. Faculty hired into these positions will join a highly collaborative group

of biologists and will contribute to a multidisciplinary research cluster that spans multiple departments in the College of Arts and Sciences, the College of Engineering and Computer Science, Falk College and Whitman School of Management. The Department of Biology also has strong research and educational ties to the adjacent Upstate Medical University and the State University of New York College of Environmental Science and Forestry.

Applicants should submit a cover letter, curriculum vitae, statements of research and teaching interests, a diversity statement describing interest or efforts in furthering diversity and inclusion, and arrange for three reviewers to submit recommendation letters to <https://www.sujobopps.com/postings/85905>, by March 15th, 2021. The search will remain open until the position is filled. Syracuse University is interested in candidates who have the communication skills and cross-cultural abilities to maximize their effectiveness with diverse groups of colleagues, students and community members. Women, military veterans, individuals with disabilities, and members of other traditionally underrepresented groups are encouraged to apply.

Syracuse University is an equal opportunity employer, as well as a federal contractor required to take affirmative action on behalf of protected veterans.

Competitive salary, start-up funds, and laboratory space will be provided. Located between the Adirondack Mountain, Finger Lakes, and Lake Ontario regions of upstate New York, the metropolitan area of Syracuse boasts myriad cultural and recreational opportunities and offers a wide array of urban, small town, and rural living. Questions can be addressed to search chair Steve Dorus at sdorus@syr.edu.

Stephen Dorus <sdorus@syr.edu>

UCincinnati 2yr TeachingEvolution

Job Overview

The Department of Biological Sciences at the University of Cincinnati invites applications for a Visiting Assistant Professor position to teach Anatomy and Physiology I and II lectures, and serve as course coordinator. The position is for two years, starting in August 2021. The Anatomy & Physiology sequence is a combined lecture and laboratory course that primarily serves students from the Colleges of Nursing and Allied Health. Our

departmental faculty have a deep interest in inclusive teaching, a proven record of excellence and quality in instruction, and can provide informal mentoring on incorporating active learning into large enrollment lectures.

This position includes instructing large enrollment A&P lecture sections: two sections of A&P one in the Fall and two sections of A&P II in Spring Semester. The successful candidate will also supervise the undergraduate Learning Assistants and Supplemental Instructors assigned to assist with the lecture sections; and coordinate the course overall and supervise the lab coordinator to ensure that content in the lecture and laboratory sections align.

The University of Cincinnati is an equal opportunity/affirmative action employer. Women, minorities, persons with disabilities, and veterans are especially encouraged to apply. Individuals with disabilities desiring accommodations in the application process should notify the Human Resources Department at 513-556-6381 by the application review date. The University of Cincinnati is the recipient of the National Science Foundation ADVANCE Institutional Transformation Award to increase the participation of women in academic science and engineering careers.

Minimum Requirements

Must have obtained a PhD in Biology or a closely related discipline.

Additional Qualifications Considered

College-level teaching experience in Anatomy and Physiology or a related area in Biology
Experience with active-learning pedagogical approaches, especially in large enrollment courses
Experience with online instruction

Application Process

All applications must be submitted online at <https://jobs.uc.edu> (Requisition #60964) To apply, submit a cover letter, curriculum vitae listing three references, and statement of teaching philosophy and experience, using the additional documents tool in the application system. As part of the application process, the applicant will need to provide a separate one-page statement addressing how the applicant's past or potential contributions to diversity and inclusion will advance UC's commitment to Inclusive Excellence. For additional information, please contact the chair of the search committee, Dr. Joshua Gross (grossja@ucmail.uc.edu). Review of applications will begin March 15, 2021, and continue until the position is filled.

Founded in 1819, the University of Cincinnati embarks upon its third century 'V building on the past and

defining the future by leading urban, public universities into a new era of innovation and impact through its strategic direction, Next Lives Here. Underscoring the power of creativity, ingenuity, invention and inclusion, what's Next will accelerate our unrivaled momentum, evidenced by eight straight years of record enrollment and rankings that include placement among America's top 100 public universities by U.S. News & World Report. Home to a diverse student body of nearly 47,000 and more than 4,200 distinguished faculty, the university combines its Research 1 (Very High Research Activity) Carnegie Classification with a physical setting that The New York Times recently acclaimed as "the most ambitious campus design program in the country.

"Gross, Josh (grossja)" <grossja@ucmail.uc.edu>

UManchester ResAssist SymbiosisEvolution

Research Assistant, University of Manchester

An exciting opportunity to join a diverse research group working in microbial evolution led by Professor Michael Brockhurst. You will be part of an interdisciplinary team of researchers investigating the evolution of symbiosis.

The project, which is funded by the Natural Environment Research Council, explores the molecular mechanisms underlying evolutionary transitions from free-living to symbiosis using the Paramecium-Chlorella model microbial symbiosis. We will exploit a powerful combination of comparative genomics, metabolomics, and laboratory experimental evolution to reveal the role of fitness trade-offs in the evolution of symbiosis.

The main responsibilities of this role include: field sampling of natural algal populations, maintenance of the strain collection, performing laboratory experiments, preparing samples for whole genome sequencing and metabolomics, collecting and analysing data, and contributing to the preparation of peer-reviewed publications and conference presentations. You will collaborate closely with the other project researchers and the investigators to deliver the research.

You will have a BSc or equivalent in Biology (or a related subject), extensive knowledge of microbial ecology and / or algal biology, and excellent technical skills in algal microbiology. Candidates with training in evolutionary biology and / or experimental evolution are strongly

encouraged to apply.

Job reference: BMH-016396 Location: Oxford Road, Manchester Closing date (DD/MM/YYYY): 18/03/2021 Salary: 27,511 to 28,331 per annum depending on relevant experience Employment type: Fixed Term Faculty/Organisation: Biology, Medicine & Health School/Directorate: Evolution & Genomic Sciences Hours per week: Full time Contract Duration: Fixed term from 3 May 2021 until 2 May 2024

Enquiries about the vacancy, shortlisting and interviews: Name: Prof. Michael Brockhurst Email: michael.brockhurst@manchester.ac.uk

General enquiries: Email: hrservices@manchester.ac.uk

<https://www.jobs.manchester.ac.uk/-displayjob.aspx?jobid=19791> Michael Brockhurst <michael.brockhurst@manchester.ac.uk>

Uppsala Fellowship EvolutionaryBiology

Call for Applications

Fellowships, Spring 2022 The Natural Sciences Programme

Located in the Botanic Garden in Uppsala, the Swedish Collegium for Advanced Study (SCAS) is a national institute for advanced study. The collections of Carolina Rediviva Library and other scientific facilities at Uppsala University are situated nearby.

For the spring semester of 2022 the Collegium offers residential fellowships for senior and early-career scholars from all countries. The fellowships afford scholars the opportunity to concentrate on their own research interests. Fellows are expected to be in residence and to participate in academic events beyond their own fields of specialization.

The Natural Sciences Programme aims at advancing cutting-edge research in the natural sciences, as well as at bridging the gap between these and the humanities and social sciences. The focus of the programme is on research that involves synthesis, data analysis and conceptual and theoretical work. There are four thematic foci of the programme, namely 1) Theoretical Biology; 2) Human Brains and Societies; 3) Measurable Man; and 4) Exoplanets and Biological Activity on Other Worlds.

At the time of application, the candidate must have held a PhD (or equivalent degree) for at least three years. Candidates should have a track record of significant and original research achievements, and be active at the international forefront of his/her research field.

The holder of a fellowship receives a monthly salary. Accommodation for Fellows who do not live in the Stockholm-Uppsala region is arranged by the Collegium and all Fellows have their own fully equipped office at the Collegium.

The application deadline is 31 March, 2021.

For full details about the programme, the eligibility criteria and how to apply, please see:

www.swedishcollegium.se Hans Ellegren
<hans.ellegren@ebc.uu.se>

USorbonne ParisNord EvolutionAnimalBehaviour

We are recruiting an Assistant Professor (Maître de Conférences) in Animal Behaviour starting in Sept. 2021 and tenured after 1 year. Teaching in French. All applications via the portal GALAXIE, deadline 30 March 2021 16:00 CET. Please RT. http://leec.univ-paris13.fr/-documents/FOPC_0931238R_4411.pdf best, Cristina

Maria Cristina Lorenzi

LEEC-Laboratoire d'Éthologie Expérimentale et Comparée Université Sorbonne Paris Nord 99 avenue J.-B. Clément 93430 Villetaneuse, France Phone: +33(0)149403260 ***** NEW Email: lorenzi@univ-paris13.fr Publication list LEEC website Master d'Éthologie, Sorbonne ParisNord

Maria Cristina Lorenzi <lorenzi@univ-paris13.fr>

USouthernCalifornia LabManager MarineMicrobialEvoluiton

AVAILABLE IMMEDIATELY, February 2021

Lab Manager and Technical Specialist in Marine Microbial Ecology

APPLY at

* <https://uscareers.usc.edu/job/los-angeles/research-lab-specialist/1209/5116983264> *The Fuhrman Lab* at the USC Dept. of Biological Sciences is looking for someone to make measurements, perform experiments in the lab and field (shipboard and possibly marine lab on Catalina island), and help keep the 10-person lab running smoothly.

Duties include:

- Performing molecular biological procedures (from field-collected samples), including DNA and RNA extraction, PCR, electrophoresis, library preparation and sequencing (and all associated reagent preparation), fluorescence microscopy for counting microbes, rate measurements (including use of radioisotopes), basic flow cytometry, nutrient analysis, and growing lab microbial cultures..
- *Experience with microbiology and molecular biology laboratory work required (prefer 5 years beyond Bachelors degree). up to 1/3 of time*

- Ordering supplies and keeping inventory of supplies and stored samples, organizing sample sets and shared resources and datasets, keeping the lab in good working order, managing compliance with safety regulations, and maintaining laboratory and field equipment. *up to 1/3 of time*
- *Data processing and analysis, including Excel spreadsheets; experience with basic bioinformatics for sequence analysis preferred*.
- *Prefer experience with bioinformatics command line programming in UNIX. On the job training can be provided. Up to 1/4 of time*
- Organizing and performing fieldwork on San Pedro Ocean Time-series cruises approximately monthly (including loading/unloading equipment, sample collection and preparation, experiments). Possibly other fieldwork on boat or Catalina marine lab. *Previous at-sea experience preferred. Training in ecology, especially aquatic microbial ecology, strongly preferred. Up to 1/4 of time*
- Supervising/training undergraduate lab assistants. Assist and train graduate students and postdocs in lab/field/analysis procedures. *Up to 1/6 of time*

The University of Southern California (USC), founded in 1880, is located in the heart of downtown L.A. and is the largest private employer in the City of Los Angeles. As an employee of USC, you will be a part of a world-class research university and a member of the "Trojan Family," which is comprised of the faculty, students and staff that make the university what it is.

See Position Requirements on the application site:

* <https://uscareers.usc.edu/job/los-angeles/research-lab-specialist/1209/5116983264> - *Jake L. Weissman, Ph.D* *pronouns: he/him/his* Simons Foundation Postdoctoral Fellow in Marine Microbial Ecol

ogy jakeweis@usc.edu <https://jlw-ecoevo.github.io>
 “jakeweis@usc.edu” <jakeweis@usc.edu>

Vienna Biology Statistician

Grade: Postdoc

Level of employment: 40 hours

Length of employment: 2 years but extension is anticipated

Deadline for applications: April, 7

We are seeking a postdoctoral statistician to provide statistical consultancy for the Vetmeduni Vienna, with a focus on two groups of the Department 5 (Unit of Comparative Cognition, Messerli Research Institute, and Domestication Group of the Institute of Ethology). The staff and student researchers in these two groups investigate the underlying mechanisms, the functions, the evolution and the development of cognitive abilities of dogs, wolves, parrots and pigs. These are examined in observational and experimental settings, using specific, well-controlled behavioural tests and state-of-the-art analysis tools (video analysis, machine learning, eye tracking).

The main duty of the post-holder will be to provide statistical consultancy to all staff and students, supported by a well-established statistics training programme. She/he will collaborate on the design and analysis of lab and field experiments and the application of a wide range of modern statistical modelling and multivariate analysis methods. Therefore, a broad working knowledge of the application of statistics in this scientific area is required; in particular, experience related to the application of statistical approaches to behavioural data and a good understanding of animal behaviour studies, in both the field and in the experimental context. The applicant should have in-depth experience with modelling approaches, taking into account small sample sizes and repeated measures designs, as well as unbalanced data sets with missing values and categorical variables. Furthermore, experience with a priori power analysis and (automated) data processing are desirable. Importantly, the applicant should also have a good capacity and strong commitment to communicate with and support colleagues and students at all levels (Masters, PhDs etc) with the statistical requirements of their project and design, help students to fit models, writing up the methods and results parts for

publications and teach both introductory and advanced in-house statistical courses including modelling in R. Finally, the applicant should be keen to advise scientists in other disciplines, especially in neuroscience, psychology, genetics, and (veterinary and human) medicine.

Required qualifications

- PhD in statistics, mathematics, biology, medicine or veterinary medicine
- Substantial statistical experience within the life sciences
- Expertise with a wide range of modern statistical modelling and multivariate analysis methods
- Sound experience with statistical software (preferably R)
- Fluency in both written and spoken English

Preferred qualifications

- Experience in planning and designing behavioural or cognitive tests
- Very good knowledge in (Generalized) Linear Mixed Models
- Experience with conducting a priori power analyses
- Experience with (statistical) programming and automated data processing
- Knowledge of Bayesian statistics
- Experience with automated video image analysis and big data analysis
- Experience in small-group teaching
- Experience of communicating statistical concepts to non-statisticians

- Proven publication skills

In the application letter the candidate should explicitly refer to these qualifications.

The University of Veterinary Medicine Vienna expects the successful candidate to acquire sufficient German language proficiency (within 3 years) for teaching and participating in University bodies.

Applications should be accompanied by the following documents:

§ Application letter (including preferred and earliest possible start date) together with a statement of personal motivation

§ Academic curriculum vitae (including a list of publications, a list of courses and students supervised, a list of talks given)

§ Copies of relevant certificates

§ Contact details of people who could provide a letter of reference (reference letters are not required at this stage)

Contact / Further Information

Prof. Ludwig Huber

Messerli Research Institute

ludwig.huber@vetmeduni.ac.at

<https://www.vetmeduni.ac.at/en/messerli/> Dr. Mar-

lies Dolezal

Bioinformatics and Biostatistics Platform

marlies.dolezal@vetmeduni.ac.at

<https://www.vetmeduni.ac.at/en/bioinformatics-and-biostatistics/about-us/> Associate Prof. Dr. Friederike Range

Domestication Lab, Konrad Lorenz Institute of Ethology

Friederike.range@vetmeduni.ac.at

— / —

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>

**WildlifeConservation
DirectorOfScientificAffairs**

Wild Animal Initiative is a 501(c)(3) nonprofit working to understand and improve the lives of wild animals. We are seeking a Director of Scientific Affairs to lead the planning and implementation of our programs that directly serve researchers. This full time position will primarily involve research, outreach, program design and evaluation, and management of our scientific team.

The successful applicant will have familiarity with the scientific community and funding environment in the US or the UK, at least 3 years of prior management experience, and significant research experience in a field related to zoology, ecology, evolution, or conservation.

Complete information about the role is available at <https://www.wildanimalinitiative.org/careers>. Applications should be submitted at <https://airtable.com/shrISVoekyNVrmGPf> by March 31st. Feel free to email info@wildanimalinitiative.org at any time with any questions about the job or application process.

The success of our mission depends on the diversity of our team. We strongly encourage people of every color, age, orientation, gender, origin, and physical ability to apply.

Michelle Graham <michelle.graham@wildanimalinitiative.org>

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BIOME Inst teaching

Caitlin Hayes

Apply for the 2021 BIOME Institute!

From Pieces to Patterns: Building a Scientific Worldview Summer Session: July 19 - August 6, 2021 Fall Working Groups: September 6 - November 19, 2021

During the 2021 BIOME Institute, participants will explore how pedagogy can guide students to see the forest and the trees—we'll focus on practices and resources that help learners incorporate detailed understandings into a meaningful framework, a scientific worldview, that will enable them to make predictions, solve problems, and see science in a broader, interdisciplinary context. The theme takes its cues from education research which indicates that providing overarching concepts can help students better retain and contextualize the details of biological processes.

The Institute will have a parallel emphasis on how our scientific worldviews are enriched by the diversity of our communities. We aim to support faculty in incorporating more inclusive teaching practices, with the goal of better preparing students to build a broad scientific worldview that reflects the interdisciplinarity of modern scientific practice. We also want to help faculty empower students to communicate scientific ideas effectively both within and beyond the classroom.

Find the full description and schedule on the BIOME webpage, and feel free to contact Hayley Orndorf (hco1@pitt.edu) with questions.

Caitlin Hayes Communications Manager

Cincinnati REU Evolutionary Biology

Dear Colleague:

This is to announce a new, paid summer research opportunity for undergraduate students, at the University of Cincinnati's Department of Biological Sciences - the National Science Foundation-sponsored Research Experiences for Undergraduates (REU) Site in Sensory Ecology. Our program is focused on research at the

intersection of neurobiology, behavior, ecology and evolution, and is directed at understanding how animals use their senses to respond to their environment at functional and evolutionary levels. Sophomore and junior Biology major students will be chosen to join active lab groups for the summer and conduct cutting edge research over a broad spectrum of topics in sensory ecology, including:

* Genomics and development of sensory systems * Neural mechanisms of sensory system function * Sensory perception and behavioral influences of the physical environment * Neuroethology * Animal communication * Behavioral ecology of animal movement and dispersal

An educational program will develop student research and professional skills and prepare them for graduate school or careers.

* ~10 weeks in summer (June 1 - Aug 6, 2021) * Students will receive a summer stipend plus dorm and meal expenses * Students will work in labs, interact w/ faculty mentors, post-docs and grad students * Weekly group seminars and meetings for students (e.g., career development, responsible research conduct, science communication training) * Social events for students (e.g., trips to Cincinnati Zoo, Reds baseball) * Concluding student research "mini-symposium" presentation session

Student applicants will be selected based on multiple criteria. Applications for the REU program will be screened by a committee to select individuals whose interests match with faculty in the program. Emphasis will be placed on faculty recommendations and student statements, along with academic performance and other indicators of future research success. Note: In-person implementation of the REU program is contingent on UC COVID 19 restrictions.

The application review will begin March 12, 2021, and will close March 24. Students can apply online at: <https://www.artsci.uc.edu/departments/biology/-special-programs/reu.html> We hope you will encourage your students to visit our website and consider applying.

Thank you.

Stephanie Rollmann, PhD (stephanie.rollmann@uc.edu) and John Layne, PhD (john.layne@uc.edu)

"Layne, John (laynejn)" <laynejn@UCMAIL.UC.EDU>

ESEB Equal Opportunities Initiative Fund Deadline Mar 31

** ESEB EQUAL OPPORTUNITIES INITIATIVE FUND **

The European Society for Evolutionary Biology is pleased to announce the open call for proposals for activities that increase knowledge and awareness of unequal opportunities. Such proposals can include, but are not limited to, short workshops (for instance, on unconscious bias) and/or seminars (with invited speakers) at your home organization, data collection, publication activities and similar events. It must be clear from the proposal how the activity will improve our knowledge and awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in the ESEB specifically, or Evolutionary Biology as a field in general. There are two calls per year, with the next upcoming deadline being the 31st of March 2021. More information about the Equal Opportunities (EO) Initiative is available at <https://eseb.org/prizes-funding/equal-opportunities-initiative/equal-opportunities-initiative-fund/>. *ELIGIBILITY*

- The main applicant must be ESEB member (to become a member of ESEB, please visit <https://eseb.org/society/membership/>) - Applications can be submitted by scientists at any stage of a professional career (e.g., undergraduate, Masters and PhD students, postdocs, and lecturers). - Applicants must provide proof of support of the host institution where the activity should take place, if applicable (letter from head of department) - Applicants must explain explicitly how their activity will improve our knowledge, awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in ESEB specifically, or Evolutionary Biology as a field in general. - Applicants must detail which group of people, and how many, will benefit from this activity (for instance, 50 undergraduates, 10 graduate students, 15 faculty members) - Budgets should be reasonable (usually not exceeding 1000 EUR, if more is required, please contact EO committee first), and, if applicable, detail costs per person (that benefit from this event).

HOW TO APPLY

The application should be no more than 3 pages long

(excluding CV and support letter) and include: - Name of the applicant(s), please indicate the main applicant if appropriate. - A proposal of the activity - A justification of how the activity will improve our knowledge, awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in ESEB specifically, or Evolutionary Biology as a field in general. - Which group of people will benefit (students, staff, general public), and how many - A detailed, justified budget (including cost per beneficiary) - A time schedule - A short summary to be published on the website (100-150 words) - CVs of the applicants (1-2 pages) - A letter of support of the host institution's head of the department

Please submit the application as a single PDF-file by email to Ute Moniatte (office@eseb.org; Subject: EO Fund) at the ESEB Office at the ESEB Office and take care to limit the size of attachments (total < 10 MB) in any one email.

Deadline 31 March, 2021

Successful applications must hand in a report about the activity, including details of how funds were spent, within 3 months of the event.

Dr. Ute Moniatte | ESEB Office Manager European Society for Evolutionary Biology | www.eseb.org ESEB <office@eseb.org>

Evolutionary Data Visualization Survey

Dear colleagues,

We are seeking evolutionary biologists to take a short survey (2 min) for our research on how data are interpreted in biology: <https://bit.ly/3t8EEem8> After completing the survey, participants will have the option to enter a draw for a \$40 gift card.

Many thanks for your consideration. If you have any questions, please feel free to contact us:

Roslyn Dakin and Ashley Irwin Department of Biology Carleton University roslyn.dakin@carleton.ca

Roslyn Dakin <roslyn.dakin@gmail.com>

ISEMPH- EvMedMembershipDiscount UntilMar31

The International Society for Evolution, Medicine, and Public Health is offering a 20% discount on memberships and renewals until March 31, 2021. Use code “COVIDYEAR” at checkout. Full information at <https://isemph.org/membership> Scientists, scholars, clinicians and students with an interest in evolutionary medicine are all invited to join ISEMPH. The 2021 annual meeting will be all online; registration and abstract submission are open now. <https://isemph.org/ISEMPH-2021>

The mission of the International Society for Evolution, Medicine, and Public Health is to foster communication among scientists, students, clinicians and public health professionals who want to use evolutionary insights to improve medical research and practice, and to use studies of human health and disease to advance evolutionary biology. To accomplish this mission ISEMPH sponsors annual meetings, the journal *Evolution, Medicine, & Public Health*, *The Evolution and Medicine Review*, and *EvMedEd*. Join ISEMPH to help us discover new ways that evolutionary biology can improve human health. Special discounts on membership and renewal until March 30, 2021

BENEFITS INCLUDE: Reduced meeting fees Early notice about events, funding opportunities and the ISEMPH Newsletter A 50% discount on publication fees (save \$1000) for articles in the Society’s journal, *Evolution, Medicine & Public Health* A 25% discount on all Oxford University Press academic books (use your email or ISEMPH member number) Notification of new publications in *Evolution, Medicine, & Public Health* (1 click unsubscribe) Advanced search and download functions for all 1500+ resources on *EvMedEd* Nomination and voting rights in Society elections Your information listed online to facilitate connections with other members (you can specify what is displayed) Access to more information about other members of ISEMPH Opportunities to collaborate with other members to help develop the field of evolutionary medicine

rmnesse@gmail.com

JMolEvol ClassicPapers

50 years ago, Emile Zuckerkandl founded the *Journal of Molecular Evolution* as a new journal dedicated to the field of molecular evolution. To celebrate this, members of our editorial board were given the opportunity to pick a classic paper from the journal and write a perspectives piece describing the paper, the research it subsequently spawned, and future directions in the field. Ten such pieces were contributed by members of our editorial board and are available at: <https://www.springer.com/journal/239/updates/18894136> together with a link to the original paper referenced. We hope you will enjoy these perspectives on the field.

David Liberles

David A Liberles <tuf77157@temple.edu>

MolEcolPrize2021 Nominations

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, and Victoria Sork.

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 Scott Edwards (sedwards@fas.harvard.edu) by Friday, April 16, 2021. 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

"Edwards, Scott V." <sedwards@fas.harvard.edu>

MustRead papers

Dear colleagues,

We are two PhD students (evolutionary theory & behavioural ecology, University of Groningen, Netherlands) who are planning to start a new literature club. We would like to cover a wide range research themes, in order to attract a diverse audience and broaden our knowledge. The title of the literature club will be "Current Themes in Ecology and Evolution". We heard that there are lists of "must-read" papers in evolutionary biology available online 'V these would form an ideal basis for our purpose!

We were therefore wondering if you could recommend any such online resources? Thank you very much!

If you have suggestions, we would greatly appreciate it if you could send them to j.m.riederer@rug.nl or to x.long@rug.nl. We will share any answers that we receive on evoldir.

All the best, Jana Riederer and Xiaoyan Long

"Riederer, J.M." <j.m.riederer@rug.nl>

OmennPrize BestEvolMedArticle DeadlineApr30

The \$5000 Gilbert S. Omenn Prize is awarded by the International Society for Evolution, Medicine, and Public Health for best article published in the previous calendar year on a topic related to evolution in the context

of medicine and public health. Nominations for articles published in 2020, including self-nominations, are welcome until April 30, 2021. Caleb Finch will chair the prize jury.

Full information here: <https://isemph.org/Omenn-Prize> Link for submission here: <https://airtable.com/-shrFQfv2sKrCUevpA> The International Society for Evolution, Medicine & Public Health invites nominations for the Omenn Prize of \$5000 for the best article published in the previous calendar year in any scientific journal on a topic related to evolution in the context of medicine and public health.

The prize, provided by the generosity of Gilbert S. Omenn, will be awarded to the first author of the winning article. The Committee, chaired this year by Caleb Finch, may elect to recognize more than one article. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome. Directions for Nominations Please submit your nomination using this brief form. The form requests a reference for the nominated article, along with a brief statement in support of your nomination.

Peer-reviewed articles with a publication date of 2020 that use evolutionary principles to advance understanding of a disease or disease process are eligible. The prize committee will give priority to articles with implications for human health, but many basic science or theoretical articles have such implications.

The prize is made possible by a generous donation by Gilbert Omenn, M.D., PhD. Director of the Center for Computational Medicine and Bioinformatics at the University of Michigan where he is a Professor of Internal Medicine, Human Genetics, and Public Health. Dr. Omenn served as Executive Vice President for Medical Affairs as Chief Executive Officer of the University of Michigan Health System from 1997-2002. He is a past president of the American Association for the Advancement of Science and a member of the Institute of Medicine of the National Academy of Sciences.

rmnesse@gmail.com

OnlineEcologyConferences listing

New mailing list for academics looking to keep up to date with upcoming online ecology conferences and seminars.

If you are an academic and want to keep up with all the societal conferences and seminars that have gone online

then sign up at www.ecologyconferences.com Jonathan Clegg <clegg.jonathan@rocketmail.com>

Rocky Mountain Biological Lab REU Plant Evolutionary Ecology

Dear colleagues,

The Anderson lab at the University of Georgia is searching for an enthusiastic undergraduate with a strong interest in evolutionary ecology for field research in an NSF REU position (National Science Foundation, Research Experience for Undergraduates) from June-August 2021. We study the ecological and evolutionary consequences of climate change for natural plant populations. We focus on research on Drummond's rockcress (*Boechera stricta* in the plant family Brassicaceae), a mustard plant native to the Rocky Mountains. Our studies take place around the Rocky Mountain Biological Lab (<http://www.rmbll.org/>), which is located in Gothic, Colorado near the wildflower capital of Colorado (Crested Butte). We quantify plant fitness and traits to ask whether climate change could disrupt long-standing patterns of local adaptation, and to test whether phenotypic plasticity will enable populations to persist in the short-term. We perform large-scale reciprocal transplant experiments to examine patterns of adaptive evolution and natural selection in contemporary landscapes. Since fall 2013, we have planted >150,000 seeds and seedlings into five experimental gardens ranging in elevation from 2500 m to 3340 m (8202 feet to 11000 feet). Our summer research involves intensive monitoring of these experimental plants to record data on germination success, survival, growth, reproductive success, as well as life history and morphological traits. We conduct most of our work in the field, with a small proportion of indoor lab work.

Undergraduate students are eligible for this REU position. If you will graduate prior to field work, please consider applying to our field technician positions.

The successful candidate will assist with ongoing fieldwork. In addition, there are many opportunities for students to develop independent projects associated with our overall objectives, including studies on: 1) population divergence in ecologically-relevant traits, especially drought, UV tolerance, and herbivore resistance; 2) phenotypic plasticity at multiple spatial scales; 3) population density and species composition of the herbivore community that attacks Drummond's rockcress;

4) flower color polymorphism; and 5) the importance of maternal effects in biological responses to climate change.

We are offering a stipend of \$500/week for a full time REU student (40 hours/week) for 10 weeks. The exact start and end dates are flexible. We will cover room and board at the Rocky Mountain Biological Laboratory and reimburse travel expenses up to \$500. Fieldwork will involve hiking to experimental gardens through rough terrain (1-3 miles one-way daily).

The University of Georgia is committed to maintaining a fair and respectful environment for living, work, and study. We celebrate diversity in human identity, experience, and perspective. Collectively, we excel when we learn from each other and when we remain open to new points of view. We seek to cultivate an inclusive lab culture, open to people of all racial, socioeconomic, religious, cultural backgrounds, family structure, gender identities, and sexual orientations, and to people with disabilities. To this purpose, we encourage applications from individuals excited to study evolutionary ecology in nature. Members of the Anderson field team are expected to be masked and maintain social distancing in public locations as detailed in RMBL and Gunnison county public health guidelines (covid19.gunnisoncounty.org). Vaccinations against COVID-19 are strongly encouraged but not required.

The application consists of a cover letter listing your qualifications, a CV/ or résumé and contact information for two references, all of which can be emailed to Dr. Jill Anderson at: jta24@uga.edu.

Applications are due by March 25th, 2021

Feel free to contact Dr. Anderson if you have any questions about the position. Additional information about our work can be found at: <https://research.franklin.uga.edu/Anderson/> Jill T Anderson <jta24@uga.edu>

Rohlf Medal Call Nominations

CALL FOR NOMINATIONS: 2021 Rohlf Medal The Rohlf Medal was established in 2006 by the family and friends of F. James Rohlf to mark his 70th birthday. He has been a longtime Stony Brook University faculty member and is currently Emeritus Distinguished Professor in the Department of Ecology and Evolution, and

Research Professor in the Department of Anthropology. Recipients of the Rohlf Medal will be recognized for excellence in their sustained body of work on the development of new morphometric methods or for their applications in the biomedical sciences, including evolutionary biology, population biology, physical anthropology, and medicine. The term “morphometrics” is intended to include high-dimensional pattern analyses of biological shape, especially those that analyse shape in a comprehensive way, or of covariation of shape with other variables. The award can recognize a body of work that has significantly advanced the field, including: mathematical or statistical theory underlying morphometric methods, software that implements or visualizes new methods, or a body of biological findings that rely crucially on contemporary morphometric methods and represent major advances.

Candidates for the Rohlf Medal may be self-nominated or nominated by others. They must possess a Ph.D. degree or the equivalent.

The winning candidate must agree to attend the award ceremony in person in order to accept the Rohlf Medal and then deliver the award lecture. Note: the event may have to be virtual this year due to COVID-19. A decision will be announced later.

Nomination packages should include, 1. 1: a description of the body of work (not to exceed two pages) on which the candidacy is based, 2. 2: reprints of no more than three relevant papers and/or software products, 3. 3: a curriculum vitae, and 4. 4: the names and addresses of three referees.

Nominating packages should be uploaded to the Rohlf Medal application < <http://sbmorphometrics.org/RohlfMedal/nominations/apply.html> > website and received by 5 pm, EST, 15 July 2021 to be assured of full consideration. Note that upon request nominations from 2019 can be retained for the 2021 selection (though updates of some of the information will likely be needed).

The successful candidate will receive the Rohlf Medal and a cash prize at Stony Brook University, planned for on or about October 24th, 2021. She or he will deliver a lecture that is appropriate for a broad audience, ranging from the exact sciences to the humanities, concerning the morphometric methodology, software, or findings for which the Rohlf Medal was awarded.

If you have questions about this nomination or need information, please contact Dean Adams <dcadams@iastate.edu> (Chair).

Dean (on behalf of the Rohlf Medal committee)

Dr. Dean C. Adams Director of Graduate Education,

EEB Program Professor Department of Ecology, Evolution, and Organismal Biology Iowa State University <https://www.eeob.iastate.edu/faculty/adams/> phone: 515-294-3834

“Adams, Dean [EEOB]” <dcadams@iastate.edu>

RoyalSocietyPublishing

Royal Society Publishing has recently published a special issue of Philosophical Transactions B entitled Ageing and sociality: why, when and how does sociality change ageing patterns? compiled and edited by Judith Korb and Jürgen Heinze and the articles can be accessed directly www.bit.ly/PTB1823 < <http://www.bit.ly/PTB1823> >

A print version is also available at the special price of £35.00 per issue from Debbie.vaughan@royalsociety.org

Felicity Davie Felicity.Davie@royalsociety.org

RoyalSociety Publishing 3

The following Royal Society Phil Trans B key issues are published and completely FREE to access:

The role of plasticity in phenotypic adaptation to rapid environmental change, compiled and edited by Jennifer M Donelson, Juan D Gaitán-Espitia, Rebecca J Fox, Celia Schunter and Timothy Ravasi -<https://royalsocietypublishing.org/toc/rstb/2019/374/1768> Developing differences: early-life effects and evolutionary medicine, compiled and edited by Bram Kuijper, Mark A Hanson, Emma I K Vitikainen, Harry H Marshall, Susan E Ozanne and Michael A Cant -<https://royalsocietypublishing.org/toc/rstb/2019/374/1770>

The evolution of complete metamorphosis, compiled and edited by Paul R Johnston, Stuart E Reynolds and Jens Rolff -<https://royalsocietypublishing.org/toc/rstb/2019/374/1783> Felicity Davie Royal Society Publishing

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Lawrence, KS | 66044 US

SMBE Nominations President-Elect And 2 Councillors

Nominations for President-elect and 2 Councillors - due by Friday, April 09, 2021 -

Dear SMBE Members,

I am writing to solicit nominations for SMBE President-Elect and 2 Councillors whose terms will begin on January 1, 2022. All of these positions are for a duration of three years.

As the society grows and thrives, council members play very important roles in guiding its development and in soliciting and implementing programs that support our members, while enriching opportunities for young scientists from around the world, and overseeing our two excellent journals (MBE and GBE) as well as our annual meeting and satellite meetings.

Nominations will be reviewed by the nomination committee* who will then put forward a slate of two candidates for each position for membership vote. Past and current council members are listed on <https://www.smbe.org/-smbe/ABOUT/Council.aspx>. Please send nominations with a brief statement in support of your suggestion (self nominations are accepted)

Juliette de Meaux jdemeaux@uni-koeln.de and Nadia Singh secretary.smbe@gmail.com.

*Nota bene: we ask the nominators to confirm explicitly that the person they are nominating has already confirmed their willingness to run for office.

Please send your nominations by Friday, April 09, 2021.

We look forward to hearing from you!

Sincerely yours, Nadia Singh Secretary of SMBE, on behalf of the Nomination Committee*

*The Nomination Committee is composed as follows:

Juliette de Meaux (Chair), University of Cologne Laurent Duret, Universite Lyon, France Ya-Long Guo, Beijing University, China Kelley Harris University of Washington, USA Martin Lysak, Masaryk University, Brno, Czech Republic Amanda Larracuente, University of Rochester, USA Tanja Slotte, Stockholm University, Sweden Nadia Singh (ex officio), University of Oregon, Eugene, USA

Spanish Pyrenees Fieldwork Volunteers Snapdragons

Fieldwork volunteers wanted: Help us study plant evolution in the Spanish Pyrenees!

Nick Barton's group at the Institute of Science and Technology (IST) Austria <https://ist.ac.at/en/research/-barton-group/> is looking for volunteers to assist with field work on plant speciation in the Pyrenees (Spain) this coming summer (late May - early August). This is a great opportunity for anybody looking to obtain experience in field work relating to evolutionary biology, speciation, plant ecology and plant-animal interactions.

The project: We study evolutionary dynamics and speciation in snapdragons. The study which has been running since 2011 involves field work on natural hybrid zones between two subspecies with different coloured flowers. The goal is to understand how different evolutionary forces like natural selection have shaped this diversity.

The fieldwork: We are seeking volunteers to assist with the field work, which involves working in teams to map the location of individual plants (GPS), tag and sample them for leaves and flowers, measuring traits, and processing material for later DNA extraction. There may also be opportunities to be involved in other projects focusing on pollinator behaviour and plant-insect interactions. Most of the work is outdoors, but we do spend some time indoors processing samples. The work is highly team orientated, typically in groups of 2-3 in the field and larger groups processing samples back at the research station.

The location: is near Ripoll in a beautiful part of the Pyrenees of North Eastern Spain (Catalonia). We stay in comfortable apartments overlooking a picturesque valley, with close access to hiking trails and small villages.

The ideal applicant: is an enthusiastic, hardworking biology student with strong interest in working outdoors. You must be meticulous with recording data and also be comfortable working as part of a team. Experience with field-based projects and plants is helpful but not essential. Climbing experience is useful as some work is conducted on ropes. We are looking for volunteers between the 29th May and the 1st of August. The length of stay is flexible but we ask people to commit to a minimum 3 week stay. Applicants must be located in the Europe or the UK.

What we cover: All food, lodgings and any travel within Europe/UK are covered.

How to apply? By the closing date of April 10th, please send (i) your CV, (ii) a short explanation about why you are interested, and (iii) your availability between the above dates to fieldvolunteer2021@gmail.com

Please send any questions to the same address.

*A note about Covid19 Although we are planning the field season optimistically, the Covid19 pandemic may force use to change/cancel our plans at very short notice. We will give as much notice as possible regarding any changes. Assuming the field season proceeds normally, all and volunteers will be required to present a negative Covid test prior to their arrival in the field.

Sean STANKOWSKI <sean.stankowski@ist.ac.at>

UOklahoma REU MateChoice

REU position available

The Schlupp lab at the University of Oklahoma in Norman has an NSF funded 8-week REU position available for this summer. You would investigate mating preferences of two species of livebearing fishes and their F1 hybrids. This project is part of a bigger project trying to retrace the origin of the Amazon molly, *Poecilia formosa*. You will be part of an international and diverse research team.

The position comes with an \$1800 stipend per month, a travel allowance and optional free housing on campus. The best start date would be June 1st, but this can be negotiated.

To apply send a statement of interest, your CV, and contact information for one reference in a single pdf to schlupp@ou.edu. In your statement, tell us please why you are interested in the position and if you ???

for example - already have experience working with fishes. Experience is not required, but helpful. Review of applications will start on April 4th.

You must be an undergraduate student and a citizen or permanent residents of the United States of America and its possessions. For questions, please e-mail Ingo Schlupp (schlupp@ou.edu)

For more information about the Department of Biology look here: <https://www.ou.edu/cas/biology> For more information about the Schlupp lab go here: <https://www.ou.edu/cas/biology/people/faculty/ingo-schlupp> Dr. Ingo Schlupp Presidential Professor of Biology Department of Biology, University of Oklahoma

Upcoming book on Male Mate Choice: <https://global.oup.com/academic/product/male-choice-female-competition-and-female-ornaments-in-sexual-selection-9780198818946?cc=de&lang=en&#> "Schlupp, Ingo B." <schlupp@ou.edu>

WebinarSeries PopulationGeneticsVienna

The Vienna Graduate School of Population Genetics runs an internationally recognized seminar series featuring weekly talks by leading experts in population genetics. The Covid-19 crisis forced us to go online, so we invite interested listeners to join our Tuesday webinars (17:00 CET/CEST).

If you would like to listen to a talk, sign up here: <https://forms.gle/nKqGmmTe4yVUUBot6> We will send you a Webex link and reminders for the webinars.

Summer term webinar program:

02.03.21 - Michael Rose (Univ. of California, Irvine, US) Machine learning for the omics of experimental evolution.

09.03.21 - JJ Emerson (Univ. of California, Irvine, US) Genome structure and variation: Hidden, heterogeneous, and functional.

16.03.21 - Jeffrey Ross-Ibarra (Univ. of California, Davis, US) The two teosintes that made maize.

23.03.21 - Brandon Gaut (Univ. of California, Irvine, US) The evolutionary genomics of Vitis: Domestication, sex and introgression.

06.04.21 - Daniel Ortiz-Barrientos (Univ. of Queensland, AU) tba.

13.04.21 - Michael Purugganan (New York Univ., US)
The geographic spread of domesticated crops.

20.04.21 - Franjo Weissing (Univ. of Groningen, NL)
A mechanistic perspective on the evolution of adaptive plasticity.

27.04.21 - Tiffany Taylor (Univ. of Bath, UK) Revealing the silent drivers of extreme parallel evolution.

04.05.21 - David Begun (Univ. of California, Davis, US)
Evolutionary genetics of male reproductive tissue transcriptomes in *Drosophila*.

11.05.21 - Katie Lotterhos (Northeastern Univ., US)
tba.

25.05.21 - Göran Arnqvist (Uppsala Univ., SE) Repeatability of adaptive life history evolution in seed beetles.

01.06.21 - Isabel Gordo (Inst. Gulbenkian de Ciencia, PT) tba.

08.06.21 - Conrad Burden (Australian National Univ., AU)
The diffusion limit of Wright-Fisher and branching models.

15.06.21 - David Reich (Harvard Univ., US) Ancient DNA and the new science of the human past.

22.06.21 - Sarah Signor (North Dakota State Univ., US)
The evolution of piRNA defense against genomic parasites in *Drosophila simulans*.

29.06.21 - Jeremy Berg (Univ. of Chicago, US) Population structure and polygenic scores: is stratification a solved problem yet?

All information about schedule updates, times and re-viewing recorded talks: <https://www.popgen-vienna.at/news/seminars/> Kind regards, Julia on behalf of PopGen Vienna

– Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator

www.popgen-vienna.at <https://twitter.com/PopGenViennaPhD> c/o Institut für Populationsgenetik Veterinärmedizinische Universität Wien (Vetmeduni Vienna) Veterinärplatz 1, 1210 Wien

Current home office contact via Skype: julia.hosp Office:

+43 1 25077 4338 (currently unavailable)

<http://www.vetmeduni.ac.at/en/population-genetics/>
<https://twitter.com/PopGenVienna> Julia Hosp
<Julia.Hosp@vetmeduni.ac.at>

YouTube aDNA network

Dear colleagues,

The ADAPT network (www.aDNA.network) is now running an online seminar series accessible through YouTube https://www.youtube.com/channel/UCry3eutQ_-eP4ThL5jPK-gw/featured In the first seminar, Dr Patrícia Chrzanová Peřnerová presents findings of the study 'Million-year-old DNA sheds light on the genomic history of mammoths' recently published in Nature.

With a focus on the most recently published evolutionary biology studies harnessing ancient DNA, presented mainly by ECRs, we hope to find a niche among the existing excellent online evolutionary biology seminar series.

The A.D.A.P.T. (Ancient DNA studies of Adaptive Processes through Time) network is a Special Topic Network funded by the €European Society for Evolutionary Biology. This seminar series marks the first of several online network activities we have planned for 2021.

Subscribe to the channel to receive alerts of newly poster seminars.

Andy Foote on behalf of the ADAPT network

YouTuber and Associate Professor

Institute of Natural History

NTNU Science Museum

Andrew Foote <andrew.foote@ntnu.no> Andrew Foote
<andrew.foote@ntnu.no>

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AMNH New York Vertebrate Evolution

Postdoctoral Fellow, Vertebrate Zoology, American Museum of Natural History, New York, USA

The American Museum of Natural History is recruiting an exceptional postdoc to be part of a highly innovative project to optimize techniques in isolating historical DNA (hDNA), modeling DNA degradation, and analyzing DNA from specimens in the herpetology and ornithology collections at the (AMNH). This project is funded by a National Science Foundation award to Christopher Raxworthy and Brian T. Smith in the Division of Vertebrate Zoology, AMNH.

This NSF-funded project aims to develop efficient and

open-source protocols for yielding genome-scale molecular data from typical traditional museum specimens, based on rigorous experiments using time-series collections at the AMNH. Museum specimens of amphibians, reptiles, and birds will be sampled for DNA across two collecting periods of: 1) <1V30 years for field-frozen, dry and fluid preserved voucher tissues, all taken from the same specimens for which alternative DNA prep types will be directly compared; and 2) 30V150 years, for older traditional voucher specimens which lack frozen tissue samples. This combined approach will determine the optimal source and extraction methods for hDNA, develop improved methods for reverse crosslinking with formalin-fixed DNA, and provide a much deeper understanding of how DNA degrades due to exposure to formalin, alcohol, tissue buffers, and archival storage time. This project will also develop pipelines for bioinformatics processing of hDNA, to better detect contamination, evaluate the effects of hDNA on phylogenetic

inference, and improve the utility of hDNA in all aspects of comparative biology.

Responsibilities include, but are not limited to: conduct and co-design experimental tests of DNA extraction; prepare samples for molecular sequencing; analyze molecular data; model DNA degradation across sample types and time; manage project internet portal and web pages; co-mentor undergraduate and high school students; co-develop best-practices for bioinformatics processing of hDNA; and prepare results for publication as lead author. The postdoc will have opportunities to present their work at conferences, attend various professional development activities, and get to participate on an expedition to Madagascar to collect samples for the project. Currently, this is a 2.5 year term position.

Required experience

Ph.D. or equivalent in evolutionary biology, computational biology, or related fields and demonstrated record of productivity and publications. Experience with DNA extraction, next-generation sequencing, wetlab methods (ideally including 'clean room' DNA labs), computer programming (e.g., python; R), genomics, molecular evolution, and vertebrate biology.

For full details about this position please see: <https://careers.amnh.org/postings/2397> Application review will begin on March 29, 2021, with a desired start date of July 1, 2021 Please contact Christopher Raxworthy (rax@amnh.org) with any questions regarding the position.

Christopher Raxworthy <rax@amnh.org>

Antwerp Evolutionary Genomics

===== Final call =====Apply before April 2nd 2021.

The Svardal lab at the University of Antwerp, Belgium, is looking for Postdoc candidates to be part of an exciting funded project to study the rapid adaptive diversification of cichlid fishes.

In one of two available project you will either

(1) establish novel molecular and computational techniques to identify structural variants

or

(2) develop machine learning and population genomic approaches to model the evolutionary and adaptive his-

tory of these structural variants and understand their role in adaptive radiation.

But also different project depending on your interest and background can be considered. A quantitative background (computational genomics, population genetics) is a plus, but also candidates with a different background interested in these topics are encouraged to apply.

The vacancy is open until filled. Applications will be evaluated on April 2nd 2021.— Start date can be negotiated. Remote work possible.

Direct application link:

<https://www.uantwerpen.be/en/jobs/vacancies/-academic-staff/?q=1432&descr=Postdoctoral-scholarship-holder-Evolutionary-computational-genomics> Postdoc fellowships are for up to 3 years with an initial contract of 1 year.

For more information feel free to contact me: hannes.svardal@uantwerpen.be

– Hannes Svardal Research Professor in Evolutionary, Ecological and Environmental Omics Department of Biology University of Antwerp

Campus Groenenborger, room U758

Hannes.Svardal@uantwerpen.be

Arizona Comparative Genomics

Interested candidates can feel free to send any questions to marc.tollis@nau.edu

Arizona State University: Office of the Executive Vice President Knowledge Enterprise: Biodesign Institute: Biodesign BSS Location Tempe, AZ Open Date Mar 19, 2021

Deadline Apr 7, 2021 at 11:59 PM Eastern Time Description Job Description

The Arizona Cancer Evolution Center (ACE) based at the Biodesign Institute at Arizona State University (ASU) seeks applications for a Postdoctoral Research Scholar that will contribute to research in the field of cancer comparative genomics. We are particularly interested in candidates with experience in bioinformatics and a background in molecular evolution and comparative biology. This full-time, non-tenure-track, benefits-eligible, fiscal year (July 1 'V June 30) position is for one year with subsequent renewal contingent upon satisfactory performance, the needs of the university,

and availability of resources. Salary range: \$53,760 - \$56,712 per year; DOE.

Beginning in 2018, ACE is funded by the NCI Cancer Systems Biology Consortium. Our group uses interdisciplinary approaches to understand the mechanisms underlying cancer defenses in nature. The successful candidate will leverage their expertise in genomics to uncover the roles that changes in protein coding genes, gene duplications, and structural arrangements in cancer-related pathways or across the genome have had in the evolution of cancer suppression in animals, including large and long lived mammals such as elephants and whales. The candidate will also help determine the genetic basis of DNA damage response in treated animal cells.

The postdoctoral scholar will conduct research with Dr. Carlo Maley, Director of ACE, as well as Dr. Marc Tollis at Northern Arizona University and Dr. Amy Boddy at UC Santa Barbara. The successful candidate will also work closely with ACE research staff and other research collaborators and partners, particularly Dr. Lisa Abeglen and Dr. Josh Schiffman at U. Utah. The candidate will contribute to multiple projects, each with numerous publication opportunities.

Essential Duties:

Analyze genomic data across species

Establish and maintain bioinformatic workflows on supercomputers

Conduct literature reviews, data analyses, and report/manuscript preparation

Identify, coordinate, and lead the writing of manuscripts

Contribute to identifying relevant research funding opportunities.

Disseminate research outcomes in peer-reviewed publications and at professional conferences.

Coordinate among team members and lead the team's efforts for accomplishing and delivering milestones for projects

Participate in collaborations with the other faculty and partners.

Working Environment

The position will be primarily based at an office within the Biodesign Institute facility in Tempe, Arizona, and will have flexibility in working arrangements to accommodate remote work.

Qualifications: Required Qualifications:

A recent (within the past 4 years) Ph.D. in biology, genomics, bioinformatics or a related field by the time

of appointment.

Desired Qualifications:

Familiarity writing or compiling software and running analyses on large DNA and RNA-seq datasets using high performance computing clusters

Knowledge and hands-on experience with common tools in genomics such as genome assembly, variant calling, annotation, gene expression and evolutionary analysis

Knowledge of UNIX/Linux environments, common programming languages, R

Demonstrated record of scientific publications

Demonstrated verbal and written communication skills (in English).

Application Instructions: Applicants are responsible for including a cover letter, CV, and the names of three professional references in their application through the Interfolio website. Emailed applications will not be accepted.

Application deadline is April 7, 2021. Applications will continue to be accepted on a rolling basis for a reserve pool. Applications in the reserve pool may then be reviewed in the order in which they were received until the position is filled.

For the sixth year in a row, ASU has been named the most innovative school in the nation, recognizing the university's culture of groundbreaking research and partnerships, as well as its commitment to helping students thrive in college and beyond. U.S. News and World Report has named ASU as the most innovative university all five years the category has existed.

ASU Knowledge Enterprise advances research, innovation, strategic partnerships, entrepreneurship, and international development. Our success arises from solutions-focused, interdisciplinary research; an entrepreneurial approach that is embedded in every school and department; and a commitment to transform society in a positive way. <http://research.asu.edu/> Interested candidates can feel free to send any questions to marc.tollis@asu.edu

Marc Tollis, Ph.D. Assistant Professor

— / —

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>

Barcelona Biomedical Informatics

Gabriel Santpere Lab. Neurogenomics group. Research Programme on Biomedical Informatics (GRIB), Hospital del Mar Medical Research Institute (IMIM), DCEXS, Universitat Pompeu Fabra, Barcelona, Spain

Project and Tasks: Genome-wide taxonomy of transcription factors and binding sites across primates for the study of human brain specializations in health and disease.

The candidate will conduct functional genomics analysis to study the evolution of human brain development and the genetic risk of neuropsychiatric disorders leveraging multiple sources of omics data at the bulk and single-cell level.

Project and Institution that finance the contract :

The work is supported with AGENCIA ESTATAL DE INVESTIGACIONES Científicas Funds, by grant (2019/8909/I) "Taxonomía de la unión de factores de transcripción en el genoma completo de primates para el estudio de especializaciones del cerebro humano en salud y en enfermedad".

Official number reference: Fundación IMIM (G.SANTPERE/PID/AEI-19)

Skills and Experience: 1) To have a PhD in the fields of biology or bioinformatics. 2) A background in neuroscience and/or comparative genomics will help in the application. 3) Experience in programming, statistics, single-cell, transcriptomics, epigenomics and molecular evolution. 4) High english level (written/spoken)

Benefits of the opening: We offer a one year contract (extendable), 40hrs week, yearly gross salary around 31.000 EUR. Envisaged starting date, April 2021. Information on the application process: Submit the requested information at the IMIM website page (*)

* https://www.imim.es/ofertes-treball/-view_contracte.php?id=1713 Gabriel Santpere Baró <gabrielsantperebaro@gmail.com>

Bolzano Italy Barkbeetle Mycobiome

A Postdoctoral position is being offered at the Free University of Bozen-Bolzano (Italy) in the lab of Hannes Schuler. The project is funded for one year renewable for six months and aims to study the microbial and fungal community of the European spruce bark beetle *Ips typographus*.

The European spruce bark beetle *Ips typographus* is one of the most important forest pests in Europe. In addition to factors such as a high fecundity and the establishment of several generations per year, symbiotic associations with fungi and bacteria are responsible for its potential to cause forest mortality. The focus of this project is to study the associations of Central European bark beetle populations with symbiotic bacteria and fungi to obtain a more holistic understanding of the biology, ecology and harmful potential of this important pest species. The project is in collaboration with Martin Schebeck and Christian Stauffer (Boku, Vienna) and Massimo Faccoli and Andrea Battisti (University of Padova).

We are looking for an enthusiastic candidate with a strong background in molecular biology and experience with bioinformatic analyses of bacterial and/or fungal communities associated with insects. The candidate will be responsible to develop an amplicon-sequencing approach for fungi optimized for this species and perform PacBio full-length amplicon sequencing of both mycobiome and bacterial microbiome.

The Free University of Bozen-Bolzano is located in one of the most fascinating European regions, at the crossroads between the German-speaking and Italian cultures. Its trilingualism in teaching and research, its high level of internationalization as well as an ideal research environment guaranteed by its excellent facilities are some of the reasons why unibz regularly reaches top positions in national and international rankings. Our lab is part of the newly funded competence Centre for Plant Health within the Department of Science and Technology <https://www.unibz.it/en/-/home/research/competence-centre-plant-health>. We are a young and dynamic research group studying various aspects of insect-microbe interactions in a collaborative atmosphere <http://hschuler.people.unibz.it> General requirements for the position: A PhD degree in Biology or Evolution or related fields. The candidate should have

excellent communication skills and should be fluent in English.

The project is expected to start in May 2021, but the starting date is negotiable.

Application deadline is 01.04.2021

All documents for the application procedure can be found at: <https://www.unibz.it/en/home/position-calls/positions-for-academic-staff/5121-entomologia-generale-e-applicata-dr-schuler?group=> For informal inquiries, and for questions about the hiring process, please contact Hannes Schuler hannes.schuler@unibz.it.

Dr. Hannes Schuler Competence Centre for Plant Health Faculty of Science and Technology Free University of Bozen-Bolzano Universitätsplatz 5 I-39100 Bozen Tel: +39 0471 017648 <http://hschuler.people.unibz.it> Hannes.Schuler@unibz.it

CarnegieStanford PopulationGenetics

Postdoc Position: Population Genetics in Plant Evolve & Resequencing Experiments

Summary Moi Exposito-Alonso Lab - www.moisesexpositoalonso.org Carnegie Institution for Science & Stanford University, 260 Panama st., California 94305, USA Annual salary \$64,268 2 years with potential extensions up to 5 years Earliest starting date: immediately available, flexible Closing date: accepting applications until filled

Description We aim to recruit highly motivated and creative people with strong training in statistical population genetics. Our group seeks to understand how and whether populations genetically adapt rapidly to different climates. The project involves using and developing population genetics theory and conducting analyses with whole-genome sequence data from evolution experiments with *Arabidopsis thaliana*. These experiments are being conducted in ~50 locations around the world and populations are re-sequenced for 3+ consecutive years (GrENE-net.org). With this data some questions we aim to address are: How strong, polygenic, and repeatable is natural selection in realistic environments? Can we predict it? How does selection vary across dense climate gradients? Did evolutionary rescue occur? Can we detect statistical signals preceding extinction or adaptation of experimental populations? The position requires leading research independently

using large genomic and experimental datasets, participating in collaborative projects, preparing publications, and presenting research in scientific meetings.

Equal opportunity employer Carnegie is an equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, religion, color, national origin, sex, sexual orientation, gender identity, age, veteran status, disability or any other protected status in accordance with applicable laws. We aim to have a vibrantly diverse lab, which is essential to tackle scientific questions from different creative angles. The main requirement for these positions is that you are passionate about the topics above, so please apply!

Requirements Required qualifications for these positions are a doctoral degree in any of the following areas: molecular biology, population genetics, evolutionary biology, ecology, bioinformatics, computer sciences, or statistics; a track record of research productivity and independence, and a willingness to work closely with collaborators and lab members. Position details This is a full-time position with a competitive annual salary of \$64,638 and benefits. The lab is located in the Carnegie Institution for Science's Department of Plant Biology on the Stanford University campus. Carnegie Postdocs have access to Stanford facilities. Stanford campus is a vibrant community embedded in the San Francisco Bay area, with opportunities for extensive social and scientific interactions. The initial position will be for one year with potential renewal of up to five years depending upon performance.

Additional information The Department of Plant Biology of the Carnegie Institution for Science (formerly known as the Carnegie Institution of Washington) is a private endowment U.S.-based non-profit, located on the campus of Stanford University since 1928. Andrew Carnegie founded the Carnegie Institution of Washington in 1902 as an organization for scientific discovery to serve as a home to exceptional individuals - men and women - with imagination and extraordinary dedication capable of working at the cutting edge of their fields. Today, Carnegie scientists work in six scientific departments on the west and east coasts and at the Las Campanas Observatory in Chile. Carnegie investigators have made key discoveries in plant biology, including early experiments of local adaptation (Clausen, Keck, Hiesey), the discovery of transposable elements (McClintock), plant ecophysiology at global scales (Berry, Field), the discovery of key photosynthesis and phototropism genes (Grossman, Briggs), or The *Arabidopsis* Information Resource TAIR (Rhee, Somerville). The Department of Plant Biology (<https://dpb.carnegiescience.edu>) and Global Ecology (<https://>

[/dgc.carnegiescience.edu](http://dgc.carnegiescience.edu)) have state-of-the-art facilities for molecular genetic studies of plants, greenhouses and field sites, and computer resources. The lab is co-affiliated with the Department of Biology at Stanford University (<https://biology.stanford.edu>) and with the center of Computational Evolutionary and Human Genetics (<http://cehg.stanford.edu>). The ideal candidate would become an active member of this community and would strengthen collaborative connections with grad students, postdocs, and faculty members across campus.

Contact

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ColoradoStateU CropAdaptationGenomics

Use evolutionary quantitative genomics to support food security of smallholder farmers!

The Morris Lab at Colorado State University is looking a postdoc with expertise in quantitative trait genomics and/or evolutionary & ecological genomics for a project on crop adaptation genetics.

The postdoc will conduct hypothesis-driven research to understand the genetic basis of adaptation of sorghum to drought and a global aphid outbreak. Sorghum is a staple food and forage crop for smallholder farmers around the world and a genomic model system for stress adaptation. The knowledge gained will be used to develop technology to accelerate adaptation of sorghum in Haiti and other developing countries.

Apply here: <https://jobs.colostate.edu/postings/84844>
Geoff Morris Associate Professor, Crop Quantitative Genomics Colorado State University, Soil & Crop Sciences Plant Sciences Building, Fort Collins CO Geoff.Morris@colostate.edu | Mobile: 312-909-1330 <http://www.morrislab.org> | <http://www.gohy.org>

“Morris,Geoffrey” <Geoff.Morris@colostate.edu>

CornellU EvolFungalBacterialSymbioses

Postdoctoral position in ecology and evolution of fungal-bacterial symbioses Cornell University, Ithaca, NY, USA

A postdoctoral position is available in the Pawlowska Lab at Cornell University to work on the NSF-funded project “Unravelling the influence of endosymbiotic bacteria on the biodiversity of Mucoromycota fungi.” The postdoctoral associate will investigate how endosymbiotic bacteria (EB) contribute to ecological community assembly and evolutionary diversification of early-divergent fungi in the phylum Mucoromycota, with a particular focus on the subphylum Glomeromycotina, arbuscular mycorrhizal fungi.

The project is an exciting collaboration between the Pawlowska lab at Cornell and partners at Oregon State University and North-West University in South Africa.

Responsibilities will include: (1) addressing project objectives of field sample collection, identification of fungi and their EB using culture-dependent and culture-independent methods, ecological analyses of fungal diversity across spatial scales, experimental manipulation of fungal communities to understand the role of EB in fungal community assembly, phylogenetic analyses of coevolution between fungal hosts and EB, as well as gene expression, proteome and metabolome profiling of fungal-bacterial symbioses, (2) mentoring undergraduate assistants working on the project, and (3) assisting with outreach activities.

Preference will be given to candidates with knowledge of fungal and bacterial biology as well as experience in working with early-divergent fungi, with a particular focus on arbuscular mycorrhizal fungi. Review of applications will start April 1, 2021.

To apply, please visit <https://academicjobsonline.org/ajo/jobs/18254> . Teresa E. Pawlowska Associate Professor School of Integrative Plant Science Plant Pathology & Plant-Microbe Biology 334 Plant Science Building 236 Tower Road Cornell University Ithaca, NY 14853-5904 Cell phone: (607) 342 3866 E-mail: tep8@cornell.edu Lab web site: www.plantpath.cornell.edu/labs/-pawlowska/index.html Office: 218 Plant Science Phone: (607) 254 8726 Lab: 219 Plant Science Microbial Friends & Foes REU: bit.ly/CIHMID-REU

“Teresa E. Pawlowska” <tep8@cornell.edu>

CRG Barcelona ModelingSequenceEvolution

Computational 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 in human genomes using computational data analysis, population genetics and statistical methods.

Read more and apply here:

<https://recruitment.crg.eu/content/jobs/-position/%E2%80%9Cpostdoctoral-researcher-group-%E2%80%9CEvolutionary-processes-modeling%E2%80%9D%E2%80%9D> Deadline: 9 April 2021.

About 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 shares principles of an interdisciplinary, motivated and creative scientific team that is supported by high-end and innovative technologies and a flexible and efficient administration.

In 2013, the CRG received the 'HR Excellence in Research' logo 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.

For further information, see <https://www.crg.eu/>.
About the group

Cancer is a genetic disease, subject to population genetics forces like mutation, selection and stochasticity. We have previously demonstrated that coding sequences of cancer tumors not only exhibit positively selected mutations that drive cancer (www.nature.com/articles/s41588-019-0572-y), but that there exist genes that the tumor cannot afford to lose to the mutational pressure (www.nature.com/articles/ng.3987). In addition to genes, we have also identified cancer driver loci in the non-coding part of the genome (www.nature.com/articles/s41467-017-00100-x), which is another ongoing research effort in the group.

Our group is particularly interested in how the evolution and survival of cancer cell populations relies on mutation influx as well as in the selection inference from allele frequency information. To this end, we develop mathematical and computational approaches to estimate mutation rates and selection from the data. 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 have also studied mutation and selection in the framework of human polymorphisms (www.nature.com/articles/ng.3831 and academic.oup.com/mbe/article-abstract/36/8/1701/5475505) and de novo variants (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-groups/weghornlab. Your profile

- You hold a PhD degree in population genetics, statistics, bioinformatics, or a related discipline.
- You have worked with DNA sequencing or other biological datasets and have substantial programming experience.
- You are familiar with the principles of population genetics, modeling and statistical analysis.

The ideal candidate should be highly motivated and eager to work on evolutionary and biological problems through the use and development of computational and theoretical approaches.

The offer

Contract duration: 1 year (with possibility of extension).
Estimated annual gross salary: Salary is commensurate with qualifications and consistent with our pay scales.
Target start date: As soon as possible.

We provide a highly stimulating environment with state-of-the-art infrastructure and unique professional career development opportunities. We offer and promote a diverse and inclusive environment and welcome applicants regardless of age, disability, gender, nationality, race, religion or sexual orientation. The CRG is committed to reconcile a work and family life of its employees and offers extended vacation

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

DalhousieU ModellingDisease

Location: Department of Mathematics and Statistics, Dalhousie University, Halifax, NS, Canada

Duration: 1 year (renewable depending on availability of funding and satisfactory performance)

Deadline: Until filled

Start date: Immediately (negotiable)

We are seeking a postdoctoral fellow who will work with Drs. Lam Ho and Edward Susko to develop statistical methods for stochastic models of infectious disease epidemics. The project will primarily focus on stochastic compartmental models and their applications in phylogenetics. It is part of a larger collaborative effort involving a network of biostatisticians across Canada as part of the new NSERC Emerging Infectious Diseases Modelling Initiative. A fundamental challenge for stochastic compartmental models is that the likelihood function is intractable. Our goal is to develop efficient methods for making inferences under these models.

Requirements:

- PhD in statistics or related fields.
- Good communication skills in English.
- Strong background in stochastic models and statistical inference.
- Expertise in R and C/C++ is highly desirable.

We offer:

- Salary: 50,000 CAD/year and benefits.
- No teaching duties are involved.

Application: Send your CV and 2 reference contacts to Drs. Lam Ho (Lam.Ho@dal.ca) and Edward Susko (Edward.Susko@dal.ca).

Lam Ho | Assistant Professor FACULTY OF SCIENCE
Department of Mathematics and Statistics 902.494.1069

Dalhousie University dal.ca

Lam Ho <Lam.Ho@dal.ca>

Finland PDF PhD FungalEvolution

The Department of Biological and Environmental Science at University of Jyväskylä, Finland, is currently seeking to recruit candidates to the positions of

TWO POSTDOCTORAL RESEARCHERS and/or DOCTORAL RESEARCHERS in COMMUNITY ECOLOGY and/or FUNGAL ECOLOGY

The positions starts on 1st May 2021 or as soon as possible thereafter, for a fixed term of three years for the post doc and for four years for the Doctoral Researcher.

Qualifications we are looking for

We are seeking a highly motivated researcher with background in empirical community ecology, in theoretical community ecology, or in fungal ecology. The successful candidate will join Professor Otso Ovaskainen's and Senior Researcher Nerea Abrego's research team at the Department of Biological and Environmental Science, University of Jyväskylä. Professor Ovaskainen leads the ERC-synergy project LIFEPLAN 2020-2026 ("Planetary Inventory of Life") that combines a global biodiversity sampling campaign (based on DNA-, audio- and image-based methods) with the development of novel bioinformatics and statistical methods for big ecological data. LIFEPLAN is implemented in close collaboration with professor Tomas Roslin (Uppsala, Sweden; biodiversity research) and professor David Dunson (Duke, USA; statistics and machine learning). Senior Researcher Nerea Abrego uses fungal communities as a model system to integrate theoretical and empirical research in community ecology. The successful candidate will become integrated in this international consortium with world leading expertise in biodiversity research, community ecology, statistical ecology and bioinformatics.

You are the person we are looking for if you have a Doctoral/Master's degree, or be about to obtain a Doctoral/Master's degree, in ecology or a related field.

While the exact application field can be selected based on the expertise and interests of the applicant, we are particularly interested in combining experimental, observational and theoretical research to yield an increasingly mechanistic understanding of community ecology. We are interested in research on all taxonomical groups, yet applicants with a background in fungal ecology are especially encouraged to apply. Knowledge about molecular methods and especially species identification through

DNA barcoding is counted as a plus.

More info and apply here by April 15 2021: https://rekry.saima.fi/certiahome/-open_job_view.html?did=5600&jc=12&id=-000010907&lang=fi&utm_source=dlvr.it&utm_
“Hardwick, Bess V P” <bess.hardwick@helsinki.fi>

Harvard MalariaGenomics

The Neafsey Lab at the Harvard T.H. Chan School of Public Health (HSPH) is seeking an early stage or senior Postdoctoral Fellow to contribute to our research program in the evolutionary genomics of malaria (<https://sites.sph.harvard.edu/neafsey-lab/>). Our lab generates and analyzes large genomic datasets from malaria parasites and vector mosquitoes to understand transmission patterns, demographic history, drug resistance, immune evasion, and host/vector/pathogen interactions. In our wet lab, we generate new genetic assays for parasites and vectors, such as multiplexed Illumina amplicon sequencing panels, and we apply assays to cross sectional as well as longitudinal sample collections, driving a need for innovative approaches to data analysis. The successful candidate will work collaboratively with other group members to develop innovative bioinformatic approaches for exploring malaria parasite and Anopheles mosquito genomic datasets. We have experimental capacity at HSPH, where we are part of a close-knit community of molecular parasitologists and vector biologists. Our lab also extends to the Broad Institute, where we belong to the Broad Institute Genomic Center for Infectious Disease and benefit from a community of expert microbial genomicists and computational biologists.

Ideal applicants will have a PhD in a relevant field, with strong background in population genetics and/or molecular epidemiology. Applicants will be expected to develop a research program that is original but fits within the general priorities of the group and funded grants, taking into account the relevant literature, own experience, and advice from other scientists.

Basic Qualifications: Candidates are required to have a Ph.D. in biology/computational biology/epidemiology or equivalent. Experience in at least one scripting language and familiarity with Unix/Linux computing environments are required.

Additional Qualifications: Experience with next generation sequencing data analysis and statistical fluency are strongly desired. Candidates should demonstrate a

track record of consistent publication, have strong organizational, written, and oral communication skills, and should be able to work both independently and as part of a team. Spanish language proficiency is a plus, as we have several active collaborations in Latin America. Molecular biology laboratory skills are welcomed but not essential.

Contact Email: Please contact Daniel Neafsey by email: neafsey@hsph.harvard.edu with CV, letter of interest, and names of at least three references.

Equal Opportunity Employer:

We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability status, protected veteran status, or any other characteristic protected by law.

Daniel Neafsey <neafsey@broadinstitute.org>

HaverfordCollege MachineLearningGenomics

Post-baccalaureate or Post-doctoral research position at Haverford College Machine Learning and Genomics

The Mathieson Lab (<https://smathieson.sites.haverford.edu/>) at Haverford College is hiring a Research Associate at the post-baccalaureate or postdoc level, to work on projects related to machine learning and genomics. Please feel free to reach out to Sara Mathieson (smathieson@haverford.edu) with any questions. The deadline is listed as March 19 but it is flexible.

<https://www.haverford.edu/human-resources/news/postdocpostbac-research-associate> “smathieson@haverford.edu” <smathieson@haverford.edu>

ImperialC London 3 ComputationalEvolution

I am advertising three Postdoctoral Research Associate positions in computational ecology. The project is to create a virtual rainforest: a general ecosystem model

replicating all physical and biotic components of the ecosystem and their interactions, with a view to understanding system-level emergent properties. We require team members who provide complementary technical skills and disciplinary knowledge, so applicants from any ecological background and with any relevant skillset are encouraged to apply.

More details and information about the application process can be found on Imperial College London's website (job reference NAT00878). <https://www.imperial.ac.uk/jobs/description/NAT00878/-research-associate-computational-ecology> Rob Ewers Professor of Ecology Imperial College London <https://www.imperial.ac.uk/people/r.ewers> "Ewers, Robert M" <r.ewers@imperial.ac.uk>

journals; Involvement in work during irregular working hours (during field work); Strong motivation for work in the project; Fluency in English, written and spoken; Valid driving license; Experience in and enthusiasm for working in an international team would be an asset.

I have funding from Norway grants under the Norwegian Financial Mechanism 2014-2021.

Principal investigator: Dr hab. inÂ¿. Szymon Â¿niegula, <http://www.iop.krakow.pl/-pracownicy,102,szymon.sniegula.html> Feel free to contact me at ecopond@iop.krakow.pl

The posting is here https://www.iop.krakow.pl/-files/317/ecopond_post.doc.en.pdf Szymon Sniegula <szymon.sniegula@gmail.com>

Krakow EvolutionStressors

Institute of Nature Conservation PAS Krakow Poland.PlasticityTranscriptomics

Postdoc position in the project 'Integrating effects of anthropogenic and natural stressors: phenotypic and genetic expression approach' at the Institute of Nature Conservation PAS, Krakow, Poland in collaboration with the Jagiellonian U. U of Lodz, Norwegian Institute for Nature Research and Norwegian Veterinary Institute.

Cities as 'heat islands' are often hot spots for alien invasive species that can drastically alter population dynamics of native species. In addition, natural stressors such as seasonal time and thermal constraints at high latitudes can strongly affect organism fitness. The aim of the project is to understand how anthropogenic and natural stressors: urbanization, native and invasive alien predators, and latitudinal gradient affect traits linked to fitness down to gene expression level in a common bluetail damselfly.

Requirements: PhD in biology, ecology or related field (PhD defense not earlier than 7 years before the year of employment in the project); Experience in field and laboratory work on aquatic/semi-aquatic invertebrates; An experience in using molecular methods to address ecological or evolutionary questions, with an appropriate publication track record; Good working knowledge of R environment, including advanced skills in statistical modelling; Working knowledge of standard bioinformatics tools in the Linux environment; Publication record including articles in leading ecological and evolutionary

Krakow JagiellonianU AdaptationGenomics

PostDoc:Krakow_JagiellonianU.Genomics_of_Adaptation

A postdoctoral position funded from the Polish National Science Centre grant Environment-dependent balancing selection in a gene involved in sexual conflict is available in Genomics and Experimental Evolution Group at Jagiellonian University, Institute of Environmental Sciences. The position is offered for two years. The position is available from late spring/summer, but the starting date is flexible. Institute of Environmental Sciences, Jagiellonian University, Krakow, Poland (www.eko.uj.edu.pl/en) is one of the strongest centres of research in evolutionary biology in Central Europe. Krakow is a beautiful medieval city with a rich history and a lively cultural life.

The project The maintenance of genetic variation, enabling populations to adapt to novel environments, is one of the greatest puzzles in evolutionary biology, because ubiquitous directional selection should lead to depletion of genetic variation in selected traits. This is especially the case with sexually selected traits, in which directional selection is particularly strong. Yet, substantial genetic variance in these traits is maintained. A potent force proposed to maintain genetic variation is balancing selection, but cases of a detailed dissection of the mechanisms of that maintain balanced polymorphisms are extremely rare. The project will likely provide a textbook example of balancing selection in action.

We aim to investigate the maintenance of polymorphism

in Phosphogluconate dehydrogenase (6Pgdh), a sexually selected gene associated with sexual conflict in the bulb mite *Rhizoglyphus robini*. 6Pgdh polymorphism (with two alleles, S and F) is associated with differences in male reproductive success. The S-bearers have advantage in male-male competition, but decrease fecundity of their partners. Previous studies suggest that the nonsynonymous polymorphism defining F and S alleles is under (relatively) long-term environment-dependent balancing selection. The project is aimed at identifying mechanisms driving this selection and investigating its molecular signatures.

Responsibilities A PostDoc will look for the molecular signatures of balancing selection around the 6Pgdh gene and attempt to estimate the age of the 6Pgdh. We expect a strong signal of long-term balancing selection within the genomic region centered on the F/S defining nonsynonymous polymorphism. The PostDoc will also be involved in gathering/analyzing field data to evaluate the levels of 6Pgdh polymorphism in natural populations and determine environmental factors affecting 6Pgdh allele frequencies in the field. This second task will be realized with the cooperation of a PhD student and PI.

Requirements

The successful candidate will have a PhD in biology, or other relevant field acquired no sooner than in 2014. The candidate will have experience in the analyses of population genomics data, including searching for the signals of balancing selection in the genome. We are looking for a candidate with a strong publication record, strong background in Evolutionary Biology and skills in data analysis. Excellent English, organizational and communication skills are also required.

Salary

The salary is 100000 PLN/year gross (ca. 23000 euro; before taxes and insurances). Note that living costs in Poland are substantially lower than in the west of the EU, so this amount of money ensures a sufficiently good life standard.

Documents

Please send a CV including contact details for two references and a cover letter to Agata Plesnar-Bielak (agata.plesnar@uj.edu.pl) till March 20th. For more information, please e-mail Agata Plesnar-Bielak.

Agata Plesnar-Bielak <agata.plesnar@gmail.com>

Krakow JagiellonianU GenomicsAdaptation

PostDoc:Krakow_JagiellonianU.Genomics_of_Adaptation

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Agata Plesnar-Bielak <agata.plesnar@gmail.com>

Lienss France WildlifeCancerEvolution

POSTDOCTORAL POSITION AT LIENSS (LA ROCHELLE, France), ONE HEALTH AND EVOLUTION OF WILDLIFE CANCER

We are seeking to incorporate postdoctoral researchers in our group through the

MOPGA program (Make Our Planet Great Again), financed by the French government (<https://www.campusfrance.org/en/visiting-fellowship-program-for-young-researchers-mopga-4>).

We are looking for researchers that have an excellent

track record in Evolutionary biology and Ecology to develop a project on wildlife health (new field studies or project focusing on the analysis of large databases in our possession).

More information on our research program can be found here: <https://giraudeaumathieu.wixsite.com/site-2015> Foreign researchers holding a *doctoral degree for less than 5 years* can respond to this call for proposals. This opportunity is open to researchers of all nationalities, except the French one.

The fellowship includes the following benefits: - Monthly allowance of *2,500 euros* - Moving allowance of 500 euros - Support for social security coverage - Support for health insurance

Please contact Mathieu Giraudeau (giraudeau.mathieu@gmail.com) if you have any questions.

- GIRAUDEAU Mathieu Centre de Recherches Ecologiques et Evolutives sur le Cancer (CREEC) CNRS, MIVEGEC, UMR5290 911 avenue Agropolis, 34394 Montpellier cedex 5 - FRANCE https://www.researchgate.net/profile/Mathieu_Giraudeau Mathieu Giraudeau <giraudeau.mathieu@gmail.com>

McMasterU COVIDmodelling

COVID modeling position.

The Theobio group at McMaster is seeking a post-doctoral fellow for COVID modeling projects. This is a chance to do practical work at the interface between dynamical modeling and public health. For more information, please see <https://www.mathjobs.org/jobs?joblist-135-17444> . “Dushoff, Jonathan” <dushoff@mcmaster.ca>

MichiganStateU InvasiveCrayfishGenomics

Postdoctoral Position, Genomic Investigations of Invasive Crayfish, Department of Fisheries and Wildlife, Michigan State University

Position Summary: The Department of Fisheries and

Wildlife at Michigan State University invites applications for the position of Postdoctoral Research Associate, under the supervision of Drs. Kim Scribner and John Robinson in the Department of Fisheries and Wildlife at Michigan State University. The successful applicant will join an established collaborative network of researchers at Michigan State University, the Michigan Department of Natural Resources (MDNR), and Michigan Department of Environment, Great Lakes & Energy (EGLE). The successful candidate will contribute to a state-funded project focused on utilizing a large suite of established Red Swamp Crayfish SNP loci to reconstruct pedigrees to characterize environmental features associated with aspects of the species' mating system, invasion routes, historical demography, and colonization history across Michigan landscapes. The appointment is for 18 months beginning in July 2021 through December 2022. The successful applicant will be provided opportunities to engage in a wide variety of professional development activities, depending on their areas of interest (e.g., participation in scientific meetings, mentoring in programming and scientific ethics, workshops in a targeted area of study, guest lectures, participation in other collaborative population genomics research). Some travel is possible to participate in field collection activities with project collaborators. Opportunities to participate in planned outreach efforts associated with this project are also available.

Background: Improved understanding of Red Swamp Crayfish population dynamics would greatly aid Red Swamp Crayfish control efforts in Michigan. Currently, little is known about mating ecology and movement dynamics among waterbodies across heterogeneous and human-altered landscapes. The specific source populations, sexes, ages, and rate of dispersal and demographic changes associated with colonization are unclear, particularly due to the recency of founding events, yet such information is critical for targeted management actions. The over-arching project goal is to utilize a large panel of SNP loci established by our group to improve the understanding of Red Swamp Crayfish population dynamics in Michigan to improve control strategies. Specific objectives are to 1) use genomic methods to quantify gene flow among infested waterbodies in Michigan, 2) identify landscape features associated with increased gene flow, and 3) estimate effective number of breeders and inter-individual variation in reproductive success.

Qualifications: A doctorate in Genetics, Ecology, Evolutionary Biology, or a related field is required. Demonstrated experience in population genetics and well-developed computational skills are also required for this position. In particular, experience with production of genome-wide single nucleotide polymorphism

(SNP) data sets is required. Previous experience with programming (R, Python, C++) and analysis of population genomic data (pedigree analysis, Approximate Bayesian Computation, unsupervised clustering) is desirable. Other desired qualifications include a strong work ethic, problem-solving and time management skills, experience working with a team and communicating scientific results. Applicants should demonstrate an interest in joining an established interdisciplinary research team working at the interface of population genomics, landscape ecology, and natural resource management.

Application Materials: Interested applicants should submit a cover letter, statement of research interests, and contact information for three references through the Careers @ MSU website - careers.msu.edu (job posting #: 694182). In addition to the required materials above, code (e.g., link to a GitHub repository) and writing samples (i.e., one or more recent publications) are also strongly encouraged, and will be considered during review. Review of applications will begin on 03/26/2021. For questions about the position or application process, contact Dr. Kim Scribner (scribne3@msu.edu) or Dr. John Robinson (jdrob@msu.edu).

Michigan State University has been advancing the common good with uncommon will for more than 160 years. One of the top research universities in the world, MSU pushes the boundaries of discovery and forges enduring partnerships to solve the most pressing global challenges while providing life-changing opportunities to a diverse and inclusive academic community through more than 200 programs of study in 17 degree-granting colleges. The Department of Fisheries and Wildlife was established in 1950 with faculty drawn from several different units. Since that time, both the faculty and the issues of importance in fisheries and wildlife have changed significantly. Our Mission, Vision, and Values build on our



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MissouriBotGarden RestorationPopulationGenomics

The Center for Conservation and Sustainable Development (CCSD) at the Missouri Botanical Garden seeks

to hire a full-time postdoctoral scholar to work in the Conservation Genetics Laboratory (PI, Dr. Christy Edwards). The candidate will 1) develop and implement collaborative research project(s) that employ population-genomic techniques to evaluate the effects of restoration techniques on the genetic diversity, genetic structure, and population dynamics of restorations in woodlands, savannahs, and grasslands at MBG's Shaw Nature Reserve and the broader region; 2) train and mentor undergraduate and graduate students; 3) assist MBG scientists with coordinating grant-funded activities including recruitment and mentoring of students, organizing and participating in outreach events and workshops, and presenting lectures to professional organizations and the general public; 4) prepare and submit manuscripts for publication; 5) build relationships with SNR staff and collaborative partners; and 6) actively participate in events with the St. Louis Ecology, Evolution, and Conservation community.

MBG's Shaw Nature Reserve contains over 2000 acres of fire-maintained woodlands, grasslands, and glades. Ecological restoration (i.e., selective tree thinning, removal of invasive species, prescribed fire) has been ongoing at SNR over the last 3 decades. The restorations have also involved seeding of native species from local and regional seed sources, and the successful candidate will be expected to work on research projects related to these restored populations of native plants at SNR and other field sites and natural areas in the region. The postdoctoral fellow will be expected to develop a research project involving testing how factors such as seed source or life history characteristics (such as mating system, pollinator, or seed disperser) affect the genetic diversity and population dynamics of restored plant populations. Candidates should have prior experience with field sampling techniques, next-generation DNA sequencing approaches, population genomics lab techniques (i.e., rad-seq, genotyping-by-sequencing), bioinformatics, and statistical analysis of population genomic data. Candidates who are interested in understanding the effects of plant life-history traits or ecological factors on the genetic diversity and structure of plant populations are particularly encouraged to apply. The successful candidates will have opportunities to collaborate with MBG scientists active in conservation genetics, reintroduction biology, restoration ecology, and community ecology.

Candidates with a completed Ph.D. or that will soon graduate with a Ph.D. in Ecology and Evolutionary Biology, Botany, Genetics, Restoration Science, Environmental Science, Conservation Biology, or a related field are encouraged to apply. The ideal start time is before summer 2021, but this is negotiable. The term for this grant-funded position will be up to 2 years,

with renewal in the 2nd year contingent on satisfactory performance. Salary will be commensurate with experience, and this position includes a comprehensive benefits package.

The position will be based in St. Louis, where a vibrant community of ecologists, conservation practitioners, and evolutionary biologists interact through partnerships among MBG, Washington University, the University of Missouri-St. Louis, Saint Louis University, plus other area institutions. The position will be seated in the CCSD, which explores and implements new, science-based approaches to the conservation and sustainable use of plant diversity. CCSD's strategies for conservation are based on a sound, scientific understanding of the occurrence and distribution of plants. CCSD applies the knowledge of plant diversity accumulated by Missouri Botanical Garden researchers over many years, making that knowledge usable for conservation planning and decision-making. Operating under the auspices of the Garden and as part of its division of Science and Conservation, CCSD builds upon the Garden's institutional expertise, scientific programs, influence, and resources.

If interested, please apply online at <https://us59.dayforcehcm.com/CandidatePortal/en-US/-mbg/Posting/View/612> Review of applicants will begin immediately and will continue until a suitable candidate is found

– Christine E. Edwards, PhD Stephen and Camilla Brauer Conservation Geneticist Center for Conservation and Sustainable Development Missouri Botanical Garden 4344 Shaw Blvd. | St. Louis MO 63110
Christy.edwards@mobot.org

Christy Edwards <Christine.Edwards@mobot.org>

MIZ Poland Canid genomics

A postdoctoral researcher/ research assistant position is now open in a research group led by Dr Małgorzata Pilot at the Museum and Institute of Zoology of the Polish Academy of Sciences. The research group is focused on mammalian evolutionary genomics, and this position will be focused on canid genomics. Specific topics to be studied include the evolutionary history of Eurasian *Canis* species, causes and consequences of admixture among *Canis* species and subspecies, and the evolution of behavioural traits in the genus *Canis*.

The position is available for 2 years and 4 months, from April 2021 until July 2023. The position may be extended for a longer period, depending on research funding availability. The research group is based at the Research Station of the Museum and Institute of Zoology (MIZ), Polish Academy of Sciences in Gdańsk, and maintains strong links with the main research facilities of the MIZ in Warsaw.

Work description

This position will involve the analysis of genomic data and preparation of manuscripts for publication, participation in the supervision of PhD students, and contribution to administrative tasks associated with research projects. Depending on the selected candidate's experience, the position may also involve laboratory work. The position will require learning and development of new methods of data analysis, and therefore strong motivation and willingness to learn is essential. The successful applicant will be expected to contribute to grant applications submitted by the group, and will be encouraged to apply for independent funding available for early career researchers. The postdoctoral researcher will thus have the opportunity to propose and explore new research questions within the general remit of the research group.

Requirements

The position requires expertise in evolutionary genomics and/or bioinformatics, and the candidate must either hold a PhD degree in a relevant area or hold a MSc degree and be able to demonstrate research independence. The ideal candidate should have the following skills:

- * good knowledge of Linux/Unix environment;
- * experience with processing DNA sequence data;
- * experience with population genetic data analysis;
- * ability to work independently and to communicate with a multi-disciplinary team;
- * good scientific writing skills, evidenced by a first authorship of at least one research paper (which will be evaluated in the selection process);
- * excellent spoken and written English.

Desirable skills include:

- * experience with the analysis of NGS data, including whole-genome sequence data;
- * proficiency with at least one scripting language (e.g. Python, Perl, Unix Shell scripts);
- * experience with laboratory methods used in experimental population genetics and genomics;
- * experience with sample processing for NGS.

Research environment

The research at the MIZ is focused on a broad range of themes in animal biology, including systematics, biogeography, evolutionary biology, ecology and population

genetics. Małgorzata Pilot's research group is part of the Laboratory of the Molecular and Biometric Techniques led by Prof. Wiesław Bogdanowicz, grouping researchers focused on population genetics, phylogeography and evolutionary genomics of a broad range of animal taxa. MIZ laboratories contain modern equipment for genomic analyses, including Pacific Biosciences RSII long-read sequencer and Illumina MiSeq System. The state-of-the-art ancient DNA laboratory carries out work on mammalian palaeogenetics. The Museum's zoological collection is among the largest and most valuable in Europe.

Employment conditions

Employment period: 28 months, subject to a 3-month probation period. Start date: 12 April 2021 or as soon as possible after that date. The salary is funded by the Polish National Agency for Academic Exchange (NAWA).

Documents required in the application

- * Copy of a PhD certificate
- * Curriculum vitae including the publication list, with the following statement provided at the end and signed:

"I agree to the processing of personal data provided in this document for realising the recruitment process pursuant to the Personal Data Protection Act of 10 May 2018 (Journal of Laws 2018, item 1000) and in agreement with Regulation (EU) 2016/679 of the European Parliament and of the Council of 27 April 2016 on the protection of natural persons with regard to the processing of personal data and on the free movement of such data, and repealing Directive 95/46/EC (General Data Protection Regulation). I also consent to the processing of my personal data by the Museum and Institute of Zoology of the Polish Academy of Sciences for the purposes of any future recruitment processes."

Applications that do not include this statement won't be considered.

- * Motivation letter (maximum one A4 page)

— / —

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>

Nottingham Evolutionary Genomics Polyploidy

3-year Leverhulme-funded Postdoc: “PREADAPT: revealing the basis of whole genome duplication-mediated adaptation”

Closing Date: Wednesday 24 March 2021

Context: Whole genome duplication (WGD) is an engine of adaptation and speciation across kingdoms, but the basis for this ‘WGD-advantage’ has been mysterious since Haldane considered it in the 1920s. Based on our preliminary data, we hypothesise that specific cellular adaptations to WGD itself preadapt certain lineages to survive subsequent extracellular challenges. We test this using our unique genomic dataset of thousands of individually sequenced genomes (including ~200 long-read sequenced) from pre- and post-WGD lineages, both before and after adaptation to challenging habitats, providing the first genomic assessment of WGD-mediated adaptability. Further, we seek to determine precisely what functional adaptive advantage WGD provides, addressing a fundamental mystery. See <https://www.yantlab.net/> for more on our group.

Role: Primary activities will include leading large-scale population genomic projects. This includes exhaustive demographic and selection analyses. We seek candidates who are not only motivated to run with these objectives, but who can also propose new creative project contributions. By the end of your postdoc with us, we expect you to be able to, for example, begin your own group, bringing along your project from our work together. We also expect to engender the development of new directions as a result of discoveries in our group that can spur independent trajectories for your future research.

Applicants passionate about evolutionary genetics or population genomics are encouraged to apply. Candidates must hold a PhD or equivalent in Genetics, Evolution, Bioinformatics, or a closely related area. The role holder must have demonstrable programming skills (e.g. scripting in Python or extensive skills in R). Experience with large scale population genomic data in HPC environments as well as practical experience of applying population genomics to biological problems is required. We are looking for a candidate with good knowledge of population genetics and demonstrable use of computational methods in an evolutionary context.

Apply here: <https://www.nottingham.ac.uk/jobs/currentvacancies/ref/MED014921> Please include a brief cover letter expressing your motivations.

This fixed-term post is available from 1 April 2021 to 29 February 2024. Informal enquiries may be addressed Levi Yant at Levi.Yant@nottingham.ac.uk

The School of Life Sciences holds an Athena Silver SWAN Award, in recognition of our commitment to supporting and advancing women’s careers in the life sciences (STEMM).

Levi Yant <Levi.Yant@nottingham.ac.uk>

OpenU TelAviv IREvolution

The Hazkani-Covo lab in the Department of Natural and Life Sciences at the Open University of Israel, Tel Aviv, is seeking a full-time self-motivated postdoc. Our lab (https://www.openu.ac.il/personal_sites/einat-hazkani-covo/) broadly studies signatures of genome instability during evolutionary timelines. The position aims to study the evolution of inverted repeats using molecular evolution and comparative genomics analysis, as well as analysis of NGS.

The ideal applicant will have a Ph.D. in evolution, bioinformatics, Genetics, or a similar discipline and good programming skills in Python or PERL. Experience with NGS analysis is preferable.

The position is based in the Open University of Israel and is located in Tel Aviv. The position can start as soon as possible. Deadline to apply: Ongoing (Open until filled). This is a multi-year postdoctoral position (run for an initial 1-year period, with the possibility of extension to 3 years given satisfactory performance).

To apply, or for more details, please contact Einat Hazkani-Covo (einatco@openu.ac.il). Applications should include a cover letter stating qualifications, previous work and motivation, your CV, publication list, and contact information of three references.

Einat Hazkani-Covo Senior Lecturer Department of Natural and Life Sciences The Open University of Israel einatco@openu.ac.il https://www.openu.ac.il/personal_sites/einat-hazkani-covo/ Einat Hazkani-Covo <einatco@openu.ac.il>

Patagonia Argentina Plant Diversity

We are looking for candidates for a postdoctoral fellowship to be developed within the framework of an Argentinian already funded project (Project PICT-2018-02145) “Patterns, causes and consequences of intra-individual genetic diversity in plants”. The chosen person will be involved in field work, laboratory and desk tasks related on the one hand with the collection of pollen and the quantification of their viability, and on the other hand with the application of molecular and bioinformatics tools to answer the questions of the project. The ideal person for this fellowship should have a broad and integrative view of biology, and be willing to embrace diverse study areas and open up to learn and develop new approaches. Any previous experience in fieldwork, pollination biology, microscopy, genetics and genomics, statistics, bioinformatics and modeling will be welcome, but it is not an exclusive requirement, as long as there is clear interest in learning new things.

Duration: 24 months, approximately from May 2021 to April 2023

Requirements: (1) Complete doctoral studies (2) Adequate level of English language (fluency in Spanish recommended but not exclusive) (3) Availability to move to the work area (Bariloche, Rio Negro, Argentina) during the fellowship period.

How to apply: Please, communicate your interest to us by sending an email with a CV and intent letter to the address below: ezattara@comahue-conicet.gob.ar

Project summary:

The foundations of modern evolutionary theory assume that genetic information is transported through a germ line isolated from the rest of an individual’s body, as a result of early germline segregation. However, this pattern of early segregation is only observed in a subset of animals, while other animals, all fungi, and all plants presumably show late germline segregation. This late segregation has important implications for modular organisms such as plants, especially in long-lived or clonally propagated species, since with time individuals acquire an increasing level of genetic mosaicism, due to the accumulation of somatic mutations that are transmitted directly to gametic cells. Consequently, older individuals are expected to show greater intra-individual genetic diversity, which affects both their contribution

to the genetic diversity of the population and their own reproductive capacities. Despite the clear ecological, evolutionary and even agricultural implications of a late segregation of the germ line in plants, to date studies focused on this issue are very scarce. In this project, we propose as general objectives to characterize and contrast detectable intra-individual genetic diversity along a range of life strategies and a mutagenic gradient in natural and artificial systems, and to analyze the implications of early or late germline segregation in the ecology, genetics and evolution of plant populations. Working under the general hypothesis that plants show late germline segregation, we will model and test the consequences of mutational load on individual genetic variability and the resulting phenotypic variation. If the observed results contradict the predictions derived from an absence or late segregation of the germ line, this would imply evidence in favor of the alternative hypothesis that early segregation mechanisms exist in plants. Our research program combines a theoretical approach for the inference of qualitative and quantitative predictions, with a phylogenetically broad sampling of the variation in pollen viability, a variable for which a differential response is expected depending on whether germline segregation is early or late, complemented by a detailed characterization at the molecular level of the pattern of somatic mutations and their effects in individuals of grapefruit, a species of great productive value. We hope that this project reinforces the current knowledge about the diversity of germline segregation strategies, and also generates knowledge with significant impact both in basic disciplines (Evolution and Ecology) and in applied areas (agricultural production). –

Gabriela L. Gleiser. CONICET Researcher Bariloche, Argentina

Gabriela.Gleiser@uv.es

San Francisco State U Forensic Population Genetics

We are looking to hire an NIJ-funded post-doc to collaborate on a project to better understand the accuracy of forensic genetic genealogical searching. The postdoc will gain experience in pedigree-based IBD analysis considering population genetic variation. The lab encourages innovative communication and examination of social justice questions related to our work.

This is a great opportunity for a scientist who is looking

to do population/statistical genetics research with a social impact, and who is interested in collaborating with brilliant, tenacious, and creative SFSU students.

While the postdoc's primary role will be in research, they will also be well-positioned to mentor masters and undergraduate students in the lab. The postdoc will also have flexible teaching opportunities, but not requirements. Depending on the postdoc's interests, this project may include collaborations with population geneticists Graham Coop at UC Davis and Doc Edge at USC, bioethicist Malia Fullerton at UW, and/or law professor Erin Murphy at NYU. Happy to discuss long-term remote working options.

Interested scientists can email Rori Rohlf's rrohlf@sfsu.edu with a 1-2 page cover letter describing your specific interest in this position and CV. Don't hesitate to be in touch with any questions!

Rori Rohlf's (she/her) Assistant Professor of Biology San Francisco State University Ramaytush Ohlone land

<https://rohlfslab.weebly.com/> Rori Rohlf's
<rrohlf@sfsu.edu>

Texas Biomed Primate Genetic Variation

Texas Biomed Position: Staff Scientist/Postdoctoral Scientist (req119) Southwest National Primate Research Center (SNPRC)

POSITION DESCRIPTION: Texas Biomed is searching for an exceptional staff scientist or postdoctoral scientist to work on understanding the consequences of genetic variation in pedigreed primate populations. The position will be in the Southwest National Primate Research Center (SNPRC) Colony Administration and Genomics Component, which functions to support and advise the SNPRC on its non-human Primate (NHP) genomics resource and research activities. Over the last 50 years the SNPRC has developed several large, pedigreed, nonhuman primate colonies (baboons, rhesus macaque, and marmoset). Animals in these pedigrees have been extensively characterized at the genetic and phenotypic level. A goal of the component is to support genetic characterization of the NHP colonies and develop breeding strategies to maintain genetic diversity. The successful applicant will work directly with Drs. Ian Cheeseman and Shelley Cole, and will have imme-

diated opportunities to collaborate with an active team of investigators to perform population and statistical genetic analyses, publish results, interact with NPRC working groups and contribute data and results to the field of NHP genomics.

Qualified and interested applicants are encouraged to apply.

EDUCATION/EXPERIENCE/SKILLS: Required: Doctoral degree. Experience with next generation sequencing data (genomic, transcriptomic or epigenetic) and statistical or population genetic analysis is essential. Candidates with a strong bioinformatics background and knowledge of scientific programming languages (for example, R, python, C++) are strongly encouraged to apply.

OTHER: This is a full-time salaried (exempt) position. Texas Biomed business hours are Mondays through Fridays 8:00 a.m. to 5:00 p.m. Texas Biomed is committed to a drug-free workplace. Pre-employment drug screen is required.

Application packets are accepted electronically or in hard copy. A completed application packet is a requirement for all positions. Incomplete applications will not be accepted. Equal Employment Opportunity/M/F/Disability/Protected Veteran Status

scole@txbiomed.org

UA Aarhus Population Genomics

A 12 month postdoctoral position will be available at the Department of Biology, Aarhus University, Denmark, starting 15 April 2021 or as soon as possible thereafter. The deadline for application is 8 March 2021.

The appointed postdoc will work on a project that will study genomic variation in two species of sea ducks of unfavourable conservation status that have recently experienced major declines in abundance [velvet scoter (*Melanitta fusca*) and long-tailed duck (*Clangula hyemalis*)]. Using whole genome sequencing data, demographic histories will be reconstructed and contemporary and historical declines will be compared, and possible selective sweeps will be identified.

Applicants should have a Ph.D. in population genomics or evolutionary biology and must document skills in population genomics analysis and bioinformatics. Experience and efficiency in writing scientific papers is

also important. Finally, applicants should be ambitious, show strong collaborative skills, and should also be able to take initiatives and responsibility.

The project involves collaboration between Prof. Michael M. Hansen and Prof. Anthony Fox, both Aarhus University, and Consultant Iben Hove Sørensen, the Danish Hunters' Association. It is funded by the Danish 15 June Foundation and the Hunters' Nature Foundation.

For further information and for applying, please see <https://international.au.dk/about/profile/vacant-positions/job/postdoc-position-in-conservation-and-population-genomics/> In case of questions, please contact Michael M. Hansen, mmh@bio.au.dk

Michael M. Hansen Professor Department of Biology Aarhus University Ny Munkegade 114-116 DK-8000 Aarhus C Denmark E-mail: mmh@bio.au.dk Web page: <http://person.au.dk/michael.m.hansen@biology> Tel.: +45 40247191

mmh@bio.au.dk

UAlabama 2 Tardigrade Evolution

Two postdoctoral research positions in integrative evolutionary biology are available in the laboratory of Dr. Jason Pienaar (<https://bsc.ua.edu/profiles/jason-pienaar/>) in the Department of Biological Sciences at the University of Alabama, Tuscaloosa.

These positions will explore cryptobiosis in tardigrades and their bryophyte hosts (the ability to suspend metabolic activity and enact morphological and physiological changes to survive harsh environmental conditions). The successful applicants will in addition interact with the laboratories of Dr. Janna Fierst (<https://bsc.ua.edu/profiles/janna-fierst/>), Dr. Stanislava Chtarbanova (<https://bsc.ua.edu/profiles/-stanislava-chtarbanova-rudloff/>) and Dr. Lukasz Ciesla (<https://bsc.ua.edu/profiles/lukas-ciesla/>) to decipher the genomics, transcriptomics and across kingdom communication mechanisms underlying cryptobiosis. The Pienaar lab also continues to develop phylogenetic comparative methods for testing adaptive hypotheses in collaboration with Dr. Krzysztof Bartozek (<https://liu.se/en/employee/krzba67>) and Dr. Thomas Hansen (<https://www.mn.uio.no/cees/english/people/-core/thomasha/>), and candidates with mathematical modeling experience or experience with phylogenetic comparative methods will also be considered.

The positions are available for highly enthusiastic post-doctoral research associates whose primary career interests are to develop expertise in integrative approaches to addressing mechanistic and evolutionary questions using “the toughest animals on earth”, tardigrades, as well as their host bryophytes or lichens as a model. Depending on academic experience, the primary responsibilities of the post doc could be any combination of: genomic and transcriptomic assembly and analyses; molecular phylogeny development or phylogenomic analysis; refining culture techniques to establish lab populations and managing field collections and/or; experimental induction of cryptobiotic states and data collection for phylogenetic comparative method analyses and / or development. Other duties will consist of gathering and managing data from the field, participating in experimental design, aiding in grant writing, collaborating with undergraduate, graduate students and other faculty as appropriate and participating in service-learning based tardigrade discovery outreach. The expectation is that findings will be published in peer reviewed journals and presented at relevant conferences.

Applicants with diverse research backgrounds are encouraged to apply. Candidates must have received a Ph.D. in a relevant field by the start date.

Funding is available for 2.5 years for each of the positions with annual renewal dependent on performance evaluation, and will include a competitive salary, full benefits, and conference travel allowance. The University of Alabama offers a range of professional development opportunities. Application review will continue until the position is filled. Start dates are negotiable, but the successful applicants should preferably be able to start in the Fall 2021 academic semester.

Applicants interested in the position should contact Dr. Jason Pienaar (jpienaar@ua.edu) Applicants must apply by submitting an application to the Fall 2021 Biological Sciences Departmental postdoctoral pool at

<https://staffjobs.ua.edu/en-us/job/512600/-postdocvisiting-scientist-biological-sciences-512600>

Materials should include: 1. Cover letter stating your application for the “Comparative cryptobiosis” position, a brief description of research accomplishments and interests, and career goals.

2. The names and contact information for 3 references (or you can arrange to have three recommendation letters sent to jpienaar@ua.edu).

3. Curriculum vitae.

4. Representative publications.

About the University of Alabama: The University of Al-

abama is the flagship campus of the University System of Alabama, with an enrollment of over 35,000 students. The University is committed to achieving excellence as one of the country's primary centers of research and education. It is located in the vibrant college town of Tuscaloosa, AL, which boasts many cultural and athletic activities. The campus also benefits from the close proximity to the Birmingham metropolitan community.

The University of Alabama is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

Jason Pienaar <jasonpienaar@gmail.com>

UBritishColumbia MarineInvertsProtists

Postdoctoral Research Position: Evolutionary Morphology of Marine Invertebrates and/or Predatory Protists

Applications are invited for a three-year postdoctoral research fellowship centered on species discovery, evolutionary morphology and trophic/symbiotic interactions of marine invertebrates and/or predatory protists. As a member of the Leander Lab (www3.botany.ubc.ca/bleander) at the University of British Columbia and in collaboration with researchers at the Hakai Institute (www.hakai.org), the PDF will have the opportunity to apply their specific expertise in marine organismal diversity and natural history by routinely sampling pristine environments in the Pacific Northwest. The field collections and sample-specific processing will primarily target different marine environments near the Hakai field stations on Quadra Island and Calvert Island (www.hakai.org/quadra and www.hakai.org/calvert). The goals of the research are to discover novel organisms and characterize their morphological traits, behaviors, feeding preferences, symbiotic/parasitic interactions and phylogenetic relationships using high-resolution microscopy and genetic/genomic techniques.

The primary responsibilities of the position include leading fieldwork, collecting molecular and morphological data using state-of-the-art approaches, building manuscripts for publication, presenting research findings at conferences, and contributing to the day-to-day training of other researchers in the lab. The postdoc will be part of a dynamic team of other researchers at UBC and the Hakai Institute with expertise in marine biodiversity. The successful applicant will have a PhD

in a relevant field (preferably earned less than 5 years ago) and a competitive publication record centered on comparative anatomy, evolutionary biology, systematics, molecular phylogenetics and high-resolution microscopy (e.g., DIC-LM, CLSM, SEM, TEM and FIB-SEM) of marine invertebrates and/or protists. This three-year PDF position is paid at a rate of \$55,000 CAD per year plus Mandatory Employment Related Benefits with an opportunity for renewal provided satisfactory performance and funding availability.

To apply, please send a concise statement of research interests, CV and the names/emails of three references as a single PDF to Brian Leander (bleander@mail.ubc.ca). Review of applications will occur on an ongoing basis in anticipation of filling the position on September 1, 2021 (negotiable).

Equity and diversity are essential to academic excellence. An open and diverse community fosters the inclusion of voices that have been underrepresented or discouraged. We encourage applications from members of groups that have been marginalized on any grounds enumerated under the B.C. Human Rights Code, including sex, sexual orientation, gender identity or expression, racialization, disability, political belief, religion, marital or family status, age, and/or status as a First Nation, Metis, Inuit, or Indigenous person.

"Leander, Brian" <bleander@mail.ubc.ca>

UCalifornia Berkeley HumanEvolutionaryGenetics

Post-doctoral position ??? University of California, Berkeley ??? Human Evolutionary Genetics.

Description: The Moorjani Lab (<https://moorjanilab.org/>) at University of California, Berkeley uses computational and statistical methods to investigate questions in human evolutionary genetics, in particular on mutation rate, demographic inference and archaic ancestry. A central aim in the lab is to understand the impact of evolutionary history on genetic variation and to apply this knowledge to learn about human history and disease. To this end, we use genetic data from ancient specimens and present-day species to learn about: (1) when key events (such as introgression and adaptations) occurred in human history, (2) how different evolutionary processes such as mutation rate evolve across primates, and (3) how we

can leverage these patterns to identify genetic variants related to human adaptation and disease. The research in the lab involves both development of new methods and large-scale genomic data analysis.

Responsibilities: A successful candidate will develop and apply computational approaches to large genomic datasets to characterize patterns of population history and evolution. The main responsibilities include conducting research, attending regular lab meetings and journal clubs, and preparing research results for publication and presentations at scientific meetings. Opportunities may also exist for mentoring graduate and undergraduate students.

Required qualifications: Ph.D. or equivalent in genetics, genomics, computational biology or related fields and demonstrated record of productivity and publications. Experience with programming (e.g. C/C++, Python/Perl, R or other programming languages), genomic data analysis and methods development.

Please contact Priya with your CV and a brief overview of research questions you are interested in pursuing. Please also request three recommenders to send a letter of reference on your behalf.

Salary: This is a multi-year postdoctoral position (initial appointment is for 12 months and renewable annually up to three more years). Salary is commensurate with qualifications and experience.

Contact: Priya Moorjani Assistant Professor Department of Molecular and Cell Biology Center for Computational Biology <https://moorjanilab.org/> Email: moorjani@berkeley.edu

Priya Moorjani <moorjani@berkeley.edu>

UCalifornia Berkeley MicrobiomeEvolution

Description:

The Department of Integrative Biology at the University of California, Berkeley seeks applications for a Postdoctoral scholar in the Koskella Lab, in the area of disease ecology and microbiome sciences, at 100 % time with an expected start date of September 2021. Bacteriophage viruses (phages) impact microbial communities across habitats, including the host-associated microbiome, structuring both microbial composition and function. Since 2017, the Koskella lab has been developing a new

urban disease ecology system that allows for temporal sampling of microbial communities from healthy and diseased tissues across a spatially structured population of Callery ('Bradford') pear trees infected with the agriculturally relevant pathogen *Erwinia amylovora*, the causal agent of Fire Blight. The department is seeking a postdoctoral researcher to lead a new NSF funded project that combines culture-dependent screening and culture-independent 'omics' approaches to explore bacteriophage dynamics over both short (monthly) and long (yearly) time scales to better understand the ecology and evolution of phage host range, the scale of phage adaptation and bacterial counter-adaptation, and the role phages play in shaping pathogen invasion and disease. The project is based around a tight integration of research and teaching, and includes the development of a four module undergraduate research program with high-throughput, culture independent sequencing of both bacterial and viral communities to examine the role of phages in bacterial community turnover and disease in this Pear Tree system. The work will take place in the laboratory of Dr. Britt Koskella, at UC Berkeley, and will include a combination of local fieldwork and bacterial viral community profiling/'omics' approaches.

Responsibilities: Responsibilities include field sampling of trees, microbiological culturing, extraction and analysis of both amplicon and metagenomic datasets, statistical analyses, and preparation of manuscripts for publication. In addition, the researcher will work with the PI to lead a team of up to 12 undergraduate researchers to isolate and characterize phages from the phyllosphere. There also exists ample opportunity to design and implement additional projects of mutual interest.

Minimum/Basic Qualifications required at the time of application: PhD (or equivalent international degree) or enrolled in a PhD degree program (or equivalent international degree program) at the time of application.

Preferred Qualifications: Given the undergraduate research component of this project, the preferred candidate would have a keen interest in integration of teaching and research and undergraduate mentoring. Moreover, preference will be given to applicants with experience in bioinformatics, microbial ecology, molecular biology, statistics, and/or disease ecology, as well as excellent writing and communication skills.

Salary:

This is a full-time position. Salary is commensurate with experience.

How to apply: To apply, please go to the following link: —<http://aprecruit.berkeley.edu/apply/JPF02889> Next

review date: —Tuesday, Mar 9, 2021 at 11:59pm (Pacific Time) Apply by this date to ensure full consideration by the committee.

Final date: —Thursday, Mar 25, 2021 at 11:59pm (Pacific Time) Applications will continue to be accepted until this date, but those received after the review date will only be considered if the position has not yet been filled.

“bkoskella@berkeley.edu” <bkoskella@berkeley.edu>

UCalifornia Berkeley MosquitoLandscapeGenomics

POSTDOC POSITION IN MOSQUITO SURVEILLANCE & LANDSCAPE GENOMICS

The Marshall Lab (<https://www.marshalllab.com/>) at the UC Berkeley School of Public Health is seeking to hire a postdoctoral scholar to work on mathematical and ecological aspects of gene drive systems in mosquito vectors of malaria, dengue and other mosquito-borne diseases. The position is initially for one year, with the possibility of extension, and is available mid-2021. Salary is commensurate with experience, and full benefits are included.

The successful candidate will work on exciting collaborative projects with a consortium of mathematical modelers, molecular biologists, ecologists and epidemiologists, mostly throughout the University of California system. Molecular biology labs that we collaborate with include the Akbari Lab (<https://www.akbarilab.com/>), Bier Lab (<http://bierlab.weebly.com/>) and Gantz Lab (<http://www.gantzlab.org/>) at UCSD, and the James Lab at UC Irvine. Ecology labs that we collaborate with include the Vector Genetics Lab (<https://vectorgeneticslab.ucdavis.edu/>) at UC Davis and the Mosquito Control Lab at QIMR Berghofer in Australia. We also collaborate with TIGS-UCSD (<https://tigs.ucsd.edu/>) and the Debug Project (<https://debug.com/>) at Verily Life Sciences (<https://verily.com/>), and serve as modeling lead for the UC Irvine Malaria Initiative (<https://ucimi.org/>).

Tasks that we are seeking help with include: * Developing methods to infer mosquito movement patterns and demography from landscape genomic data, * Informing mosquito monitoring and surveillance protocols to assess intervention efficacy and unintended spread, * Contributing to development of our modeling frame-

work, the Mosquito Gene Drive Explorer (MGDrive) (<https://marshalllab.github.io/MGDrive/>), & * Mentoring PhD, Masters and undergraduate students.

An ideal candidate will have: * A strong background in applied mathematics, statistics and/or computer science, * Experience with population genetics, genomics or ecological and epidemiological modeling, * An interest in mosquitoes and/or mosquito-borne diseases, & * An interest in mentoring students and promoting diversity, equity and inclusion in research.

If you are interested in the position, please send: i) your CV, including a list of publications and the names and email addresses of three potential referees, ii) PDFs of your two most significant publications or manuscripts to date, and iii) a cover letter describing your research interests and motivations for joining our lab to John Marshall at john.marshall@berkeley.edu. Inquiries are also welcome. Additional information about the research in our lab can be found at <https://www.marshalllab.com/>. The position will remain open until filled. The first review date will be April 16th 2021.

UC Berkeley has large and vibrant public health, ecology and computational biology communities spanning the School of Public Health, the Department of Integrative Biology, the Department of Environmental Science, Policy and Management, the Center for Computational Biology, the Innovative Genomics Institute, and more. UC Berkeley offers competitive salaries, excellent benefits and is an equal opportunity employer. The City of Berkeley and the surrounding San Francisco Bay Area is known for its progressive values, vibrant social and cultural scene, and beautiful surrounding environment.

“Marshall, John M.” <john.marshall@berkeley.edu>

UCentralFlorida EvolutionPlantSecondaryMetabolism

Postdoctoral Scholar in Genetics and Evolution of Plant Secondary Metabolism

The Mason Lab in the Department of Biology at the University of Central Florida is currently seeking a postdoctoral scholar to assist with a research project funded by the Foundation for Food and Agriculture Research exploring the evolution, genetic architecture, and ecological and agricultural consequences of inducible chemical defenses and broader plant secondary metabolism in cultivated and wild sunflowers (*Helianthus*). This work

seeks to identify endogenous chemical defense systems in sunflower to provide quantitative resistance for the sustainable control of pests and pathogens.

The postdoctoral scholar will work closely with faculty with expertise in:

- (1) Plant ecophysiology and secondary metabolism
- (2) Insect and microbial plant-biotic interactions
- (3) Genome-wide association mapping
- (4) Phylogenetic comparative methods and multivariate statistics.

The primary duties will involve organizing empirical data collection, conducting data analysis, and leading research dissemination. The scholar will organize greenhouse and laboratory experiments, conduct plant tissue analytical chemistry analysis via gas chromatography-mass spectrometry, perform analysis of genomic datasets including genome-wide association mapping, and prepare manuscripts for publication. The initial duration of this postdoctoral position will be one year, extendable up to 32 months (2.66 years) with satisfactory performance toward project objectives. The salary is \$50,000 per year. In addition to salary and benefits, the UCF preminent postdoctoral program provides an additional \$5,000 travel/research allowance to the postdoctoral scholar outside of the scope of project funding.

This postdoctoral scholar position is especially targeted at researchers interested in aggressively pursuing a faculty position. The PI is dedicated to working with the postdoctoral scholar in establishing themselves as an independent researcher. This includes writing grant proposals as a co-PI and leading a small research team. The Mason lab engages a large number of undergraduates in plant science, and the postdoctoral researcher will have the opportunity to advise a broad range of undergraduate projects as well as work closely with PhD students. In addition, the postdoctoral scholar will be expected to contribute to an inclusive lab culture, and will be encouraged to participate in diversity, equity, and inclusion efforts in support of UCF's mission as a Hispanic-Serving Institution.

The minimum qualification is a Ph.D. from an accredited institution in plant science, genetics, biology, or a closely related field. Strong preference will be given to candidates with experience in analytical chemistry of plant tissues (e.g., GC-MS, HPLC-MS), or experience working with large genomic datasets, for example analyzing whole genome resequencing data or performing genome-wide association mapping in plants. Competitive applicants will have experience in at least one of these two areas, and the most competitive applicants will have experience in both. In addition, preference will be given to candidates with experience related to any of the following areas. Please note that we do not

expect applicants to necessarily have any of these skills or interests, but please indicate experience in these areas if present: plant tissue culture and transformation, analysis of gene expression, metagenomics/barcoding, flow cytometry, leaf hyperspectral reflectance, laboratory techniques in plant pathology, mycorrhizal symbiosis, plant-pollinator interactions.

UCF requires all applications and supporting documents to be submitted online through the Human Resources website at <https://jobs.ucf.edu/en-us/job/-500060/postdoctoral-scholar-biology>. In addition to the online application, candidates should also submit: 1) a cover letter, 2) a current curriculum vitae, 3) the full text of three peer-reviewed publications relevant to the project area authored or co-authored by the candidate, 4) a one-to-three page research statement summarizing past research projects and your involvement and contributions to each, and (5) a one-page diversity statement summarizing past efforts and future goals in advancing diversity, equity, and inclusion in STEM.

NOTE: Please have all application documents ready when applying so they can be attached at that time. Once the online submission process is finalized, the system does not allow applicants to submit additional documents at a later date. Only complete application materials will be considered. Active review of applications will begin immediately, but the search will continue until the position is filled.

For questions regarding the position, please contact Dr. Chase Mason, chase.mason@ucf.edu For more information about the Mason Lab, see here:

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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>

UEdinburgh BiogeographyGlobalDryTropics

Please check out the below PDRA position on the biogeography of the dry tropics. Website: <https://blogs.ed.ac.uk/seco-project/news> Contact: kyle.dexter@ed.ac.uk

As part of the SECO project we have four job opportunities available at the University of Edinburgh. The SECO

project aims to resolve the current and future carbon dynamics of the dry tropics, more details available here: <https://blogs.ed.ac.uk/seco-project/news> SECO is a 5-year Large Grant funded by the Natural Environment Research Council (NERC) in the UK that will generate the first ever estimates of key carbon fluxes across the dry tropics. Collaborators from eighteen countries will use data from over 600 forest plots and radar remote sensing to understand how the vegetation of the dry tropics is changing and why. It is the largest research effort of its kind for the dry tropics, and it aims to determine how the carbon cycle varies across continents and why. Along the way, it will address longstanding questions on the biogeography and ecosystem function of tropical dry forests and savannas. SECO is a global partnership of 22 organisations including, in the UK, the Universities of Edinburgh, Leeds, Sheffield and Exeter.

There are 3 x 4-year post-doctoral positions available at Edinburgh, with a focus on 1) geospatial analysis, 2) biogeography, and 3) carbon cycle modelling. A project officer position is also available, which would suit a recent MSc or BSc graduate. Closing dates vary from 19 April to 17 May.

Please see <https://blogs.ed.ac.uk/seco-project/news/> for more details. Informal queries can be addressed to Casey Ryan (casey.ryan@ed.ac.uk geospatial PDRA and project officer), Kyle Dexter (kyle.dexter@ed.ac.uk biogeography PDRA) and Mat Williams (mat.williams@ed.ac.uk modelling PDRA).

Kyle G. Dexter | www.phylodiversity.net/kdexter Senior Lecturer | School of GeoSciences | University of Edinburgh Research Associate | Royal Botanic Garden Edinburgh

219 Crew Building, King's Buildings, Edinburgh EH9 3FF, U.K. Phone: +44 (0) 131 650 7439

Kyle Dexter <kgdexter@gmail.com>

UIdaho DiseaseEvolution

We are seeking a postdoctoral researcher to develop phylogenomic methods to predict the risk of viral emergence. Anticipating viral emergence before it occurs creates revolutionary possibilities for reducing the risk of infectious disease through preemptive intervention. The researcher will work to develop tools to identify the genomic signature of adaptation to novel hosts within the context of Lassa virus, a hemorrhagic fever widespread

throughout West Africa that regularly spills into the human population but has yet to produce sustained human-to-human transmission. The postdoctoral researcher will work with Drs. Scott Nuismer and Chris Remien at the University of Idaho as part of a large multi-national collaboration focused on predicting the risk of viral emergence and preempting it using wildlife vaccines capable of limited self-dissemination. Although this position is based at the University of Idaho, arrangements for remote work are possible.

The ideal candidate will have a strong background in evolutionary biology and population genetics and be comfortable programming in R, Python, or C++. Prior experience working on infectious disease is not required; fresh diverse perspectives from any area of computational evolutionary biology are welcome. We anticipate this position will become available as soon as April 1, 2021. The position will be initially for one year with opportunity for renewal.

Scott Nuismer Professor Department of Biological Sciences and Mathematics Program in Bioinformatics and Computational Biology University of Idaho Moscow, ID 83844 <https://www.leef.org/> "Nuismer, Scott (snuismer@uidaho.edu)" <snuismer@uidaho.edu>

ULodz Poland Biodiversity

Post-doc Position in the project: BIODiversity PATternS and Scale: the case of peracarid Crustacea from south-eastern Australia (BIOPASS)

A postdoctoral position is available in the Marine Biology Research group at Faculty of Biology and Environmental Protection, University of Lodz (Poland).

Project: The main objective of the project addresses the lack of fundamental knowledge about biological diversity patterns in the benthic marine ecosystems off the south-eastern Australian coast. This project is an interactive approach that focuses on identification and assessing local diversity of peracarids (Tanaidacea and Isopoda) from SE Australia to point the environmental factors shaping the diversity over latitudinal and bathymetric gradients.

The project is held in University of Lodz (Poland) and forms a close collaboration with the University of Valencia (Spain) and Melbourne Museum (Australia).

Candidate: The postdoc is expected to apply a variety of methods for species delimitation (genetic/ genomic)

and testing connectivity among populations of several hundred individuals of the peracarids crustaceans from SE Australia, NW and Central Pacific, N Atlantic. The obtained data are supposed to be interpret against taxonomical finding (cooperation with taxonomists) to draw the general model of distribution (cooperation with ecologists). Finally, the genetic results will be employed to investigate phylogeny and phylogeography of most diverse taxa (family/genera).

We seek enthusiastic candidate with good communication skills, experience in genetic, systematic and phylogenetics. The candidate is expected to work both independently and as part of a large research team, and may supervise technical staff and students.

The candidate should have: Good interpersonal skills
Good written and oral communication skills
Experience in wet-lab molecular biology (e.g. DNA/RNA extraction, PCR)
Experience in generating transcriptomic/genomic data (e.g. RNAseq, NGS library preparation)
Minimum PhD in biology genetics or ecology obtained in 2014 (or latter).

The position is fully-funded. It will be initially for 1.5 years, but funding available to extend it further.

If you would like to discuss the project further, please feel free to contact with prof. Magda Blazewicz (magdalena.blazewicz@biol.uni.lodz.pl). To apply, please send a CV, and cover letter stating qualifications, previous work and motivation for the contact as above.

Prof. Magdalena Blazewicz Editor Polish Polar Research Department of Invertebrate Zoology and Hydrobiology Faculty of Biology and Environmental Protection University of Lodz ul. Banacha 12/16 90-237 Lodz
T: 42635 4297 E:magdalena.blazewicz @biol.uni.lodz.pl

Magdalena Blazewicz
<magdalena.blazewicz@biol.uni.lodz.pl>

UManchester Symbiosis Evolution

Postdoctoral Research Associate in Evolutionary Biology, University of Manchester, UK

An exciting opportunity to join a diverse research group working in microbial evolution led by Professor Michael Brockhurst. The successful candidate will be part of an interdisciplinary team of researchers investigating the evolution of symbiosis.

The project, which is funded by the Natural Environ-

ment Research Council UK, explores the molecular mechanisms underlying evolutionary transitions from free-living to symbiosis using the Paramecium-Chlorella microbial symbiosis. Using a powerful combination of comparative genomics, metabolomics, and laboratory experimental evolution we will reveal the role of fitness trade-offs in the evolution of symbiosis.

The main responsibilities of this role include: bioinformatic analyses of whole genome sequence and metabolomic datasets (including both population genetic and phylogenetic analyses), design and supervision of laboratory experiments, collecting and managing multi-omics and experimental data, statistical analysis and data visualisation, and the dissemination of the findings through peer-reviewed publications and conference presentations. You will collaborate closely with the other project researchers and the investigators to deliver the research.

The candidate will have a PhD or equivalent in evolutionary biology or genetics, extensive knowledge of evolutionary biology, and excellent technical skills in bioinformatics. Candidates with training in population genetics and / or evolutionary genomics are strongly encouraged to apply.

Job reference: BMH-016397 Location: Oxford Road, Manchester Closing date (DD/MM/YYYY): 18/03/2021 Salary: 32,816 to 33,797 per annum depending on relevant experience Employment type: Fixed Term Faculty/Organisation: Biology, Medicine & Health School/Directorate: Evolution & Genomic Sciences Hours per week: Full time Contract Duration: Fixed term from 3 May 2021 until 2 May 2024

Enquiries about the vacancy, shortlisting and interviews: Name: Prof. Michael Brockhurst Email: michael.brockhurst@manchester.ac.uk

General enquiries: Email: hrsservices@manchester.ac.uk

<https://www.jobs.manchester.ac.uk/-displayjob.aspx?jobid=19792> Michael Brockhurst <michael.brockhurst@manchester.ac.uk>

UMaryland Disease Evolution

The Bruns lab at the University of Maryland, College Park invites applications for a postdoctoral researcher to develop evolutionary models of correlated disease resistance to multiple pathogens. Plant and animal species show substantial resistance variation to pathogens that

a species does not normally encounter in nature. This resistance is often correlated, either positively or negatively, with resistance to endemic pathogens that are more frequently encountered. How do these correlations evolve? And what are the consequences of resistance correlations for invasion by a foreign pathogen? The postdoc will work to develop general theoretical models that examine the co-evolutionary processes that give rise to resistance correlations between endemic and foreign pathogens. The project is in collaboration with Michael Hood's lab at Amherst college and Janis Antonovics at University of Virginia. The theoretical models developed as part of the project at Maryland will complement empirical research into resistance correlations to anther-smut disease in the wild plant *Silene vulgaris*. The postdoc would have the opportunity to travel between labs to collaborate with a growing network of anther-smut biologists as well as to participate in field work in the western Italian Alps.

Ideal candidates would have a background in quantitative biology with a preference for experience in evolutionary biology, population genetics, or disease ecology. This is a two-year, funded appointment, with preference for a spring 2021 start date.

***To apply*:** To apply please upload a cover letter, CV, contact for 3 references to: <https://ejobs.umd.edu/postings/80175>. Or you can directly email me at: ebruns@umd.edu

– Emily (Emme) Bruns Assistant Professor of Biology University of Maryland College Park, MD 20741 (301) 405-7684 ebruns@umd.edu <http://biology.umd.edu/emily-bruns.html> “ebruns@umd.edu” <ebruns@umd.edu>

UMichigan YeastEvolution

Postdoctoral Position in Experimental Yeast Evolutionary Genomics at University of Michigan

A postdoctoral position is available in the laboratory of Jianzhi “George” Zhang at University of Michigan, Ann Arbor, Michigan. Ideal candidates will use the budding yeast *Saccharomyces cerevisiae* and its relatives as model organisms to study evolutionary processes. Potential topics include but are not limited to (1) evolution of gene expression at the levels of transcription and translation, (2) fitness landscapes across environments (including topics such as epistasis, pleiotropy, and plasticity), and (3) mechanisms of adaptation probed

by experimental evolution. The position requires a motivated individual with an interest in evolutionary biology and experience in molecular genetics or genomics. Prior training in yeast genetics will be a plus. For further information about the Zhang lab, see <http://www.umich.edu/~zhanglab/>. Applicants should email a short statement of research interests, CV, and contact information of three references to jianzhi@umich.edu.

“jianzhi@umich.edu” <jianzhi@umich.edu>

UNorthCarolina ChapelHill EvolutionGrasses

Post-doctoral associate at UNC-CH in grass evolutionary genomics.

Drs. Alan and Corbin Jones are seeking qualified applicants for a talented postdoctoral associate who will lead a project investigating the intersection of genome X environment as part of an interdisciplinary team at the University of North Carolina at Chapel Hill. The project focuses on the evolution of flickering light sensing in grasses of Ecuador. The specific job duties are the following: manage genome sequencing queues, assemble genomes, annotate genomes, molecular and comparative evolutionary analysis, manage project, and establish collaborators. This is a great opportunity for those with some background in this area who want to build their skills and expertise.

Applicants must have a PhD and some experience or training with R or Python, ideally experience handling genomic data through assembly and gene annotation. Experience with phylogenomics is a plus. A strong background in evolutionary biology, evolutionary ecology, population genetics, comparative genomics is an asset. Candidates without relevant background will be ignored.

The successful applicant will be in charge of all aspects of the project and will interact with a large team, including a collaborative team at the University of Illinois that will lead translational biology aspects of this work and a field and ecological team at Universidad San Francisco de Quito.

We have funding for this position, but strongly prefer applicants who are able to seek additional funding or are strong candidates for this NSF program (Theme 2): <https://www.nsf.gov/pubs/2020/nsf20602/-nsf20602.htm> or are competitive for NSERC and other grants.

The posting is here: <https://unc.peopleadmin.com/postings/188561> Feel free to contact us if you have questions. cdjones@email.unc.edu

Corbin D. Jones, Ph.D. Professor Department of Biology iBGS 'V Integrative Program for Biological & Genome Sciences Department of Genetics iGC & BARC Campus Box 3280, Genome Science Building UNC-Chapel Hill Chapel Hill, NC 27599-3280

“Jones, Corbin D” <cdjones@email.unc.edu>

UParma 1yr HumanPopulationGenomics

1 year Post Doctoral Position :University of Parma, Human Population Genomics

One year Post Doctoral Position (Assegno di Ricerca) in human population genomics at the Department of Chemistry, Life Sciences and Environmental Sustainability (SCVSA), University of Parma (Italy) (<https://scvsa.unipr.it/en>), as part of the Molecular Anthropology Laboratory coordinated by Prof. Cristian Capelli.

This position will take the lead on the analysis of genomic and demographic data to reconstruct micro-evolutionary dynamics in human populations. The Post Doctoral investigator will apply bioinformatics and biostatistics tools to analyse metagenomic data generated from saliva samples of human groups. The aim is to reconstruct the dynamics and the impact of migration and gene-flow in shaping genetic variation across groups within populations. Our objective is to bring together the demographic data collected via interviews of participants and the genetic variation of people and associated microbes to develop an integrated model describing how behaviour and spatial proximity shape genetic variation.

The successful applicant will be already skilled and have solid experience in all aspects of handling human genomic data in the context of population genomics and use of high-performance computational clusters. The individual will process and analyse data already available, write resulting manuscripts and contribute to the supervision of graduate and undergraduate students. Applicants will be expected to have published work relevant for the project.

The position is expected to start in September 2021. Interested candidate fulfilling the criteria are invited to contact Prof. Capelli to discuss the project (email: cristian.capelli@unipr.it)

This position is part of the special ministerial funding granted by the Italian Ministry of Education, University and Research following the recognition of SCVSA as a Department of Excellence (2018-2022).

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

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

Cristian CAPELLI <cristian.capelli@unipr.it>

USouthernCalifornia MarineMicrobialEvol

A postdoctoral position in marine microbial ecology is immediately available (February 2021) in Dr. Jed Fuhrman’s research group at USC. The overall focus of the research, funded by the CBIOMES project of the Simons Foundation, is a better understanding how the interactions between bacteria, archaea, viruses, and protists regulate the distributions and activities of marine planktonic microorganisms in the global ocean. CBIOMES is ultimately a global modeling effort, and the Fuhrman Lab contributes by studying the biogeography, genomics, growth, loss, and activities of marine microbial communities, with a focus on material most informative to models. Candidates should have a PhD degree and significant experience (and publications) in microbial ecology, including bioinformatics with ‘omics data, involving mixed natural communities of microor-

ganisms. Experience with hands-on molecular biological analysis of aquatic samples, ideally including viruses, is an advantage. Work involves analysis of new and existing very large sequence datasets (metagenomes, metatranscriptomes, 16S, 18S, other marker genes) from prior lab experiments and oceanographic measurements. Much of the work involves our San Pedro Ocean Time Series (SPOT) and vicinity. There is frequent access to fresh open-water samples via the USC boat that travels to our well-equipped marine laboratory on Santa Catalina Island. The ideal candidate has strong quantitative skills and broad microbial ecological understanding, with experience handling very large 'omics datasets. Experience in both laboratory and field based aquatic research is strongly preferred. Strong written and verbal communication skills, as well as the ability to work well in a team including modelers, are required. Post-docs are well paid and have a benefit package including health insurance. We are committed to Diversity, Equity, and Inclusion. Current funding for this position goes through late summer 2022 and there is a good expectation it will be renewed. Applicants should send their CV, a letter of intent describing their motivation, qualifications, skills, and experience relevant to this position, and contact information (including telephone numbers) for three references. *Candidates may contact Dr. Fuhrman directly at fuhrman@usc.edu.*

– *Jake L. Weissman, Ph.D* *pronouns: he/him/his*
 Simons Foundation Postdoctoral Fellow in Marine Microbial Ecology jakeweis@usc.edu
<https://jlw-ecoevo.github.io> “jakeweis@usc.edu”
 <jakeweis@usc.edu>

UTours France InsectSocialEvolutionGutMicrobes

We invite applications for a 3-year postdoctoral position at the Research Institute on Insects Biology (IRBI) located at the University of Tours, France, to work on THE ROLE OF GUT MICROBIOTA IN THE EARLY EVOLUTION OF INSECTS' SOCIAL LIFE

CONTEXT. A long-standing problem in biology is to understand why and how animal social life has emerged from a solitary state. We aim to address these questions by testing whether social life may not only emerge due to its benefits for the group members but also due to its benefits for their gut microbiota. The applicant will design and conduct a series of standardized experi-

ments with the European earwig *Forficula auricularia* to identify which gut microbes are associated with host sociality, test how these microbes can benefit from and increase the sociality of their hosts, and shed light on the mechanisms allowing these gut microbes to modify hosts sociality. The project mostly relies on metabarcoding, behavioural experiments and/or RNA-seq analyses (depending on candidate interests).

REQUIREMENTS. The position requires a PhD in biology or microbiology (or a related field) completed at the beginning of the contract. The successful candidate will have experience in developing and implementing DNA barcode approaches, ideally on insects' gut microbiota, as well as good practice in molecular biology techniques and analyses. Strong interests in evolutionary biology and social evolution, as well as experience in conducting behavioural experiments are advantageous, but not required. The position is fully funded by the ANR (project MicroSoc). The contracts may last up to 3 years (for candidates with less than 6 months of postdoc experience at the beginning of the contract) and the preferred starting date is October 2021 (negotiable). The position is an excellent opportunity for candidates who plan to defend their PhD before January 2022. All nationalities and genders are encouraged to apply.

LOCATION & HOST LAB. The city of Tours is a beautiful historic place located near Paris and the Loire Valley, and hosts many students and a rich social and cultural life. The University of Tours includes many excellent scientific institutions, among which the Institut de Recherche sur la Biologie de l'Insecte (IRBI). This institute is dedicated to the analysis of interactions between insects and their biotic and abiotic environment. The IRBI offers an international, dynamic and interactive scientific environment based on 27 permanent researchers, numerous post-doctoral researchers and PhD students for a total staff of 70 people. Following recent investments in genomics, the IRBI is equipped with a state-of-the-art molecular biology platform with a wide range of equipment, including a DNA extractor robot and a bioinformatics server facilitating the molecular analysis of insects. The person recruited will work under the direction of Dr Joël Meunier. More information on his research and publications can be found on <https://joelmeunier.wixsite.com/researchpage>. APPLICATION. The application must be submitted via the official application webpage, which will be available on 27 April 2021 on the webpage <https://joelmeunier.wixsite.com/researchpage/openpostdoc>. The deadline for application is Monday 17 May 2021.— Applications must include 3 documents: (1) a Curriculum Vitae (2) a covering letter detailing, in particular, what you think you can bring to this project (max. 2 pages) (3) a pdf including a short

summary of the PhD thesis and past or ongoing postdoc projects, one or two publications in international peer-reviewed journals of which you are one of the authors, and the names and e-mail addresses of three referees.

Candidates are encouraged to contact Joël Meunier (joel[dot]meunier[at]univ-tours[dot]fr) if they have any questions regarding the project and the application system.

Joël Meunier, PhD, HDR

CNRS Researcher

Institut de Recherche sur la Biologie de l'Insecte (IRBI) - UMR 7261 Université de Tours UFR des Sciences et Techniques Avenue Monge, Parc Grandmont 37200 Tours, FRANCE

Office: +33 (0)2 47 36 73 93 <https://irbi.univ-tours.fr/-recherche/> Joël Meunier <joel.meunier@univ-tours.fr>

UVirginia Biology 2

****ADDITIONAL TRACK ADDED TO PREVIOUS POSTING**** The Department of Biology at the University of Virginia is pleased to announce that an additional track has opened up for the Rising Scholars Postdoctoral Fellowship Program. We seek to recruit a cluster of research scholars who are interested in broad questions in biology that fit within the expertise that is represented in our Department. We seek Fellows who aspire to a tenure-track faculty position and who would benefit from our strong research programs and the mentored professional development opportunities provided through our NRT-EXPAND Program.

These positions are designed to support underrepresented scholars and are part of an ongoing commitment to diversify our programs, the professoriate and the research workforce, led by the College and Graduate School of Arts & Sciences at UVA. Interested individuals should contact potential research mentors in the Biology Department <https://bio.as.virginia.edu/>; for more information on EXPAND see <https://expand.virginia.edu/>; and for questions contact Deborah Roach, Chair of Biology droach@virginia.edu. Applications may be initiated at <https://graduate.as.virginia.edu/rising-scholars> and review will begin April 12, 2021.

lg8b@virginia.edu

UVirginia PhenotypeEvolution

The Department of Biology and the NSF NRT Expand Program at the University of Virginia is soliciting applications to the Rising Scholars Postdoctoral Fellowship Program. We seek to recruit a cluster of interdisciplinary life science scholars who are interested in research that will foster a vertical reintegration of the phenotype, such that cellular, genomic, organismal, population, evolutionary, community, and ecosystem level approaches are brought to bear on understanding the expression of traits, i.e. phenotypes. Scholars working on any phenotype, from disease, to behavior, to response to changing climates are encouraged to apply. Postdoctoral Fellows will be co-advised by two mentors that offer strengths in different disciplines within the program. We seek Fellows who aspire to a tenure-track faculty position and who would benefit from the mentored professional development opportunity provided by our EXPAND Program.

These positions are designed to support underrepresented scholars and are part of an ongoing commitment to diversify our programs, the professoriate and the research workforce, led by the College and Graduate School of Arts & Sciences at UVA. Interested individuals should contact potential research mentors in the Biology Department <https://bio.as.virginia.edu/>; for more information on EXPAND see <https://expand.virginia.edu/>; and for questions contact Deborah Roach, Chair of Biology mailto: droach@virginia.edu. Applications may be initiated at <https://graduate.as.virginia.edu/rising-scholars> and review will begin April 12, 2021.

– Laura F. Galloway Commonwealth Professor of Biology
“Galloway, Laura F (lg8b)” <lg8b@virginia.edu>

UWisconsin Madison EvolutionaryComparativeGenomics

Postdoctoral Position in Evolutionary Population and Comparative Genomics

A postdoctoral position is available to work on an NSF-funded project in the laboratory of Professor Carol Lee,

in the Department of Integrative Biology at the University of Wisconsin, Madison.

This project focuses on Rapid Evolutionary Responses to Global Change using the copepod *Eurytemora affinis* species complex as a model system. With changes in global climate, coastal high latitude waters are experiencing rapid declines in salinity, due to increases in ice melt and precipitation. We have found evolutionary shifts in ion transport function, genome-wide gene expression, and population genomic signatures of selection associated with changes in salinity (see pubs in the links below). This postdoc project will entail conducting comparative genomic and population genomic analyses associated with temperature and salinity change in wild and laboratory populations.

The *E. affinis* complex presents an exemplary model, with its short generation time (20d), ease of culturing large numbers (thousands per population), and ability to generate inbred lines. The Lee Lab is generating multiple full reference genomes (PacBio and Oxford Nanopore) from the *E. affinis* species complex to the chromosome level. Additionally, the multiple independent environmental clines have enabled us to observe exceptional cases of parallel polygenetic adaptation (to the level of SNPs).

The ideal candidate should hold a Ph.D. and have publications in peer-reviewed journals. A background in evolutionary genetics is required, especially in population genetics/genomics or comparative genomics. Relevant areas of expertise include molecular evolutionary genetics, computational and programming skills, and statistics.

Review of applications will begin immediately and will continue until the position is filled. The appointment could persist for up to three years. Interested candidates should email their application to Prof. Carol Lee (carollee@wisc.edu), including: (1) a CV, (2) a cover letter describing qualifications and relevant experience, (3) a list of references (recommenders), and (4) samples of first authored publications. Enquiries regarding this position are most welcome.

The University of Wisconsin-Madison offers a large and intellectually vibrant community of evolutionary/population biologists, providing ample opportunities for interaction with excellent scientists (see <https://evolution.wisc.edu/people/faculty/>) and first rate departments of Statistics and Biostatistics, computational facilities, and a Biotech Center. Madison is a culturally-rich community, in relative close proximity to Chicago.

Representative publications: [https://carollee.labs.wisc.edu/pdfs/-](https://carollee.labs.wisc.edu/pdfs/-Stern&Lee_NatureE&E.2020suppfiles.pdf)

[Stern&Lee_NatureE&E.2020suppfiles.pdf](https://carollee.labs.wisc.edu/pdfs/PosaviEtal.2020.pdf) <https://carollee.labs.wisc.edu/pdfs/PosaviEtal.2020.pdf>
https://carollee.labs.wisc.edu/pdfs/Eyun_et al2017.pdf
https://carollee.labs.wisc.edu/pdfs/Posavi_et al2014.pdf

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Carol Eunmi Lee Professor Department of Integrative Biology University of Wisconsin, Madison Madison, WI 53706 carollee@wisc.edu

Carol Eunmi LEE <carollee@wisc.edu>

WashingtonStateU EvolutionaryGenomics

POSTDOCTORAL RESEARCHER

Washington State University

School of Biological Sciences

We are seeking a postdoctoral researcher to work on evolutionary genomics/ modeling of Tasmanian devils and Tasmanian devil facial tumor disease, a transmissible cancer. This NSF-funded international collaboration builds on over 20 years of mark-recapture data tracking the spread of the unique infectious tumor across Tasmania and consequent endangerment of the iconic Tasmanian devil. As the top predator in Tasmania, devil declines altered the native mammal community via trophic cascades. This project bridges ecology and evolution by combining ecological and evolutionary modeling, field ecology and evolutionary genomics to predict future community dynamics. The successful applicant will have an unprecedented opportunity to analyze tens of thousands of mark-recapture records, thousands of devil genotypes and hundreds of tumor samples taken both before and after epizootics to: model coevolutionary dynamics, test for selection throughout both genomes, predict phenotypic evolution of Tasmanian devils aided by pedigree reconstruction, and conduct functional genomics studies aided by a CRISPR-Cas9 system. The position is centered in the lab of Dr. Andrew Storfer (<https://storfer-lab.org/>) at Washington State University, with the possibility for scholarly exchanges with University of South Florida, University of Tasmania and Griffith University in Australia. WSU has state-of-the-art facilities, including the WSU Genomics Core (<https://labs.wsu.edu/genomicscore/>) and the WSU Kamiak High Performance Computing cluster (<https://hpc.wsu.edu/>).

Review of applications will begin on April 1, 2021 and continue until the position is filled. A Ph.D. in Biology or a related discipline, combined with genomics and bioinformatics experience is required. A background in evolutionary modeling is strongly preferred. Desired qualities also include experience in population genomics, infectious disease evolution, and/or cancer genomics. Start date is negotiable, but is anticipated to be between May and September, 2021. Salary and benefits are competitive. Position is for 1 year, with continuation for additional year(s) pending satisfactory progress.

To apply, please send in pdf format a CV, and names, addresses and email addresses of 3 references, a research statement, and up to 3 representative reprints via email to: Andrew Storfer (astorfer@wsu.edu). Inquiries prior to application are also encouraged.

WSU is an Equal Opportunity/Affirmative Action/ADA educator and employer.

Andrew Storfer, PhD Professor School of Biological Sciences Washington State University Pullman, WA 99164-4236 (509) 335-7922 astorfer@wsu.edu www.storfer-lab.org "Storfer, Andrew" <astorfer@wsu.edu>

Workshops Courses

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Online AnalysisTransposableElements Jun14-18

Dear all,

registrations are now open for the 2nd edition of the ONLINE course "Analysis of Transposable elements"

Dates: 14th-18th June

Course website: (<https://www.physalia-courses.org/-courses-workshops/course24/>)

Instructor: Dr. Alexander Suh (University of East Anglia, UK)

In this course we will teach Transposable elements (TEs) biology, computational analyses of TEs in genome assemblies (RepeatModeler, RepeatMasker) and raw read data (dnaPipeTE), and manual analyses of TEs (consensus curation, classification).

At the end of this course, attendants should be able to conduct computational analyses of TEs, interpret the results in the light of TE biology, and improve TE annotations through manual curation. To achieve this, the first three days of the course will provide lectures and practicals on all these topics. The last two days of the course consist entirely of supervised individual practicals to further refine the attendants' skills in com-

putational and manual analyses of TEs, either in their own data or in a course-specific collaborative project.

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>

Online Bayesian Phylogenetics Using RevBayes Apr13-Jun7

We are offering a free, virtual short course on Bayesian phylogenetic inference using RevBayes.

This course will be held from mid-April to early June of 2021 (exact dates are tentative), with particular focus on (1) tree inference from molecular data, (2) analyses combining fossil and extant taxa, and (3) evaluating MCMC performance, with advanced topics including assessing model adequacy and macroevolutionary analyses. Additional topics may be added depending on the interests of the selected participants. Participants in the course will interact with the instructors and one another (via Slack and Zoom) as they complete tutorials (detailed lessons on different RevBayes analyses with pre-recorded video guides). Additionally, we will hold 3 or more interactive sessions to discuss and review tutorials and discuss practical applications of RevBayes. At the end of the course, each participant will be paired with one of the instructors in a 1-on-1 meeting where they can talk about applying the methods available in RevBayes to their own data. The dates for the interactive sessions are currently tentative and may be adjusted depending on the schedules of the participants and instructors.

We are hoping to identify up to 20 participants for this online course and targeting those residing in Asia and Pacific time zones (UTC+4 to UTC+14, including UTC-10 and UTC-11). Participants will not be charged for the course, but we will request that they commit to

completing the tutorials and attending a majority of interactive sessions.

For more details about the 2021 Stay-at-Home RevBayes Workshop and a link to the application form, please go to: <https://revbayes.github.io/workshops/online2021.html> Applications are due by March 29, 2021.

trayc7@gmail.com

Online Demographic Inference Jul12-16

Dear all,

registrations are now open for the ONLINE Physalia course “Inferring demographic history from population genomics data”: (<https://www.physalia-courses.org/courses-workshops/demoinference/>)

Dates: 12th-16th July

Instructor: Dr Vitor C Sousa (Centre for Ecology, Evolution and Environmental changes, Department of Animal Biology, Faculdade de Ciências da Universidade de Lisboa, University of Lisbon, Portugal)

Teaching Assistants: 1) Dr Bárbara Parreira (Centre for Ecology, Evolution and Environmental changes, Faculdade de Ciências da Universidade de Lisboa, University of Lisbon, Portugal)

2) Dr Isabel Alves (INSERM/CNRS UMR-1087, University of Nantes, France)

This course will provide a comprehensive introduction to population genomics data and methods to model and infer the demographic history of populations/species. It will focus on methods based on single nucleotide polymorphisms (SNPs) and the site frequency spectrum (SFS), which can be obtained from whole genome or reduced representation (e.g., GBS, RAD) sequencing data from model and non-model species.

The course will take participants through all the steps required for preparing the data, performing and interpreting results from demographic history inference. Specifically, it will go from generating the SFS from VCF files to formalize hypotheses in terms of demographic models with parameters of interest (e.g., past effective sizes, migration rates and times of split).

Participants will learn how to compare alternative models (model choice) and estimate parameters, as well

as simulate data under different demographic history scenarios. By combining lectures addressing key concepts in population genomics with hands-on exercises, participants will learn key approaches used in population genomics that can be applied to several species and types of data, including low coverage and ancient DNA. After completing the course, participants should be able to begin using NGS data to model and infer the demographic history in their study system of choice.

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
info@physalia-courses.org mobile: +49 17645230846 Follow us on (<https://twitter.com/Physacourses>)

“info@physalia-courses.org” <info@physalia-courses.org>

Online DiversityInMathematicalBiol Mar26

Dear All,

We are excited to announce an SMB (<https://www.smb.org/>) workshop in Diversity, Equity and Inclusion in Mathematical Biology *THIS FRIDAY* March 26 from 9:00am - 2:30pm Pacific. This workshop is being held in connection and in preparation for the SMB 2021 Annual Meeting (<https://www.smb2021.org/>).

We invite the community to join us as we engage in a critical reflection of our practices in order to cultivate a culture in which all voices are heard, valued and validated. Together, by sharing stories and identifying concrete actions, we can make space for everyone.

We encourage you to give us your input by completing the questionnaire on our website:

Website: <https://icqmb.ucr.edu/smb-diversity-workshop-2021> *Registration Page:* https://ucmerced.zoom.us/webinar/register/-WN_crPmkNyNTSu_YQDESIUIfQ Best,

Suzanne

– Suzanne Sindi Interim Co-Director of Cyberinfrastruc-

ture & Research Technologies Associate Professor of Applied Mathematics University of California, Merced ssindi@ucmerced.edu <http://www.SindiLab.com> 209-228-4224 she/her/hers

– Miriam Barlow University of California, Merced 209.228.4174 miriam.barlow@gmail.com

Miriam Barlow <miriam.barlow@gmail.com>

Online EnvironmentalMetagenomics Apr19-23

Dear all,

last seats available on the Physalia course on Environmental Metagenomics, which will take place ONLINE from the 19th to the 23rd of April: (<https://www.physalia-courses.org/courses-workshops/-environmental-metagenomics/>)

Instructors: Dr. Antti Karkman and Dr. Igor S Pessi (University of Helsinki, Finland).

In this course, participants will learn state-of-the-art bioinformatic approaches to analyse metagenomic data. We will cover both read- and assembly-based methods, focusing on the strength of each of these methods depending on the research question. We will use data from both short- (e.g. Illumina) and long-read (e.g. Nanopore) sequencing platforms, as it improves dramatically metagenome-assembled genomes (MAG) assembling and binning compared to short-read-only methods.

Learning Outcomes

By completing this course, you will:

- Understand the basics of metagenomic sequencing and bioinformatic approaches to the analysis of metagenomic data
- Be able to plan and execute a metagenomic sequencing project
- Have an up-to-date knowledge on the bioinformatic tools and best practices for the analysis of metagenomes
- Be able to choose the right tools and approaches to answer your specific research question
- Have confidence to learn new methods needed to answer your research question

Program: (<https://www.physalia-courses.org/courses->

[workshops/course55/curriculum55/](https://www.physalia-courses.org/courses-workshops/course55/curriculum55/))

The full list of our online courses can be found here: ((<https://www.physalia-courses.org/courses-workshops/>))

All the best,

Carlo

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www.physalia-courses.org/courses-workshops)

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

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courses.org>

Online Landscape Genomics Jun21-25

Dear all,

the 5th edition of the Landscape Genomics course will be delivered remotely from the 21st to the 25th of June. This course is aimed at all biologists, ecologists, geneticists, veterinarians that want to implement the landscape genomics approach in their own studies of evolutionary biology and conservation.

Instructors: Dr Stéphane Joost and Dr Elia Vajana (EPFL, Switzerland).

The course will provide an overview of the type of dataset that can be used for a landscape genomics analysis. Firstly, students will learn how to obtain environmental data from publicly available databases, how to process it with Geographic Information Systems (GIS) and how to use the latter to produce indicators able to describe the characteristics of the landscape. Next, the course will discuss the different approaches to obtain genetic data and subsequently show how to study genetic variation and population structure across space in the R environment. Students will be given an overview of the different statistical approaches to study local adaptation, and will be trained in using two of them, Sambada and LFMM. The course will also cover the critical task of the interpretation and validation of the results. Finally, the workshop will consider the crucial aspects and good habits to account for when planning a landscape genomics experiment (e.g. sampling design).

Course website: (<https://www.physalia-courses.org/courses-workshops/course17/>)

Full list of our courses and Workshops: ([https://](https://www.physalia-courses.org/courses-workshops/)

Online Modelling Evolution Using mvMORPH Jun7-11

Dear colleagues,

Registration is open for Transmitting Science course “Modelling and Analysing Multivariate Traits Evolution using mvMORPH”, June 7th-11th, 2021.

Online live sessions from Monday to Friday from 14:00 to 16:30 and 17:00 to 19:00 (GMT+2, Madrid time zone).

Instructors: Dr. Julien Clavel (NNRS, France)

Course overview

In this workshop students will be introduced to multivariate phylogenetic comparative methods with the mvMORPH R package.

The mvMORPH package contains tools for modelling the evolution of correlated continuous traits (e.g. morphometric measurement, geometric morphometric datasets, life history traits, gene expression data, etc.) on phylogenetic trees [with either fossil species, extant species or both] as well as statistical tools such as multivariate generalized least squares (GLS) linear models -e.g. multivariate regression, MANOVA, MANCOVA - for studying comparative datasets.

In this course, students will be first introduced to some theory with illustrative examples (both from simulated data as well as students’ own datasets) and will learn how to interpret the models, their parameters, as well as how to assess their reliability.

For more information, please check the course webpage: <https://www.transmittingscience.com/courses/-evolution/modelling-and-analysing-multivariate->

[traits-evolution-using-mvmorph/courses@transmittingscience.com](https://www.transmittingscience.com/courses@transmittingscience.com) or write to [<soledad.esteban@transmittingscience.com>](mailto:soledad.esteban@transmittingscience.com)

With best regards

Sole

– Soledad De Esteban-Trivigno, PhD. Scientific Director
www.transmittingscience.com [1]

Twitter: @soledeesteban Instagram: @soledaddeesteban Researchgate: https://www.researchgate.net/profile/Soledad_De_Esteban-Trivigno ORCID: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or <http://transmittingscience.com/additional-terms>. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www.aepd.es.

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Links:

[1] <http://www.transmittingscience.com>
Soledad De Esteban Trivigno

Online StatGenetics ScholarshipFundsRemain

Registration for the (virtual) 26th Summer Institute in Statistical Genetics is now open. Details are available at si.biostat.washington.edu/suminst/sisg Scholarship applications already submitted have been processed. New applications will be processed as they are received while funds remain, and can be submitted at

si.biostat.washington.edu/suminst/sisg/scholarships

with best wishes,

Bruce bsweir@uw.edu

Bruce S Weir <bsweir@uw.edu>

Online TamingTheBEAST June07-11

Dear colleagues,

A week ago we announced the opening of registration for the ONLINE edition of our Bayesian phylogenetics and phylodynamics summer school, “Taming the BEAST”.

This is a quick follow-up message to announce that we are able to provide a small number of fee-exempt places at the workshop. These places are intended to accommodate people who cannot afford the 150 CHF registration fee.

For more information on the workshop, including instructions for applying for a fee exemption, please visit the summer school website: <https://www.bsse.ethz.ch/-cevo/taming-the-beast/overview-2021.html> For information on previous workshop programs, tutorials etc. please visit <https://taming-the-beast.org>. We hope to see you there, the Taming the BEAST organising team

“timothy.vaughan@bsse.ethz.ch”

<timothy.vaughan@bsse.ethz.ch>

**Online
TransposableElementDetection
Jun14-18**

Dear colleagues,

Registration is open for Transmitting Science Online course “Course: Introduction to transposable element detection using sequencing data, June 14th-18th, 2021.

Schedule: Online live sessions from Monday to Friday from 13:00 to 17:00 (GMT+2, Madrid time zone), plus 5 hours of participants working on their own, with tutored exercises.

Instructors: Dr. Anna-Sophie Fiston-Lavier (Institut des Sciences de l’Evolution de Montpellier, France) and Dr. Emmanuelle Lerat (Université Lyon 1, France)

For more information, please check the course webpage:

<https://www.transmittingscience.com/courses/-genetics-and-genomics/introduction-to-transposable-element-detection-using-sequencing-data/> or write to courses@transmittingscience.com

Course overview

Transposable elements (TEs) can be major components of eukaryotic genomes. Such repeated sequences, which can make up very large proportions like about 50% of mammalian genomes to more than 80% in the genomes of some plants, can promote various types of mutations, from gene interruption and expression alteration to large-scale chromosomal rearrangements. They can also promote the formation of new genes. Despite their deleterious effects, TEs are currently considered as major actors in genome evolution due the genetic and epigenetic diversity they can generate.

Even if they have a fundamental biological role, detection and analysis of TE sequences are still technologically challenging. The length and quality of sequenced reads make their detection and annotation difficult (40% detection error). Moreover, the presence of TEs in a genome can also lead to important assembly errors due to rearrangement and the merge of repeats, and to difficulties in the identification of splicing events and in the estimation of gene expression in transcriptomic analyses. It is thus important to be able to identify these sequences in genomic and transcriptomic data.

Since several years, a large number of bioinformatic tools

have been developed allowing a better identification of TEs in genomes. New tools are released regularly to follow the progress of sequencing technologies but also to answer particular biological questions allowing to go from the TE annotation in assembled or unassembled genomes, to insertion polymorphism detection in natural populations. The result is a particularly large choice for users leading to difficulties in the determination of the best tool(s) to use according to the case.

In this course, we aim at proposing an introduction of selected bioinformatic tools for the detection and analysis of TEs in genomic data (RepeatMasker, DnaPipeTE, T-lex).

With best regards

Sole

– Soledad De Esteban-Trivigno, PhD. Scientific Director
www.transmittingscience.com [1]

Twitter: @soledeesteban Instagram: @soledaddeesteban Researchgate: https://www.researchgate.net/profile/Soledad_De_Esteban-Trivigno ORCID: <https://orcid.org/0000-0002-2049-0890> Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or <http://transmittingscience.com/additional-terms>. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www.aepd.es. Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not

— / —

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

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.