
E v o l D i r

May 1, 2020

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.



Foreword	1
Conferences	2
GradStudentPositions	7
Jobs	32
Other	45
PostDocs	52
WorkshopsCourses	68
Instructions	73
Afterword	74

Conferences

Online Bioinformatics Jul17-26	2	Online ISMB EvolCompGen Jul13-16 CallAbstracts	5
Online Demographics	3	Online ISMB EvolCompGen Jul13-16 LastCall	6
Online EvolutionEcologySeminarSeries Apr15	4	Snowbird Utah GenesAsEnvironment Nov15-18	6
Online EvolutionHIV May11-13	5		

Online Bioinformatics Jul17-26

2020 Bioinformatics Community Conference (BCC2020) Online, July 17-26 <https://bcc2020.github.io/> The 2020 Bioinformatics Community Conference (BCC2020) will be online, global, affordable, and accessible to all.

Key Dates: May 8: Deadline for submitting talk/poster abstracts (this will not be extended) June 6: Authors notified about talk/poster acceptance July 10: Early registration ends July 17-19: BCC2020 tutorials July 19-22: BCC2020 main meeting July 22-24, 24-26: CollaborationFest Core and Encore

BCC2020 -> <https://bcc2020.github.io/> BCC2020 is a joint event bringing together the BOSC and Galaxy Communities. If you are working in data intensive life science research then there will be no better event this year to share your work, and to learn from others. BCC2020 will be held July 17-26, and offer 2 days of training, a 3 day meeting, and a 4 day CollaborationFest.

BCC2020 is Online -> <https://bcc2020.github.io/blog/-going-virtual> All BCC2020 events will be held online. Training will be live and interactive. The meeting will feature keynotes, accepted talks, lightning talks, posters, demos, and birds-of-a-feather and other networking opportunities. Talks (with the possible exception of keynotes) will be pre-recorded. Posters, demos, and BoFs will be live and interactive. The CoFest will also be live and interactive.

BOSC is organized by the Open Bioinformatics Foundation (OBF), a non-profit group dedicated to promoting the practice and philosophy of open source software development and open science within the biological research community. Galaxy is an open source data integration and analysis platform for the life sciences that is used, deployed, maintained and extended by a worldwide community of researchers, students, software engineers, and infrastructure providers.

BCC2020 is Global -> <https://bcc2020.github.io/blog/-going-global> BCC2020 events will be held twice: once in the originally scheduled Toronto time zone (BCC West), and then again 12 hours later in the Eastern hemisphere (BCC East). Training will differ between East and West, with enrollment open to all, regardless of where you are. The main conference content will be presented in both East and West. We are striving to have the CoFest run continuously, with participants from every part of the world.

BCC2020 is Affordable -> <https://bcc2020.github.io/-Registration/> We have slashed registration rates for BCC2020, and are offering even larger discounts to participants based in low and lower-middle income countries. Pricing starts at US\$3 per training session, and \$12 for the 3 day meeting. The CoFest is free.

BCC2020 is Accessible Going online and global, combined with the low registration rates make this the most accessible Galaxy and BOSC conference ever. If you work in open source bioinformatics then this is 2020's best opportunity to share your work and learn from others.

Abstracts Due May 8 -> <https://bcc2020.github.io/-submit/> BCC2020 is seeking oral presentations, lighting talks, posters, and demos, from researchers working in bioinformatics, and from all over the world. Abstracts are due May 8 (and that deadline will not be extended). Please submit your work today.

Register Now -> <https://bcc2020.github.io/-Registration/> BCC2020 registration is now open. Registering early saves 50% off of the full rates.

We hope to see you in July at BCC2020, BCC2020 Organizers

Online Demographics

Dear Colleagues,

We resend the announcement for turning the SMTDA2020 International Conference and Demographics2020 Workshop in Barcelona into a web-conference the same dates and with the same program but via the facilities of the virtual event.

It is a really difficult situation, but we urge all of you to keep together via any means and by this virtual SMTDA2020 conference.

We already have done the appropriate provisions for a successful event (see details below). More information in the web at www.smtda.net < <http://www.smtda.net> > .

The deadline for reduced fees and Abstract or Paper submissions is set at April 25, 2020, see at <http://www.smtda.net/registrfeesexcursions.html> and <http://www.smtda.net/abstractsubmission.html> .

Registration fee includes: License for virtual software and training, download and participation in all virtual sessions, e-book of abstracts and e-posters, power points of presentations, full paper publication in proceedings, and considered for the Communications in Statistics Journals or in the ISTE-Wiley book publications or the Springer book series.

We are sorry for the situation in Spain and in other countries in the Globe and we wish strength and good health to all of you and your families and friends.

All the best,

Prof. Christos H Skiadas

Dear Colleague,

We are deeply concerned for the virus development in connection to the conference activities and that the World Health Organization has declared it a global pandemic.

We are quite sensitive to that constraint but equally determined to fight against the difficulties that emerged.

We are in front of the new challenges, a new historical frame, new conditions of life.

Dear colleagues,

In these conditions, and following many requests and after consulting the committee, we have turned the conference into Virtual Conference in order from the one hand to follow the international instructions about the pandemic and the other hand to turn the SMTDA2020 International Conference and Demographics2020 Workshop into a successful virtual international event (www.smtda.net).

So far the basis of the SMTDA and ASMDA Conference series will remain unchanged including the Proceedings and Publications in Books and Journals.

The web interactions, after the appropriate adaptations, will join better the groups of colleagues forming streams and workshops. A new challenge to open the international travel barriers set to stop the coronavirus spread.

While the Conference dates remain unchanged, the early registration deadline extended to 25 April including the corresponding reduced fees for the virtual participation (<http://www.smtda.net/registrfeesexcursions.html>).

If you have already paid for the conference fees, you will be issuing a refund for the difference between the early bird registration and virtual conference fee.

Special technical details and training will be provided to participants before the conference and especially to the Special, Invited Sessions and Workshop organizers and Session Chairs.

Note that the power point of your presentation is important for the Virtual Conference schedule. It should be send to the secretariat for the session/s chair as early as possible at secretariat@smtda.net <<mailto:secretariat@smtda.net>> .

On behalf of the Conference Committee,

Prof. Christos H Skiadas,

Conference Chair

Over the years several Books from leading publishers emerged from the SMTDA and ASMDA Conferences and events.

I am happy to inform you that the basic details of the 2 collective volumes we have edited for iSTE WILEY as

a result of the SMDTA2018 Conference in Chania, are now available online.

Data Analysis and Applications 3, ISBN : 9781786305343, Publication Date : April 2020 <http://www.iste.co.uk/book.php?id=1630>

Data Analysis and Applications 4, ISBN : 9781786306241, Publication Date : April 2020 <http://www.iste.co.uk/book.php?id=1635>

>From ASMDA2019 in Florence, Italy

Demography of Population Health, Aging and Health Expenditures. ISBN : 978-3-030-44695-6 : Vol 50 of The Springer Series on Demographic Methods and Population Analysis, Springer Nature Switzerland AG, 2020 <https://www.springer.com/gp/book/9783030446949>

Note that the SMTDA and ASMDA Conferences started many years earlier and our email lists include old and new addresses.

It is a very important task to update our lists. If you would like to remove your email address from our lists, please click here: [Unsubscribe](#)

— / —

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>

Online EvolutionEcologySeminarSeries Apr15

Dear EvolDir,

We are launching an online seminar series in Evolution and Ecology on Wed 15th April and would like to invite you to join the online community of evolutionary biologists and ecologists, for our upcoming talks.

We are a group of postdocs from the research groups of Alexei Maklakov, Simone Immler and Judith Mank at the University of East Anglia, UK, and the University of British Columbia, Canada.

Now that many departmental seminar talks and conferences have been cancelled or postponed, we believe there is a great opportunity to replace that otherwise missing stimulus, and to keep our international research community connected. To that end, we are inviting

some of the most exciting scientists in the community to share their research.

When: 5-6PM BST / 9-10AM PST, first talk this Wed 15 April, up to 3 seminars/week Mon, Wed, Fri

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 and Ecology Seminars' here https://join.slack.com/t/evolutionecol-x154980/shared_invite/zt-cylz6q41-IL4o9EXDEbSKQ4kh5KFvnQ Our talks this week are:

Wed 15 April: “An evolutionary perspective on meiotic recombination in vertebrates”

Prof. Molly Przeworski (Department of Biological Sciences, Columbia University, USA)

<https://biology.columbia.edu/people/przeworski> —

Fri 17 April: “Rules of engagement: molecular arms races between host and viral genomes”

Dr. Harmit Malik (Fred Hutchinson Cancer Research Center, USA)

<https://research.fhcrc.org/malik/en/labmembers/harmitmalik.html> Next week's schedule:â€

Mon 20 April

Prof. Kayla King (Department of Zoology, University of Oxford, UK)

<https://www.zoo.ox.ac.uk/people/dr-kayla-king> Wed 22 April

Prof. Doris Bachtrog (Department of Integrative Biology, UC Berkeley, USA) <https://bachtroglabberkeley.wordpress.com/> Fri 24 April

Prof. Andrew McAdam (Ecology and Evolutionary Biology, University of Colorado Boulder, USA)

<http://www.mcadamlab.ca/#evolutionaryecology>

With more speakers to come!

Please see posters attached!

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)”
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Online EvolutionHIV May11-13

The 27th International Dynamics & Evolution of HIV and Other Human Viruses conference will be held May 11-13, 2020 via webinar. This year will include a special session on SARS-CoV-2.

This International Workshop brings together biologists and immunologists working in viral pathogenesis with applied mathematicians and statisticians. The meeting fosters interdisciplinary collaboration and a new generation of young talented researchers with the aim to contribute to the understanding of HIV/AIDS and other human viruses such as SARS-CoV-2 through research that addresses the challenges of viral persistence, evolution and genetics, changing human behavior, and infection control.

It was designed to promote discussion between specialists in quantitative and computational approaches in two areas in the field of HIV and other human viruses where these are particularly important:

Modeling of viral and cellular dynamics

Viral evolution and population genetics

We actively encourage participation by members of minority groups.

Register online at <https://cme.ucsd.edu/hivdynamics/-registration.html> Follow UC San Diego CME on <http://facebook.com/ucsdcmecme> and <http://twitter.com/UCSanDiegoCME> UC San Diego School of Medicine, Continuing Medical Education 9500 Gilman Drive, MC0947 La Jolla, CA 92093-0947 Phone: (858) 534-3940 Toll-Free: (888) 229-6263 Fax: (858) 534-1896 E-mail: ocme@ucsd.edu Website: <http://cme.ucsd.edu> Content is subject to change without notice. Please refer to the activity website for the most current information.

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Online ISMB EvolCompGen Jul13-16 CallAbstracts

Dear colleagues,

We are soliciting abstract submissions for talks or posters at the Evolution and Comparative Genomics (EvolCompGen) COSI track at ISMB 2020, which will be held as a Virtual Conference, July 13-16, 2020. https://evolcompgen.org/meetings/ismb_2020 Abstract Submission Deadline: April 16th

The goal of the track is to foster exchange and collaborations between developers and users of computational methods in evolution and comparative genomics. We think that this virtual format is also an opportunity that enable more researchers from all around the world to attend the conference.

The track will feature a mix of proceedings talks and contributed talks from the submitted abstracts. In addition, there will be a poster session (PDF file with a pre-recorded audio and a tied Q&A function for each presentation). There will also be live sessions for distinguished talks and invited speakers for the whole conference.

Talks can be on unpublished work or work published after January 1, 2019, and delivered by speakers at any career stage.

The selection will be made by a committee chaired by Lars Arvestad (Stockholm University) and Edward L. Braun (University of Florida), based on the following criteria: (i) significance and novelty of the contribution; (ii) completeness of the description of methods, data, and analysis; (iii) quality of the presentation.

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

Information on abstract submission deadline and guidelines can be found here: <https://www.iscb.org/ismb2020-submit/abstracts#deadlines>

Applications should be submitted here:

https://easychair.org/account/signin_timeout?!=-L6juo5LUsqtH3rTHDpBwjs# For more information on the EvolCompGen COSI, consult our website at: <https://EvolCompGen.org> Good health wishes for all countries around the world !

Aïda Ouangraoua <Aida.Ouangraoua@USherbrooke.ca>

Online ISMB EvolCompGen Jul13-16 LastCall

PLEASE FORWARD THIS ANNOUNCEMENT!

ONLINE CONFERENCE : Intelligent Systems for Molecular Biology (ISMB 2020) - Evolution and Comparative Genomics (EvolCompGen) - July 13-16, 2020

LAST CALL : abstract submissions for Talks and/or Posters.

DEADLINE EXTENSION TO APRIL 30

Webpage: <https://evolcompgen.org/meetings/-ismb.2020> Abstract submission deadline: April 30, 2020 Talk and/or Poster acceptance notifications: May 14, 2020 Late poster submission deadline: May 28, 2020 Late poster acceptance notifications: June 04, 2020

Scope: The goal of the EvolCompGen track is to foster exchange and collaborations between developers and users of computational methods in evolution and comparative genomics. The track will feature a mix of proceedings talks and contributed talks from the submitted abstracts. In addition, there will be a poster session (PDF file with a pre-recorded audio and a tied Q&A function for each presentation). There will also be live sessions for distinguished talks and invited speakers for the whole conference.

The selection will be made by a committee chaired by Lars Arvestad (Stockholm University) and Edward L. Braun (University of Florida), based on the following criteria: (i) significance and novelty of the contribution; (ii) completeness of the description of methods, data, and analysis; (iii) quality of the presentation. Talks can be on unpublished work or work published after January 1, 2019, and delivered by speakers at any career stage.

Cost: This virtual format is an opportunity that enables more researchers from all around the world to attend the conference. Registration fees also include tiered rates based on the economic status ranking of the attendee's country. <https://www.iscb.org/>-

<ismb2020-registration#registrationfee> Moreover, selected talks/posters will be eligible for grants to cover registration fees. The procedure for application will be communicated to the relevant people in the talk/poster acceptance email.

Further information on abstract submission deadline and guidelines can be found here: <https://www.iscb.org/ismb2020-submit/abstracts> Aïda Ouangraoua <Aida.Ouangraoua@USherbrooke.ca>

Snowbird Utah GenesAsEnvironment Nov15-18

AGA2020 REDUX!

Genes as Environment: Indirect Genetic Effects in Evolution, Agriculture, and Medicine

The American Genetic Association 2020 President's Symposium has been rescheduled to take place Nov 15-18, 2020. We will still hold the meeting in Snowbird, Utah, but instead of spring flowers, anticipate snow on the mountaintops!

Early Registration will remain open until August 31st. Student and postdoc AGA members receive free registration if they submit a poster abstract by then, and have the chance to be selected for an oral presentation and \$300 travel award. Poster abstracts from all registrants will be accepted. AGA members receive significant discounts on symposium registration.

Social or indirect genetic effects (IGE) are genetic effects of an individual on the trait values of others in the same species. IGE provides a unifying framework for traditional quantitative genetics, maternal and paternal genetic effects, inclusive fitness, and multilevel selection.

We hold the friendliest symposia - small meetings in lovely settings that provide great opportunities to interact with the best in the field.

Check out our speaker lineup: Key Distinguished Lecture: Allen J. Moore Nathan Bailey Amelie Baud Piter Bijma Butch Brodie Nancy Chen Niels Dingemans Kathleen Donohue Courtney Fitzpatrick Maren Friesen Andrew McAdam Joel McGlothlin Stephanie Porter David Rand Julia Saltz Michael Wade Alastair Wilson

Join us in Snowbird! <https://www.theaga.org/-agatwentytwenty.htm> theaga@theaga.org

GradStudentPositions

AarhusU PlantMacroecologyEvolution	7	PotsdamU MarineEvolGenomics	20
AMU Poznan BorreliaCoevolution	8	SGN Frankfurt 2 MarineEvolGenomics	20
CzechRepublic PopGenetics	8	StockholmU ButterflyPlantEvolutionaryGenomics .	21
ETH Zurich Evolution	9	StockholmU StrepsipteraPhylogenomics	22
ETH Zurich GenomicDiversity	9	UAberdeen SalmonidImmunogenetics	22
ETH Zurich MicrobialEcolEvolution	10	UFerrara Italy PopConsGenomics	23
FUBerlin Insect Immun Virulence Evolution	11	UGothenburg FlatOysterEvolution	24
FUBerlin InsectMicrobiotaImmunity	11	UKonstanz DaphniaAdaptationGenetics	25
IBENS Paris EvolutionaryGenomicsPrimates	12	UManchester BirdsongEvolution	26
JagiellonianU-Krakow TardigradeEvolution	13	UMuenster GeneticBasisAdaptivePlasticity	26
Krakow OutbreakInsectGenomics	13	UMunich EvolutionaryEpigenetics	27
LilleU PleistoceneHydrosystems	14	UNaples 2 PlantEvolution ExtDeadline	28
Marseille HLA Evolution	15	USorbone Paris SexualEvolution	29
MaxPlanck Jena 3 EcolEvol	16	USouthBohemia NeoSexChromosomes LastCall . . .	30
McGillU FishConservation	17	UTurku AvianMicrobiome	31
MichiganTechU PlantEvolutionaryBiol	18	Vienna PopulationGenetics	32
NHM Basel DarwinWaspMacroevolution	18		
Nottingham Evolution	19		

AarhusU PlantMacroecologyEvolution

Applications are invited for a PhD fellowship/scholarship at Graduate School of Science and Technology, Aarhus University, Denmark, within the Biology programme. The position is available from 1 August 2020 or later. Read more and apply here: <https://phd.scitech.au.dk/for-applicants/apply-here/-may-2020/global-plant-macroecology-and-evolution-with-focus-on-tropical-rainforest/> DEADLINE 1 May 2020

Title: Global plant macroecology and evolution with focus on tropical rainforest

Research area and project description: Biological diversity is globally threatened by human activities, and to effectively preserve it for future generations we need to understand the natural processes that have generated it. We are looking for a PhD student to be part of the TropiToL project (Explaining the biological hyperdiversity of tropical rainforests using the Tree of Life) at Aarhus University. Using vascular plants as a

model, the TropiToL addresses the question: What circumstances have led to the accumulation of exceptional biodiversity in tropical rainforests, making them the most species-rich terrestrial ecosystems on Earth? The PhD research will contribute to this overall research agenda by combining macroecological Big Data and with data on the plant Tree of Life. The successful candidate will develop an in-depth understanding of biodiversity theory, and learn and work with a range of advanced quantitative methods, including methods with real-world application outside academia, such as GIS and programming/bioinformatics.

Place of employment and place of work: The PhD student will be enrolled in the Graduate School of Science and Technology (GSST) at Aarhus University. The place of employment is Aarhus University, and the place of work will be Section for Ecoinformatics and Biodiversity (ECOINF), Department of Biology, Ny Munkegade 116, 8000 Aarhus C, Denmark.

Contacts: Applicants seeking further information are invited to contact: Associate professor Wolf Eiserhardt, wolf.eiserhardt@bios.au.dk

wolf.eiserhardt@bios.au.dk

AMU Poznan BorreliaCoevolution

Graduate position: AMU_Poznan.BorreliaCoevolution

PhD position in evolutionary biology is available for four years starting from 1st October 2020 in NCN-funded project aiming to investigate coevolution between Lyme disease agent *Borrelia afzelli* and its rodent host, at the level of genes. The student will join Evolutionary Biology Group of Professor Jacek Radwan (<http://evobio.home.amu.edu.pl>) and receive a stipend of 5000 PLN/month. In addition to carrying out research in an enthusiastic team, the student will have opportunity to attend specialized courses for PhD students in English. The candidate should hold MSc degree in biological sciences or bioinformatics. Interested candidates should send their CV and a motivation letter (via email) to the project leader, who will provide further information about the project and application procedure (email: jradwan@amu.edu.pl).

CzechRepublic PopGenetics

PhD in Population Genetics and Community Ecology

We invite prospective candidates for a four-year fully funded PhD Studentship to explore exciting questions on the interface of population genetics and community ecology. How is genetic variation maintained within populations? And how do species coexist in diverse communities? These are analogous major questions, but are typically addressed separately. However, genetic variation is likely to have a key role in determining species coexistence. Similarly, species diversity may improve maintenance of genetic variation. The candidate will investigate interactions between variation and diversity using laboratory microcosm experiments, experimental evolution and field surveys. This collaborative project utilizes a novel experimental community model system of wild *Drosophila* species and their parasitoids from tropical Australia. The student will be involved in obtaining live *Drosophila* and parasitoid lines from the field, and in analysing population genomic data.

The successful applicant will join the Laboratory of

Experimental Ecology [<http://lab.hrcek.net>] at the Biology Centre, Czech Academy of Sciences, Ceske Budejovice, Czech Republic, under the supervision of Dr Jan Hrcek. The laboratory is a multinational team of PhD students, postdocs and technicians and the applicant will have the opportunity to work extensively with other team members. The laboratory obtained prestigious high-level funding for five years from 2020 to 2025 (ERC-CZ grant) and therefore can provide substantial resources and support for exceptional research. The laboratory is part of the Department of Ecology, a dynamic international centre for research on interaction networks, with regular publications in leading journals. The student will be co-advised on population genetics by Prof Jon Bridle from University College London, UK (moving from University of Bristol) [<https://scholar.google.com/citations?hl=en&user=YXLkASMAAAAJ>]. Fieldwork in Australia will be conducted in collaboration with Dr Megan Higgie from James Cook University [<https://research.jcu.edu.au/portfolio/megan.higgie/>] and additional collaborations are possible.

The deadline for applications is 10th June 2020, with a possible start date from October 2020 onwards. The student will receive a salary which comfortably covers living expenses in the Czech Republic. The working language is English and applicants from all countries are eligible. An MSc is required to enter PhD in Czech Republic. Interested candidates who do not have an MSc are invited to contact Jan, there is possibility to do MSc thesis in Jan's lab.

A strong educational track record in biological sciences is required.

Desirable: - Experience with population genetics or genomics - Experience in population genetic modelling or bioinformatics - Research experience with laboratory experiments, insect ecology or molecular ecology - Driving licence and fieldwork experience

To apply please send one document comprising a CV, contact details for two references, and a cover letter stating qualifications, previous work and motivation to Jan Hrcek [janhrcek@gmail.com].

Jan Hrcek <janhrcek@gmail.com>

ETH Zurich Evolution

The Computational Biology group in the Institute of Integrative Biology at ETH Zurich, led by Joshua L. Payne, is hiring two new Ph.D. students, with funding for up to four years. The group is broadly interested in evolution, particularly in the relationship between genotype and phenotype, and the role of mutation in the generation of adaptive phenotypic variation. We study these topics at all scales of information transmission from DNA to protein, with an emphasis on transcriptional regulation. The PhD projects available are centered around these topics.

We are looking for two highly self-motivated students to join our team, which is currently made up of 2 PhD students and one postdoc, with backgrounds in physics, developmental biology, and evolution. The successful candidates will have experience in some form of computational science, a passion for evolutionary biology, and a masters in a related discipline (math, physics, CS, life sciences...). Fluency in a major programming language is essential, as is the ability to work independently. Experience modeling evolutionary processes or analyzing large-scale biological datasets, such as from functional genomics assays, is a plus.

We will begin considering applications on May 1st, and will continue until the positions are filled. The earliest possible start date is July 1st. Given the ongoing global pandemic and the computational nature of the projects, we may begin with home office if the candidate already resides in Switzerland.

To be considered, please send a single pdf file to [joshua.payne\[at\]env.ethz.ch](mailto:joshua.payne[at]env.ethz.ch) including your CV, publication list, academic transcripts, a single-paged statement of research interests, and contact information for 2-3 academic references. Please write GPMAP2020 in the subject line.

Related papers:

Payne & Wagner (2019) "The causes of evolvability and their evolution." *Nature Reviews Genetics*, 20, 24-38.

Aguilar-Rodríguez et al. (2018) "The architecture of an empirical genotype-phenotype map." *Evolution*, 72, 1242-1260.

Payne et al. (2018) "RNA-mediated gene regulation is less evolvable than transcriptional regulation." *Proceedings of the National Academy of the Sciences*, 115,

E3481-E3490.

Aguilar-Rodríguez et al. (2017) "A thousand empirical adaptive landscapes and their navigability." *Nature Ecology & Evolution*, 1, 0045.

Payne & Wagner (2014) "The robustness and evolvability of transcription factor binding sites." *Science*, 343, pp. 875-877.

Group website:

<https://sites.google.com/site/joshualevipayne>
joshua.payne@env.ethz.ch

ETH Zurich GenomicDiversity

Understanding the changes in genetic diversity in time and space

A PhD position in population genomics is available in the Plant Ecological Genetics group at ETH Zurich. The aim of the project is to understand how anthropogenic impacts (e.g. habitat fragmentation, disturbance or pollution) shape genome-wide patterns of genetic diversity and the genetic structure of populations in time and space. It is well established that rapid environmental changes pose a threat to biodiversity. In recent years, much emphasis has been put on monitoring changes in species and habitat diversity. At the same time, we know much less about extant genetic diversity in natural populations and how it has been affected both in time and space by rapid environmental changes mediated by human impact. However, genetic diversity is considered a prerequisite for adaptation, and hence essential for the long-term persistence of populations and species under continuing environmental change. This PhD project aims to identify drivers of changes in genome-wide diversity and population genetic structure over time and space in multiple plant (and potentially animal) species using an individual whole-genome re-sequencing approach. The sampling and analysis of extant populations will be complemented by a retrospective approach in which the genetic diversity in historic herbarium or museum specimens is analysed. This allows reconstructing changes in genetic diversity over at least one century and may help identifying underlying factors driving changes in genetic diversity over time and space. Based on this knowledge, an applied goal is to develop conservation management strategies that prevent further erosion of genetic diversity and maintain the adaptive potential of populations and species.

For this project we seek highly motivated applicants with a solid background in population and conservation genomics, evolutionary biology and bioinformatics. Applicants are expected to work independently, to communicate and collaborate with a wide diversity of stakeholders and have strong analytical and writing skills.

The PhD candidate is supervised by Dr. Martin C. Fischer and Prof. Alex Widmer of the Plant Ecological Genetics group at the Institute of Integrative Biology at ETH Zurich, Switzerland (<https://peg.ethz.ch>). The project is facilitated by access to state of the art infrastructure, including the Genetic Diversity Centre (<http://www.gdc.ethz.ch/>) and the Functional Genomics Center Zurich (<http://www.fgc.ethz.ch/>). The working language is English, but advanced knowledge of German and French is important for interactions with Swiss stakeholders.

Applications consisting of a CV with names and contact information for two references, publication list and a motivation letter with a statement of research interests (not longer than 2 pages) should be prepared as a single pdf file and sent by e-mail before 10 May 2020 to Dr. Martin C. Fischer (martin.fischer@env.ethz.ch). The position can start from June 2020.

Dr. Martin C. Fischer

ETH Zurich Plant Ecological Genetics Institute of Integrative Biology (IBZ) Universitätstrasse 16 8092 Zurich, Switzerland

E-mail: martin.fischer@env.ethz.ch Phone: +41 44 633 9319 Web: www.peg.ethz.ch martin.fischer@env.ethz.ch

ETH Zurich MicrobialEcolEvolution

PhD Position in Microbial Ecology & Evolution at ETH Zürich

The Pathogen Ecology group at ETH Zürich seeks a PhD student to join our team for a project investigating antibiotic-resistance plasmids in microbial communities. The project is funded by the Swiss National Science Foundation and runs for four years, starting as soon as possible.

Our group studies microbial ecology and evolution in the context of infectious disease. Current topics include the evolution of antibiotic resistance and bacteria-virus interactions. The group is collaborative, international and

includes researchers from a range of backgrounds. For more information, see our webpage: <https://pe.ethz.ch>. The group is part of the Institute of Integrative Biology at ETH Zürich (<https://ibz.ethz.ch>).

We are looking for a highly motivated PhD student who can develop projects, carry out experiments, analyze and communicate the results, and interact with other researchers with a high degree of independence. Applicants must have a masters degree in a relevant discipline and excellent communication skills in English. ETH Zürich is an equal opportunities employer.

Research topic: The overall aim is to gain new insights into the spread of naturally occurring plasmids in multi-species microbial communities, such as those in the human gastrointestinal tract. We plan to do this by measuring parameters that drive the spread of clinical resistance plasmids in experimentally assembled communities, and by tracking plasmids in species-rich communities sampled from human gut microbiomes. By doing so, we hope to learn something new about the role of interspecific interactions in the spread of mobile genetic elements, and to identify reservoir species/strains for clinically important plasmids. The PhD student will work on some of these objectives, collaborate with a postdoc and other group members, and potentially develop related projects in microbial ecology, evolution and/or infectious disease.

Further information about PhDs at ETH Zürich is available here: <https://ethz.ch/en/doctorate.html>. Information about being employed at ETH Zürich is here: <https://ethz.ch/en/the-eth-zurich/working-teaching-and-research.html> (the PhD student will have an employment contract at ETH Zürich), and further enquiries about this position by email to alex.hall@env.ethz.ch.

To apply send a single pdf to alex.hall@env.ethz.ch including (1) cover letter, (2) CV, (3) contact details for 2-3 referees. We will start reviewing applications after 15 May and then until the position is filled. The earliest available start date is likely to be summer 2020.

Hall Alex <alex.hall@env.ethz.ch>

FUBerlin Insect Immun Virulence Evolution

—Application deadline extended to 13th April 2020—

Freie Universitaet Berlin, Germany Open PhD position: Damage, immune defence and pathogen virulence evolution Extended application deadline: 13th April 2020

The Evolution and Ecology of Insect Defences group at the Institute of Biology, Freie Universitaet (FU) Berlin, Germany, would like to invite applications for a German Research Foundation (DFG) funded doctoral candidate position (TV-L E13, 65%) for the research project: “Damage, immune defence and pathogen virulence evolution: From the wild to the lab”. The position is fixed-term and available for 4 years and it will start in June 2020, or as soon as possible thereafter.

Project background Our research lies in the field of eco-evo-immunology (<https://armitagelab.com/>). To fully understand immune defence variation and function it is essential to consider the ecological context in which defences are used and the evolutionary pressures placed on them. Much of our extensive knowledge is from carefully controlled laboratory-based studies, which is quite different from the complex environments under which the defences have evolved. Given rapid adaptation rates to lab conditions in short-lived insects, it is relevant to connect insight from the lab with that from wild organisms. To address this, in this project, the successful candidate will sample flies (*Drosophila melanogaster*) from the wild and examine their “natural state”, in terms of the degree of wounding that they have been subjected to and their cuticular microbiota. The latter will be identified and quantified using e.g. 16S rRNA metabarcoding. They will also ask how immune defences of wild- and lab-bred *D. melanogaster* differ in terms of resistance to bacterial pathogens, and whether their associated cuticular microbiota affect the virulence evolution of bacterial pathogens. A mathematical/statistical analysis will provide an understanding of the drivers of the virulence data. The results will give insight into variation in the natural selection pressures placed upon the host, and inform us about how they affect insect defences and pathogen virulence evolution.

The position is part of the “Insect Infect” Research Unit funded by the DFG. The Research Unit will give the opportunity for the candidate to interact with a diverse

group of doctoral candidates, post-docs and PIs, to obtain methodological training, to collaborate with theoreticians, and to receive bioinformatics support. There will be yearly retreats for Research Unit members and access to a graduate training programme.

Requirements A completed University Master’s degree in biology.

Desirable - We would like applications from enthusiastic and highly motivated students with a background/strong interest in evolutionary ecology. - Laboratory experience with bacteria and insects. - Good basic knowledge of statistics and experimental design. - Proficient in spoken and written English. - Good team-working and communication skills. - Ability to work independently. - A European driving licence would be an advantage. - Experience in collecting insects from the wild. - Experience in molecular biology. - Completed projects/internships on topics relevant to the research area are advantageous.

How to apply Applications should be written in English and include the following documents: (1) a cover letter detailing your suitability and motivation to join the research project (no more than one page), (2) a CV including details of your research experience, the abstract of your MSc thesis, and any publications, (3) the names of 2-3 potential referees. Please send the application as one single PDF document, to sophie.armitage@fu-berlin.de, with the following identifier in the subject field: WiMi InsectInfect_SA. The deadline for applications is the 13th April 2020. Interviews will take place as soon as possible after this date. The working language of the group is English. For further information, please contact Sophie Armitage.

– Sophie Armitage

Heisenberg Fellow Freie Universität Berlin Institute of Biology Königin-Luise-Str. 1-3 14195 Berlin <https://armitagelab.com/> “saoarmitage@zedat.fu-berlin.de” <saoarmitage@zedat.fu-berlin.de>

FUBerlin InsectMicrobiotaImmunity

** DEADLINE EXTENSION: Doctoral position on host-microbiota-pathogen interactions. New deadline for applications: 18th May 2020 **

A 4-year doctoral position (TVL-13, 65%) is available at the Institute of Biology (Prof. Dino McMahon) of the Freie Universität Berlin. The position is part of

a collaborative research unit funded by the Deutsche Forschungsgemeinschaft (DFG) to investigate the tripartite relationships between insect hosts, the microbiota and bacterial infection. This project will employ the cockroach model, *Blattella germanica*, to examine the role of host-microbiota interactions as drivers of virulence adaptation in an infectious opportunistic bacterium. Project objectives are to 1) understand how the diversity and duration of the association between the host and the microbiota shapes quantitative resistance to infection; 2) examine how microbiota-induced immune resistance is tied to host fitness and trade-offs between life-history traits; and 3) test the impact of host-microbial interactions on pathogen virulence evolution.

Qualifications for an application are a Bachelor and Master's degree (or soon to be completed) in natural sciences. Practical experience and an interest in microbiology, insects and host-parasite interactions are highly desirable, as well a very good command of English and an interest in independent scientific work.

For informal enquiries about the position, please get in touch with Dino McMahon (dino.mcmahon@fu-berlin.de).

Deadline for applications: 18th May 2020 Application documents (CV, 1-page research statement), including contact details of 2 or 3 referees, should preferably be sent by PDF to the above contact, or by post to:

Prof. Dr. Dino McMahon Unter den Eichen 87 12205 Berlin Germany Telefon: +49 30 8104-3837 Fax: +49 30 8104-1417

“McMahon, Dino Peter” <dino-peter.mcmahon@bam.de>

IBENS Paris Evolutionary Genomics Primates

Applications are invited for an ERC-funded PhD fellowship at the Institute of Biology of the Ecole Normale Supérieure (IBENS) in Paris, France, commencing on September 1st 2020 or shortly hereafter. Position is full-time and funded for three years.

We offer a fully-funded PhD position on ERC Starting Grant EVOMENS, which seeks to understand how menstruation evolved in the primate uterus. Menstruation is a recent evolutionary innovation in primates: the trait is present in some species (humans, baboons) but not

in closely related others (vervets). The molecular and genetic bases of menstruation are not fully understood, despite its involvement in critical gynecological conditions. EVOMENS aims to profile cellular populations, gene expression and gene regulation in the uterine lining of several primates across the female hormonal cycle to characterize how menstruation evolved at the functional level. The project involves cutting-edge work with functional genomics experiments (single-cell transcriptomics, cell sorting, regulatory genomics) across different primate species, to be analysed in an evolutionary and phylogenetic framework.

We seek candidates with a strong academic record, a keen interest in computational genomics, and a background in genetics, evolutionary biology, computational biology, biostatistics or a related field. Applicants must have completed their Masters degree or equivalent by September 2020. The applicant must have strong programming skills in a bioinformatics language (R, Python, etc) and a familiarity with evolutionary genetics/genomics. The position can provide opportunities to perform wet-lab work, if this suits the candidate's skills and scientific interests. Applicants should be proficient in scientific English, good team members and enthusiastic about learning new concepts and methodologies.

The successful PhD candidate will be supervised by Dr Camille Berthelot in interaction with Dr Morgane Thomas-Chollier. The candidate will join the Dynamics and Organisation of Genomes laboratory, located at the Institute of Biology of the ENS. ENS is a prestigious university with a vibrant, international academic life and is part of the Paris Sciences et Lettres (PSL) network of universities and research centers, ranking 1st in France according to the Times Higher Education's World University Ranking. The institute is located in the heart of Paris, in the Quartier Latin known for its lively student life, restaurants and bars.

Application deadline: May 1st 2020

Start date: September 1st 2020

Application: Please send your cover letter and a detailed CV including Master grades, with the names of two referees and your relationship to them to camille.berthelot@bio.ens.psl.eu

Camille Berthelot, PhD Laboratoire Dynamique et Organisation des Génomes (Dyogen) Institut de Biologie de l'ENS, CNRS, INSERM, Université PSL 46 rue d'Ulm, 75230 Paris Cedex 05, France – mail : cberthel@biologie.ens.fr tel : +33(0)144322375

Camille Berthelot <camille.berthelot@bio.ens.psl.eu>

JagiellonianU-Krakow TardigradeEvolution

PhD studentship in tardigrade evolution

Fully funded 4-year PhD studentship in tardigrade evolution at the Jagiellonian University in Krakow (Poland) in the team of Dr. ukasz Michalczyk.

The main goal of the project is to test how reproductive mode and cryptobiotic abilities affect dispersal and, in consequence, speciation and extinction rates in tardigrades. Tardigrades are a phylum of microinvertebrates that dwell a wide variety of habitats throughout the globe. They are famous for their cryptobiotic abilities that allow them to withstand extreme conditions (including outer space) and are also thought to aid dispersal of individual species. Moreover, tardigrades exhibit various reproductive modes, including dioecy and parthenogenesis. Theory predicts that both asexual reproduction and cryptobiotic survival should increase dispersal potential. On the other hand, both reproductive mode and dispersal abilities are hypothesised to affect speciation and lineage extinction rates. Thus, tardigrades are an interesting model to address some of the fundamental questions of modern evolutionary biology, biogeography and taxonomy such as mechanisms underlying the evolution of biodiversity or evolution of sex.

The successful candidate will be involved in extraction of tardigrades from moss samples, slide preparation, morphometrics and imaging in light microscope, processing specimens for scanning electron microscope, karyotyping, DNA extraction, amplification and multilocus sequencing (NGS), species identification, testing cryptobiotic abilities, and taking care of tardigrade cultures. The student will also analyse data and prepare drafts of manuscripts, and will be involved in the promotion of results at seminars and conferences.

The PhD programme in Biology at the Jagiellonian University is run entirely in English and it includes some obligatory and facultative classes. The programme is open to all nationalities and there are no tuition fees.

The PhD stipend is 4 —000 —PLN per month (typically, cost of life in Krakow for a PhD student is ca. 2 —500 PLN/month).

Deadline for applications: 20th May 2020.

Detailed information on the project, university, our team and the application procedure is available here: <http://tardigrada.edu.pl/PhD.htm> Dr. ukasz Michalczyk LM@tardigrada.net

ukasz Michalczyk <LM@tardigrada.net>

Krakow OutbreakInsectGenomics

PhD Student position in Population genomics of outbreaks

We are seeking a motivated PhD Student to join the project “Genomics of population outbreaks in an emerging model system - neutral and adaptive evolution in the spruce bark beetle”, funded by the Polish National Science Centre (NCN) SONATA BIS grant.

About the project

A major goal in evolutionary biology is to understand which processes shape genetic diversity observed in natural populations. Classic population genetic theory provides a solid mathematical framework to study genetic variation and predict efficacy of natural selection relative to drift in equilibrium conditions, for example under constant population size. However, the majority of natural populations often experience large size fluctuations that make prediction less straightforward. The main purpose of this project is to test how extreme fluctuations in population size of outbreaking species affect the dynamics of neutral and adaptive genetic variation. Many pests experience epidemic outbreaks characterized by sudden changes in population size, often spanning orders of magnitude. Such outbreaks are known from ecological studies of closely monitored species of economic importance. However, little is known about how genetic variation changes during outbreak cycles. Specifically, the rate of adaptive evolution during relatively short periods of large population size remains unknown. This can be studied in species which experience extreme fluctuations of population size, such as spruce bark beetle (*Ips typographus*). Spruce bark beetle is the most destructive pest of Norway spruce forests because under specific conditions (e.g. storms) populations may outbreak, causing mass mortalities of spruce stands. We will compare populations of spruce bark beetle that have experienced frequent, recent outbreaks and populations that did not experience outbreaks in the recent past. By combining existing knowledge on biology and ecology of the species with newly generated, large-scale genomic data, we will address specific questions about

the relationship between genome-wide variation and fluctuating effective population size: How outbreaks affect species genetic structure? Are adaptations in frequently outbreeding populations mainly driven by soft sweeps? How demographic history of the spruce bark beetle and historical fluctuations of effective population size over time affect current patterns of neutral and adaptive variation and more.

The PhD student will be working with large, whole genome resequencing data obtained from several populations and >500 individuals. The samples are being collected and the sequencing is planned for autumn 2020. Thus, the student will be able to work with the data shortly after he/she starts his/her PhD studies. The PhD student will analyse whole-genome variation patterns including differentiation, divergence and recombination rate variation along the spruce bark beetle genome. The PhD student will also infer spruce bark beetle's demographic history using coalescent-based simulations. The PhD student will gain a wide range of scientific experience including genome-wide sequence data analysis as well as demographic history modelling and will be encouraged to develop his/hers own projects using extensive datasets available.

About the place and salary

The student will be based at one of the top research institutes in the fields of Ecology and Evolution in Central Europe - Institute of Environmental Sciences, Jagiellonian University, Krakow, Poland (www.eko.uj.edu.pl/en_GB). Krakow is a beautiful city with a dynamic cultural life (European City of Culture 2000; more than 100 festivals and other events organized every year; modern museums, cinemas, theaters, restaurants etc). It has good access to outdoor activities (biking, hiking and more) and is well-connected to the rest of Europe.

The PhD student will be supported by a 48-month, tax-free research stipend: 4500 PLN (~1050 EUR) per month. This stipend may be combined with the standard PhD program scholarship (for those that will pass the entrance exam to PhD graduate school at Institute of Environmental Sciences, approximately 2200 - 3500 PLN). Note that in Poland, the living costs are relatively low (check out a cost-of-living calculator such as www.numbeo.com) and even without additional funding from graduate school the salary is more than enough to fully enjoy life in Krakow.

Requirements

The successful candidate will have an M.Sc. degree in a relevant field by October 2020. We are looking for a student with strong interest in Evolution, Molecular Ecology, Population Genetics and/or Genomics as

well as experience with, or a keen interest in learning, Bioinformatics and Computational Biology; and strong English language, communication, and organizational skills. Previous experience with population genetics,

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LilleU PleistoceneHydrosystems

Interdisciplinary PhD project - Geosciences - Evolutionary Biology (INSU-INEE)

Institutions: UMR 8198 Evo-Eco-Paleo, CNRS/Lille University; CEREGE, Aix-en-Provence; UMR 7516, CNRS/Strasbourg University Primary lab attachment: UMR 8198 Evo-Eco-Paleo, CNRS/Lille University Doctoral school: Lille University ED104 Sciences de la matière, du rayonnement et de l'environnement (SMRE) - branch: Geosciences Ecology Paleontology Oceanography

Project title: Reconstructing Plio-Pleistocene hydrosystems in the Omo-Turkana Basin with integrative studies of sedimentology and freshwater mollusks Project: EnviroMolSed (CNRS 80|PRIME project) Promotorship: Dr. Bert Van Bocxlaer (CR CNRS), Dr. Alexis Nutz (MC AMU); Dr. Mathieu Schuster (DR CNRS). Email contact: bert.van-bocxlaer[at]univ-lille.fr, nutz[at]cerege.fr, mschuster[at]unistras.fr Start date and duration: 1 October 2020 for 3 years.

Vacancy description We are pleased to announce a PhD fellowship for a highly motivated, enthusiastic and independent person with a keen interest in the paleontology of freshwater mollusks and their application to paleoenvironmental reconstruction through the integration of taphonomy and sedimentary geology. Background knowledge of evolutionary biology, morphometrics, ecological data analysis, facies analysis, sequence stratigraphy and enthusiasm to participate to fieldwork in Africa are plus-points.

Project description Freshwater mollusks are common in lakes, rivers and wetlands and, hence, they record living conditions in continental hydrosystems. They leave abundant fossil remains in the deposits of various basins in the East African Rift, but despite their unique

potential to reconstruct paleoenvironments, including those in which hominids evolved, they remain underutilized compared to terrestrial vertebrates. We propose a trans-disciplinary PhD project on the sedimentology, taphonomy and paleontology of late Cenozoic mollusk assemblages of the Omo-Turkana Basin to reconstruct hydrosystems of the basin in space and time. Although the basin harbored various paleolakes, it is unclear whether changes in aquatic communities coincide with major lacustrine transgressions and regressions, and how environmental change affected biotic communities. We propose to study freshwater mollusk communities over time from stratigraphically constrained shell beds together with depositional facies and basin-scale sequence analysis.

Setting and requirements The project is funded by the CNRS 80|PRIME initiative and will be developed in an inter-institutional collaboration between the UMR 8198 Evo-Eco-Paleo of the CNRS and Lille University, the European Centre for Research and Teaching in Environmental Geosciences (CEREGE) in Aix-en-Provence and the Institute for Earth Physics (UMR 7516) of the CNRS and Strasbourg University. Furthermore, this project is embedded in an ongoing GDR on the East African Rift that brings together a larger research consortium. Lille University is the diploma-granting institution for this PhD project, so that the successful candidate will be subscribed to a doctoral school of Lille University. Master students that are graduating over the summer are welcome to apply. More information on studying at Lille University can be found on the Lille University webpage: <https://www.univ-lille.fr/home/international-student/>. Profile of the candidate - Master's degree in a relevant field (geosciences, paleontology or paleobiology or equivalent) - Eager to acquire new competences and knowledge - Fluent in English, knowledge of French is a plus-point - Ability to work in an interdisciplinary and collaborative environment (independency, reliability, integrity) - Ability to write clear scientific reports and disseminate results - Have good non-academic attributes (e.g. maturity, open-mindedness, respectfulness)

Interested? This vacancy will be published at the beginning of May on the CNRS employment portal and will be available for 21 days. Only applications through the employment portal are eligible. In the meantime feel free to contact the abovementioned promoters for informal inquiries about the project. Feel free to contact Bert Van Bocxlaer (bert.van-bocxlaer[at]univ-lille.fr) to receive detailed application instructions from the moment they become available.

Bert Van Bocxlaer <bert.van-bocxlaer@univ-lille.fr>

Marseille HLA Evolution

Project description Our team conducts research on HLA1b molecules in alloimmunisation and inflammation (Carlini, Traore et al. 2013, Di Cristofaro, El Moujally et al. 2013, Di Cristofaro, Reynaud-Gaubert et al. 2015, Di Cristofaro, Reynaud-Gaubert et al. 2015, Carlini, Ferreira et al. 2016, Di Cristofaro, Pelardy et al. 2016, Carlini, Picard et al. 2017, Ribeyre, Carlini et al. 2018). The Major Histocompatibility Complex (MHC) region is the most studied genetic region of the human genome, in large part thanks to the presence of classical HLA class I (HLA-A, -B and -C) and HLA class II (HLA-DR and -DQ) genes. Its huge genetic diversity is challenging because of functional implication in many clinical fields such as transplant and graft outcome, or viral escape. However, this diversity also deeply contributed to anthropological science by helping to define *Homo sapiens* evolution and the earliest worldwide migration routes (Parham 1993). Conversely, less is known about worldwide genetic diversity and Linkage Disequilibrium (LD) of non-classical HLA class I genes (HLA-E, -F and -G) and of HLA class I pseudogenes. Among these, HLA-E and -G are the most studied, both at genetic diversity and at functional levels (Hviid and Christiansen 2005, Kolte, Steffensen et al. 2010).

Non classical HLA-E, -F and -G (HLA Ib) display specific features compared to classical HLA class I (HLA Ia) such as very low genetic polymorphism and restricted pattern of antigens presentation. Their role is not to elicit an immune response but rather to inhibit its activation.

HLA-G modulates NK and cytotoxic T-lymphocyte mediated activity as well as B-lymphocyte proliferation and is involved in epithelial cell differentiation (Rouas-Freiss, Goncalves et al. 1997, Allan, Lepin et al. 2002, Howangyin, Loustau et al. 2012). Many diseases involving immune tolerance were studied in regards to HLA-G expression variation, especially in pregnancy (Lynge Nilsson, Djuriscic et al. 2014, Rebmann, da Silva Nardi et al. 2014). Several studies associated genetic polymorphisms both at coding level and in regulatory regions with inter-individual expression variation (Rebmann, da Silva Nardi et al. 2014). HLA-G displays five main alleles with unequal worldwide distribution (Castelli, Mendes-Junior et al. 2007, Carlini, Traore et al. 2013, Castelli, Ramalho et al. 2014, Carlini, Ferreira et al. 2016, Castelli, Gerasimou et al. 2017, Oliveira,

Veiga-Castelli et al. 2018, Sonon, Sadissou et al. 2018, Castro, Issler et al. 2019).

HLA-E regulates natural killer cells (NK) and cytotoxic T-lymphocyte cells via its inhibitory receptor CD94/NKG2 (Allan, Lepin et al. 2002, Pratheek, Nayak et al. 2014, Celik, Kraemer et al. 2015). HLA-E mRNA is expressed in most tissues (Heinrichs and Orr 1990) and HLA-E is mobilized at the cell surface by leader peptides of HLA Ia and HLA-G molecules. HLA-E also binds peptide ligands from stress proteins and viruses (Foroni, Couto et al. 2014, Kraemer, Blasczyk et al. 2014). The two main HLA-E alleles, E*01:01 and E*01:03, display similar frequencies worldwide, suggesting an advantage for heterozygous carriers; E*01:03 is associated with higher expression (Geraghty, Koller et al. 1992, Grimley and Ober 1997, Felicio, Porto et al. 2014, Pabon, Navarro et al. 2014, Olieslagers, Voorter et al. 2017, Ramalho, Veiga-Castelli et al. 2017, Sonon, Sadissou et al. 2018, Castro, Issler et al. 2019).

HLA-F mRNA is expressed in most cell types and the protein is intracellular, and is mobilized at the cell surface of activated monocytes, NK, B-lymphocyte and T-lymphocyte (Lee, Ishitani et al. 2010, Goodridge, Burian et al. 2013). HLA-F, expressed in an open conformer form and whose function seems independent of peptide loading (Boyle, Gillingham et al. 2006, Goodridge, Lee et al. 2013) is implicated in immune system regulation in pregnancy, infection, autoimmunity and cancer, especially via its interaction with the inhibitory receptor KIR3DS1 (Burian, Wang et al. 2016, Garcia-Beltran, Holzemer et al. 2016). HLA-F displays four alleles defined at second field resolution, with F*01:01 representing 90% of allelic diversity (Carlini, Ferreira et al. 2016, Lima, Buttura et al. 2016, Buttura, Ramalho et al. 2019, Castro, Issler et al. 2019).

HLA-H (formerly named HLA-12.4 or HLA-AR), located at 55 Kbp away from the telomeric side of HLA-A, is more related to HLA-A than to HLA-B or -C (Malissen, Malissen et al. 1982, Zemmour, Koller et al. 1990) and together with HLA-J and -G forms a group defined as HLA-A related genes (Messer, Zemmour et al. 1992).

HLA-H has orthologs in chimpanzees, bonobos and gorillas, hence the separation between HLA-H and other HLA-A-related genes predates the divergence of these species (Lawlor, Warren et al. 1991, Adams and Parham 2001, Hans, Bergl et al. 2017). A proposed model of evolution suggests the duplication of an ancestral MHC-A/H block 30 million years

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MaxPlanck Jena 3 EcolEvol

3 PhD positions in Molecular and Chemical Ecology and Evolution International Max Planck Research School: “The Exploration of Ecological Interactions with Molecular and Chemical Techniques”

The International Max Planck Research School (IMPRS) “The Exploration of Ecological Interactions with Molecular and Chemical Techniques” in Jena, Germany, invites applications for 3 PhD positions beginning in October 2020 - January 2021. The overarching research topic is the use of molecular, chemical and neurobiological techniques to experimentally explore ecological interactions under natural conditions. The main focus is on the relationship between plants, microbes and herbivores, and their environment, as well as the evolutionary and behavioral consequences of these interactions. We offer 10 exciting projects focusing on different organisms and approaches. The complete list of projects offered including project descriptions is available on our website (http://imprs.ice.mpg.de/ext/index.php?id=420#header_logo). We are looking for enthusiastic PhD students with strong interests in the above-described central topic. Applicants should have or be about to obtain a Masters or equivalent degree in one of the following fields: entomology, neurobiology, molecular biology, biochemistry, analytical chemistry, plant physiology, genetics, ecology, evolutionary biology, bioinformatics, and mathematics and computer science. All our projects are highly integrative and require willingness to closely collaborate with researchers of different backgrounds.

The Research School is a joint initiative of the Max Planck Institute for Chemical Ecology and the Friedrich Schiller University. We offer state-of-the art equipment, an excellent research environment, supervision by a thesis committee and a structured training program including scientific courses, training in transferable and outreach skills and participation in research symposia. Successful candidates will receive a Max Planck support contract. There are no tuition fees and the working language is English. Application deadline is May 8, 2020.

For detailed information on the IMPRS, projects offered and application requirements, please visit our website: <http://imprs.ice.mpg.de/>. Please apply online from April 2, 2020, at: <https://imprs-reg.ice.mpg.de/>.

Projects offered in 2020 Please find below a list of projects we offer for this year's recruitment. All projects are highly integrative and require the collaboration between different research groups. Applicants can identify up to three projects of interest. It is possible to change project preferences during the recruitment in Jena.

Project 1: Communication in plant communities via a hyphal network connecting the roots of neighboring plants Supervisors: Prof. Dr. Ralf Oelmüller, Plant Physiology, Matthias Schleiden Institute, Friedrich Schiller University Jena, Priv. Doz. Dr. Axel Mithöfer, Department of Bioorganic Chemistry, Max Planck Institute for Chemical Ecology

Project 2: Mycorrhizal communication: between plant response and fungal symbiosis Supervisors: Prof. Dr. Erika Kothe, Institute for Microbiology, Friedrich Schiller University Jena, Prof. Dr. Jonathan Gershenzon, Department of Biochemistry, Max Planck Institute for Chemical Ecology, Dr. Katrin Krause, Institute for Microbiology, Friedrich Schiller University Jena

Project 3: The role of the transcription factor FLC in growth habit, fruit dimorphism and plant defense of *Aethionema arabicum* Supervisors: Prof. Dr. Günter Theißen, Genetics, Matthias Schleiden Institute, Friedrich Schiller University Jena, Prof. Dr. Jonathan Gershenzon, Department of Biochemistry, Max Planck Institute for Chemical Ecology, Prof. Dr. Ralf Oelmüller, Plant Physiology, Matthias Schleiden Institute, Friedrich Schiller University Jena

Project 4: Convergent evolution of metabolic pathways: The biosynthesis of benzoxazinoids in dicotyledonous plants Supervisors: Prof. Dr. Sarah O'Connor, Department of Natural Product Biochemistry, Max Planck Institute for Chemical Ecology, Dr. Tobias Köllner, Department of Biochemistry, Max Planck Institute for Chemical Ecology

Project 5: Towards GC-MS: Adapting SIRIUS and CSI:FingerID for electron ionization fragmentation Supervisors: Prof. Dr. Sebastian Böcker, Chair of Bioinformatics, Friedrich Schiller University Jena, Prof. Dr. Georg Pohnert, Chair of Instrumental Analytics, Friedrich Schiller University Jena, Dr. Alles Svatos, Research Group Mass Spectrometry, Max Planck Institute for Chemical Ecology

Project 6: Small bugs - global effects: Microbial communication with consequences for climate functioning Supervisors: Prof. Dr. Georg Pohnert, Chair of Instrumental Analytics,

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McGillU FishConservation

Graduate position in fish conservation genomics ??? McGill University ??? MacDonald Campus.

The fish population and conservation genomics (FPCG) lab in the Department of Natural Resource Sciences at McGill University is seeking applications from students interested in pursuing a PhD/MSc in population genomics, comparative phylogenomics, and transcriptomics of local and/or Arctic fish species. The work will consist of performing extensive population RAD and/or RNA sequencing surveys. Although fieldwork experience is not required, a strong potential exists for students to participate in sample collections in Arctic coastal and offshore marine environments, as well as in more local areas (St. Lawrence River and Lac Saint-Pierre).

Candidates should have an academic background in ecology, evolution, genetics and/or bioinformatics and be an independent learner with a strong work ethic. A working proficiency in the R script writing language would be an asset, as would familiarity with Linux/Unix based high performance computing clusters (HPCC) and the use of bioinformatics packages (e.g., SOAP, Geneious, CLC genomics workbench and GATK among others). The successful candidate should also have strong lab and interpersonal skills allowing them to work well in a laboratory setting and in a group.

Natural Resource Sciences (NRS) is a multi-disciplinary department based out of McGill's MacDonald Campus in Ste-Anne-de-Bellevue Quebec, Canada (<http://www.mcgill.ca/nrs/>). McGill University offers competitive graduate scholarships, including tuition waivers, and visa differential waivers (for international students that qualify) for applicants based on grades and research experience (please see the sites listed below for more information).

- <http://www.mcgill.ca/internalawards/> - <http://www.mcgill.ca/gps/funding/students> Although funds are available to support a PhD student, the eventual hire is expected to apply for either national/provincial support and/or institutional internal graduate scholarships.

Application

To apply, please send a current c.v., unofficial copies of academic transcripts (including undergraduate marks), brief description of your research interests (~ 1 page Max), and contact information for 2-3 referees. Applications will be considered until the position is filled, but priority will be given to those received before May 5th. Electronic applications (PDF only please) can be sent to:

denis.roy5@mcgill.ca

Denis Roy Assistant Professor Department of Natural Resource Sciences McGill University?? 21111 Lakeshore Road Ste-Anne-de-Bellevue, QC, H9X 3V9 <https://www.mcgill.ca/nrs/academic-0/denis-roy> <http://denisroy.weebly.com> Denis Roy

Assistant Professor Department of Natural Resource Sciences McGill University 21111 Lakeshore Road Ste-Anne-de-Bellevue, QC, H9X 3V9 denis.roy5@mcgill.ca / denisroy1@gmail.com <http://denisroy.weebly.com> Denis Roy <denis.roy5@mcgill.ca>

MichiganTechU PlantEvolutionaryBiol

PhD Position in Plant Community Ecology and Evolutionary Biology in the Hersch-Green Lab at Michigan Technological University

A PhD position is available with Dr. Erika Hersch-Green at Michigan Technological University to join a 5-year NSF-funded project. The overall premise of this research is to examine whether and how nutrient availability and plant genome size together contribute to the structuring of terrestrial biodiversity patterns from the molecular and functional attributes of organisms to multispecies assemblages. Student will combine field data from across the United States with phylogenetic modelling approaches to examine how changes in nutrient conditions affect functional traits and multispecies biodiversity patterns across sites that vary in multiple environmental factors. Student will work alongside a dynamic research group that includes international and national scientific and teaching collaborators and graduate and undergraduate students. Student will also have the opportunity to be involved in teaching workshops/activities to enhance their scientific teaching and communication skills.

RA funding for at least 4 years (including stipend and tuition) is provided. Candidates must have prior research

experience in plant ecology and/or evolutionary biology and in working in field settings. Desired qualifications also include: an M.S. in ecology, evolutionary biology, plant sciences or a related discipline, an excellent academic record, a good quantitative background (including statistics), and strong writing and computing skills; skills in flow cytometry, with a Li-Cor machine, and/or in community phylogenetic methods is highly favored.

Interested candidates should contact Dr. Erika Hersch-Green by email (eherschg@mtu.edu) and include a statement of research interest, an updated CV, and contact information for 3 references. Suitable candidates will be contacted for an interview and will be encouraged to submit a formal application to the graduate school at Michigan Technological University (details on Michigan Tech, the Department of Biological Sciences, and the application procedure can be found at <http://www.mtu.edu/biological/>).

Review of applicants will begin May 15th 'V Start date is flexible.

Erika Hersch-Green <eherschg@mtu.edu>

NHM Basel DarwinWaspMacroevolution

* DARWIN WASPS AND THE K-PG MASS EXTINCTION *

A PhD position in systematics and macroevolution is available at the University of Bern and the Natural History Museum Basel. The project combines entomology, palaeontology, molecular clock analyses, and computer simulations to assess the impact of the K-Pg mass extinction event on Darwin wasps (Ichneumonidae), a species-rich group of parasitoids.

Evidence of past mass extinctions is only conclusive for groups with a dense fossil record, such as hard-bodied marine taxa. Insects have been the most species-rich taxon on earth ever since the Carboniferous, but our knowledge of their fate during past mass extinctions is limited by their capricious fossil record. Bayesian phylogenetic methods potentially allow estimating the impact of mass extinction events on groups that do not fossilize well, provided a well-dated phylogeny is at hand.

Our project aims to date the tree of life of Darwin wasps using total-evidence dating, an approach that integrates morphological and molecular data of extant and fossil

taxa. The wasp time tree will then be used to assess the impact of the K-Pg extinction event on this group, which is at the top of the insect food web. The project spans a broad range of tasks, from analysing and describing new fossil species, over coding morphological characters and filtering next-generation sequencing data, to Bayesian phylogenetic and macroevolutionary analyses.

We are looking for a highly motivated and versatile applicant with an interest in morphology, palaeontology, and macroevolutionary inference. The PhD student will be enrolled at the University of Bern and will work at the Natural History Museum in Basel. He or she will be supported by a postdoc and supervised by PI Seraina Klopstein. The position is funded by the Swiss National Science Foundation for four years.

Applications should include a brief CV, two references with contact details, a publication list, and a motivation letter detailing previous experiences with any of the aspects of the project. Please send these documents in a single PDF file to seraina.klopstein@bs.ch. The deadline for applications is 31 May 2020 and the position is available at the earliest from 1 July 2020.

Seraina.Klopstein@bs.ch

Nottingham Evolution

PhD position for UK and EU students, deadline May 12th: Left-right asymmetry in Hawaiian 'Looking-glass' snails, with myself, Dr Mark Ravinet (University of Nottingham) and Dr Ken Hayes (Bishop Museum, Hawaii). Funded by 15m award from BBSRC to UoN. Email me for further details: angus.davison@nottingham.ac.uk.

Apply: [**https://nottingham.ac.uk/bbdt/**](https://nottingham.ac.uk/bbdt/) Advert: [**https://findaphd.com/phds/project/left-right-asymmetry-in-hawaiian-looking-glass-snails/?p75229**](https://findaphd.com/phds/project/left-right-asymmetry-in-hawaiian-looking-glass-snails/?p75229)
 Twitter: [**https://twitter.com/angus_davison/status/1247481772650180610**](https://twitter.com/angus_davison/status/1247481772650180610) Key papers:

Davison, A., McDowell, G.S., Holden, J.M., Johnson, H.F., Koutsovoulos, G.D., Liu, M.M., Hulpiau, P., Van Roy, F., Wade, C.M., Banerjee, R., et al. (2016). Formin is associated with left-right asymmetry in the pond snail and the frog. *Curr. Biol.* 26, 654-660. [**https://doi.org/10.1016/j.cub.2015.12.071**](https://doi.org/10.1016/j.cub.2015.12.071) Yeung, N.W., and Hayes, K.A. (2018). Biodiversity and Extinction of Hawaiian Land Snails: How Many Are Left Now and What Must We Do To Conserve Them-A Reply to Solem (1990). *Integr. Comp. Biol.* 58, 1157-1169.

Davison, A. (2019). Flipping shells! Unwinding LR asymmetry in mirror-image molluscs. *Trends in Genetics* 36:189-202. [**https://doi.org/10.1016/j.tig.2019.12.003**](https://doi.org/10.1016/j.tig.2019.12.003) Project Description

While most animal bodies are bilaterally symmetric on the outside, the internal organs usually show a consistent left-right (LR) asymmetry. Defining this LR asymmetry is a critical part of early development, such that left/right positional errors are an important class of human birth defect, and in later life numerous diseases affect apparently symmetric organs in an asymmetric fashion. Yet, in trying to understand how this LR asymmetry is established, it is straightforward to conceive how the LR axis is defined relative to front/back and top/bottom, but more difficult to comprehend how left and right are consistently orientated in the same direction. In the classic view, the solution is that LR asymmetry is signalled by a chiral structure, the fabled "F-molecule", which is directionally orientated relative to the other axes.

To date, a wealth of studies have revealed the genes that promote the propagation of asymmetric signals, but the earliest LR symmetry-breaking events are not clear. In seeking to understand if there is a common pathway, an emerging consensus is that LR asymmetry in diverse organisms originates from the cytoskeletal dynamics that underlie the asymmetric behaviour of individual cells. Nonetheless, a central problem remains - how and why are left and right consistently orientated in the same direction? The main approach to understanding this invariance has been to use rare mutants or manipulations in model animals (vertebrates, nematode/fly), to create individuals that are partly or wholly orientated in the opposite direction. This methodology has been fruitful, of course, but unfortunately, scientists have largely ignored the only animal group - snails - in which ordinary development can produce individuals that are LR orientated in different directions. Studies of LR asymmetry ("chirality") in snails may be key to understanding how and why are left and right consistently orientated in the same direction in nearly all other animals. In this project, we propose to use association mapping and long read genome sequencing to identify the gene that underpins natural variation in the LR asymmetry of Hawaiian snails of the genus *Lymnaea* or *Auricullela*. This knowledge will then be used to understand how molecular chirality defines the LR asymmetry of cells, organs and bodies, with implications for understanding human health and development. The project will involve cutting-edge methods in DNA sequencing / bioinformatics, and may also require field or lab work in Hawaii.

Angus Davison <Angus.Davison@nottingham.ac.uk>

PotsdamU MarineEvolGenomics

PhD position in Evolutionary Genomics of Marine Mammals 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 July 1st 2020.

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> for recent work).

The successful applicant will work on the genomic basis of adaptation in marine mammals. The project will have a strong bioinformatics component and may involve field work.

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, bioinformatics, or a related discipline). Familiarity with modern genetic and genomics techniques, genomic data analysis, and/or multivariate statistics is essential. Experience in R and Linux is strongly appreciated.

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 15th of May 2020 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>

SGN Frankfurt 2 MarineEvolGenomics

Job offer ref. # 12-20008

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG) is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology IME aiming to intensify biodiversity genomics in basic and applied research. We will establish a new and taxonomically broad genome collection to study genomic and functional diversity across the tree of life and make genomic resources accessible for societal-demand driven applied research.

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

Evolutionary genomics of marine vertebrates (part time, 50 %)

Your tasks:

Comparative genomic analysis of non-model organisms, with a focus on marine animals, especially venomous fish Evolutionary inference of mobile DNA to study dynamics, phylogeny, and/or mode of transmission Phylogenomic inference and introgression analysis across populations

Your profile:

A master degree in the fields of biology, evolution or bioinformatics Preferred experience with genome assemblies, bioinformatics and basic scripting languages (bash, perl and/or python) Interest in mobile DNA and its genomic influences Experience and exceptional interest in comparative genomics, evolutionary biology research and phylogenomics Teamwork oriented and excellent communication skills in written and spoken English, you also work independently and meet deadlines

What is awaiting you?

Become part of a dynamic team of researchers in an international research group and join the new LOEWE excellence centre with its 20 new research groups. Ac-

cess to unpublished genomes from exotic animal phyla. The possibility to create a network with scientists in interdisciplinary fields in translational biodiversity genomics.

Salary and benefits are according to a part time public service position in Germany (TV-H E13, 50%). The contract should start as soon as possible and will initially be limited for 36 months. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung. Equally qualified handicapped applicants will be given preference.

Please send your application, mentioning the reference of this job offer (ref. #12-20008) before April 29th, 2020 by e-mail (attachment in a single pdf document) and including a cover letter detailing research interests and experience, a detailed CV and a copy of your certification to:

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

E-Mail: recruiting@senckenberg.de

For more information please contact Prof. Dr. Axel Janke (axel.janke@senckenberg.de).

Mit freundlichen Grüßen / Best Regards

Jessica Helm

Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung
(Rechtsfähiger Verein gemäß § 22 BGB) Senckenberganlage 25

60325 Frankfurt am Main

Besucheradresse: Mertonstraße 17-21, 60325 Frankfurt am Main (1. OG)

Telefon/Phone: 0049 (0)69/ 7542 -

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales - 1319 Elsen, Carina

Team Personalbeschaffung (Recruiting) -1564 di-Biase, Maria - 1313 Helm, Jessica - 1478 Gajcevic, Isabel

Fax: 0049 (0)69/ 7542-1445

Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Karsten Wesche

Präsidentin: Dr. h. c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Mitglied der Leibniz-Gemeinschaft

Vernetzen Sie sich mit uns: www.senckenberg.de/-socialmedia Jessica Helm <recruiting@senckenberg.de>

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG) is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology IME aiming to intensify biodiversity genomics in basic and applied research. We will establish a new and taxonomically broad genome collection to study genomic and functional diversity across the tree of life and make genomic resources accessible for societal-demand driven applied research.

The Senckenberg Gesellschaft für Naturforschung and the LOEWE-TBG invite applications for a

PhD Position (m/f/d)

Evolutionary genomics of invertebrates

(part time, 50 %)

Your tasks:

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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>

StockholmU ButterflyPlantEvolutionaryGenomics

PhD position in Evolutionary genomics of butterfly-plant associations (deadline April 23)

A PhD position has been announced at the Department of Zoology, Stockholm University, Sweden, as part of the project “Evolving modularity in the adaptations of phytophagous insects to their host plants”, newly funded by the Swedish Research Council.

The Department of Zoology is a vibrant international community, consisting of five interactive and collaborative divisions: Ecology, Ethology, Functional Morphology, Population Genetics, and Systematics and Evolu-

tion. The advertised PhD will be part of the Division of Ecology.

The project aims to improve our understanding of the causal mechanisms behind the evolutionary patterns observed in insect-plant associations, and is based on the idea that adaptations to specific host plants can best be understood as “modules” of co-expressed genes and the corresponding phenotypes – in particular larval performance on different hosts.

Work in the PhD project will focus on butterflies, and will involve field collection and laboratory rearing of insects, including short-term selection experiments, as well as genomic analysis of in particular RNA-sequencing data. Experience from rearing and genomics of non-model insects is thus particularly meriting.

The position is for four years full time, with salary and social security. To be eligible you need a degree corresponding to at least four years of higher education, including an independent project at an advanced level in animal ecology, evolutionary biology or similar subject (i.e. a Master’s degree or similar).

The project will be supervised by Prof. Sören Nylin:

<https://www.su.se/english/profiles/snylin-1.183643>
and co-supervised by Prof. Niklas Janz:

<https://www.su.se/english/profiles/janz-1.182966> Informal inquiries and expressions of interest are welcome to soren.nylin@zoologi.su.se.

Formal advertisement and link to application (deadline April 23):

<https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=11873&rmlang=UK> Soren Nylin Professor i Zoologisk Ekologi/Professor of Animal Ecology Biology Section Dean

Department of Zoology Stockholm University S-106 91 Stockholm SWEDEN

Soren.Nylin@zoologi.su.se

Soren Nylin <soren.nylin@zoologi.su.se>

StockholmU StrepsipteraPhylogenomics

A PhD student position in Systematic Zoology at Stockholm University/Swedish Museum of Natural History, Stockholm, in Dr. Johannes Bergsten’s Lab, is now open in the projectPhylogenomic species delimitation of Strepsiptera parasitizing wild bees.

Closing date for applications:23rd of April 2020.

<https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=12058&rmlang=UK> Johannes Bergsten, PhD Senior Curator/ Förste Intendent of Coleoptera Department of Zoology Swedish Museum of Natural History Box 50007 SE-104 05 Stockholm SWEDEN Visiting address: Frescativägen 40 Phone: +46 8 5195 4192 E-mail: johannes.bergsten@nrm.se http://www.nrm.se/english/researchandcollections/zoology/staff/johannesbergsten.6881_en.html Johannes Bergsten <Johannes.Bergsten@nrm.se>

UAberdeen SalmonidImmunogenetics

Project title: Immunogenetic status of salmonid populations in Scotland

Institutions: School of Biological Sciences, University of Aberdeen, and Marine Scotland Science Freshwater Fisheries lab.

Supervisors: Stuart Piertney, Marius Wenzel, David Morris, John Gilbey

Application: Deadline 1 May 2020 via Findaphd at www.tinyurl.com/salmonPhD About the project

The genetic integrity of wild salmon in Scotland is being challenged by interaction with escaped farmed fish. Gene introgression from farmed to wild fish can result in genetic pollution of maladaptive alleles, the dilution and disruption of natural adaptive gene complexes, and in declining populations the erosion of standing genetic diversity which compromises the relationship between genetic variation and resilience to immune insult. Moreover, the spill over of pathogens and parasites

from aquaculture can exert strong selective pressures on wild individuals that drive selective sweeps within populations, or expose wild fish to novel immunogenetic challenge.

There is a recognised need to characterise immunogenomic diversity in wild Atlantic salmon around Scotland, and examine how this is influenced by interaction with aquaculture mediated by both gene introgression and novel selection pressures. This project will detail immune gene diversity in natural populations using multiple approaches including targeted sequencing of key genes such as the MHC, and RADseq to identify genomic regions associated with immunological adaptation to or elevated levels of population genetic divergence consistent with the effects of directional selection. The project will exploit two unique sample sets that allow for assessment of both spatial and temporal variation in immunogenetic diversity in salmon populations. First, samples collected as part of the National Electrofishing Programme for Scotland (NEPS) that covers over 400 sites and 11,000 samples across Scotland. Second, historic material (scales and tissue samples) held at Marine Scotland Science Freshwater Fisheries Lab.

The studentship will be structured around key questions that include: How much spatial and temporal immunogenetic variation exists among populations of wild salmon in Scotland? Do the levels of diversity and patterns of structure at adaptive immunogenetic markers mirror those observed for non-functional, neutral markers? How much genetic introgression has there been through escapes of farmed genetic variants associated with pathogen resistance? Can signatures of adaptation to pathogens associated with farming be detected in wild populations? Are these signatures more acute in areas associated with aquaculture? Does any historical variation in the frequency of gene variants associated with introgression or adaptation correspond with farming activity?

It is an exceptional training opportunity for a student to exploit leading edge molecular genetic approaches in an applied context that interfaces with both industry and conservation. You will become part of a vibrant, supportive and international research team, and receive in-depth training in modern molecular and sequencing techniques, bioinformatics and statistical modelling.

The student will also benefit from wider interactions with other projects funded by the Scottish Universities Partnership for Environmental Research (SUPER) Doctoral Training Partnership (NERC) and collaboration with the Marine Scotland Science freshwater fisheries laboratory.

Funding Notes

This project is funded by the SUPER-DTP and is available to UK/EU nationals who meet the RCUK eligibility criteria. The studentship provides funding for tuition fees, stipend and a research training and support grant, subject to eligibility.

Professor Stuart B Piertney School of Biological Sciences
University of Aberdeen Zoology Building Tillydrone Avenue Aberdeen AB24 2TZ UK

Email: s.piertney@abdn.ac.uk Web: www.abdn.ac.uk/sbs/people/profiles/s.piertney Follow me @Piertney <<https://twitter.com/piertney>>

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“s.piertney@abdn.ac.uk” <s.piertney@abdn.ac.uk>

UFerrara Italy PopConsGenomics

We are seeking expressions of interest for one PhD position on a project led by the University of Ferrara (Italy).

Using five iconic endangered Italian endemics as model species, we plan to obtain chromosome-scale, fully-annotated genome assemblies and whole-genome resequencing data to investigate the dynamics of the accumulation of deleterious mutations in small populations, and their impact on individual fitness.

This three-year project was selected in 2019 by the Italian Ministry for Education and Research, but funding was delayed until February 2020.

Additional details can be found at www.endemics.it. Interested candidates should contact Giorgio Bertorelle (ggb@unife.it). The phd student will be enrolled in November.

Giorgio Bertorelle Department of Life Sciences and Biotechnology University of Ferrara
<http://docente.unife.it/giorgio.bertorelle>
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scholar.google.com/citations?user=zjz86D4AAAAJ&hl=en
“ggb@unife.it” <ggb@unife.it>

UGothenburg FlatOysterEvolution

Ph.D. candidate in molecular ecology of flat oysters

The University of Gothenburg meets the challenges of society with diverse knowledge. 47,500 students and 6,400 employees make the university a great and inspiring workplace. Strong research and attractive programs attract researchers and students from all over the world. With new knowledge and new perspectives, the University of Gothenburg is contributing to a better future.

The Department of Marine Sciences (<http://marine.gu.se>) is Sweden's most complete marine research and education environment, and is one of the few such organizations in Europe. The Department of Marine Sciences, established in 2015, brings together expertise in physical oceanography, marine chemistry, marine biology, marine geology and marine cultural conservation. The department thus has excellent conditions for meeting future challenges in marine research and education. The Department of Marine Sciences is located and has permanent staff in three locations: in Gothenburg and at the research stations Kristineberg and Tjärnö in Bohuslän.

Subject

Marine molecular ecology

Subject description

Although European flat oysters (*Ostrea edulis*) constitute a potentially important marine resource, and that Scandinavian populations are still unaffected by the parasites that have decimated populations on the European mainland, little has been done to investigate where there may be barriers to gene flow along the coasts of Scandinavia, or if there are differences in genetic diversity between geographic areas or local adaptations to environmental factors. With new genomic methods, there are now also excellent conditions for dramatically increasing the understanding of the underlying factors behind adaptations, and for predicting which factors will be important for stocks when the marine environment changes in the future due to global environmental changes (especially climate change and ocean acidification). This project is based on a combination of field studies, breeding of oysters and laboratory experiments linked to genomic and bioinformatic methods to increase the knowledge of flat oyster ecology and population genetics. The project is also linked to ma-

rine management through the development of a better classification scheme for management based on genetic data.

Employment conditions

Applicants will work in an international research group within a project aimed at investigating population structure, local adaptations, and resilience to global environmental changes in European flat oysters (*Ostrea edulis*) in Scandinavia. This group includes researchers at the Department of Marine Sciences, the Technical University of Denmark, the University of Agder and the Swedish Environmental Institute IVL.

The doctoral student is expected to work with combinations of field and laboratory experiments of local adaptations, tolerance to e.g. pH and temperature changes, and to examine the genomic background to differences in tolerance levels between individuals and between populations.

Eligibility

Basic qualifications for postgraduate education is given by: a completed degree at an advanced level, completed course requirements of at least 240 higher education credits, of which at least 60 higher education credits are obtained at an advanced level, or in some other way in or outside the country acquired essentially equivalent knowledge.

The applicant must have an education in evolutionary biology, evolutionary genetics or similar fields.

Evaluation criteria

Regulations for employment as a doctoral student are found in Swedish Code of Statutes 1998: 80. Only those who are or have been admitted to PhD-studies may be appointed to doctoral studentships. When appointing, the primary focus is on the ability of the student to take advantage of the postgraduate education. In addition to the obligation to engage in his / her own postgraduate education, the holder may be required to perform duties relating to education, research and administrative work in accordance with specific provisions in the Statutes.

We are looking for a highly motivated and independent person with basic knowledge of evolution and / or genetics, to conduct doctoral studies in science with a focus on biology. The applicant is expected to have a deep interest in research in marine evolutionary biology, willingness to work in a team, ambitions to learn new tasks, and good ability to handle data and to communicate with others.

A good ability to communicate orally and in writing in English is a requirement.

The highest ranked applicants are called for an interview that may be conducted in English and in some cases by telephone / internet.

Employment

Employment form: Temporary position, up to 48 months. Full-time. Placement: Department of Marine Sciences, Tjärnö Marine Laboratory First day of employment: Upon agreement

Contact information for the employment

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UKonstanz DaphniaAdaptationGenetics

DAAD Graduate School Scholarship Program - Call for applications for a Doctoral Scholarship integrated in the DFG Research Training Group R3

The Research Training Group R3 - Resilience of Lake Ecosystems at the University of Konstanz studies the response of aquatic ecosystems, and their resilience and reversibility to changing abiotic and biotic conditions, using Lake Constance as model system. More information can be found at <https://www.rtg-resilience.uni-konstanz.de> A 4-year doctoral scholarship funded by the DAAD is available for the following research topic: “Changing baselines” Egg banks as a tool to assess genetic diversity and phenotypic response of Daphnia populations from Lake Constance to nutrient differences over time“

Project Description: Daphnia resting eggs can be resurrected and provide a tool to assess the genetic diversity of past and current populations to respond to changing environmental conditions. Here we will test how the genetic and phenotypic diversity of standing Daphnia populations from lake Constance from different time periods determine the Response of Daphnia to experimental eutrophication/oligotrophication conditions, the Resilience (i.e., changes in diversity) of Daphnia populations to such changes, and whether or not genetic and phenotypic diversity will Reverse to the genetic and phenotypic diversity state of sampled reference populations. Briefly, we plan to expose Daphnia populations

from different time periods to eutrophic and oligotrophic conditions. We will measure genotype/allele frequencies using whole genome pool sequencing, determine juvenile growth rates under standardized conditions as a means to assess fitness differences, and collect samples for phytoplankton dynamics. Further, to allow assessment of a putative role of associated bacteria to aid ecological adaptation, we will determine microbial community composition using 16S marker gene sequencing. The project is collaborative effort between the Becks, Meyer, Martin-Creuzburg, and Voolstra labs, integrated in the doctoral program of University of Konstanz & the Research Training Group R3 (www.rtg-resilience.uni-konstanz.de), and funded by the German Academic Exchange Service DAAD.

Application: We search for a highly motivated doctoral researcher with a MSc degree in Molecular Biology, Genetics/Genomics, Microbiology, Limnology, or a related discipline. Experience in molecular work and bioinformatics analysis is a plus. High proficiency in English is expected.

At the time when DAAD receives the nomination letter, the last final exam (Master Degree or equivalent) must have taken place no longer than six years ago and applicants must not have resided in Germany for more than 15 months prior to the nomination.

For more information on this project contact Professor Dr. Christian R Voolstra (Christian.voolstra@uni-konstanz.de), group leader: Adaptation Genetics in Aquatic Systems.

To apply, please send the following documents as a single PDF file to Dr. Tina Romer, applicationRTGR3@uni-konstanz.de, coordinator of the Research Training Group R3 until 30th of June 2020.

- Letter of Motivation (1 page) - Overview of your ideas on experimental strategies and methods for addressing the research question (1 page). - Curriculum vitae (including list of publications) - Certificates of education. - Two letters of recommendation from faculty members of your home university (using the forms <https://www.daad.de/medien/-deutschland/stipendien/formulare/recommendation.pdf> or <https://www.daad.de/medien/deutschland/-stipendien/formulare/recommendation.doc>).

Details on the DAAD Graduate School Scholarship Program, the application procedure and eligibility criteria: <https://www.daad.de/go/en/stipa57034100> and https://www.daad.de/medien/hochschulen/ww-programme/gssp/gssp.2019_guideline_applicants.pdf chris.voolstra@gmail.com

UManchester Birdsong Evolution

Modelling Birdsong Evolution at the University of Manchester

In many bird species, young males learn their songs from their fathers. But, learning occurs with error, so songs can change over generations. This culturally transmitted behaviour fascinates the public and has important implications for conservation. Birds use songs to choose mates. If songs diverge among partly isolated populations, this may prevent those populations from exchanging genes and threaten species viability. Data-driven mechanistic models of the evolution of birdsong could help us understand birdsong evolution, but few such models exist.

Birdsong evolution is in some ways analogous to genome evolution. Notes are like nucleotides, and mutations (i.e., errors in copying) can change one note to another. Notes or song segments can be inserted, deleted, or duplicated. Tools from molecular phylogenetics may thus provide a foundation for modelling such changes. However, there are important differences between genomes and birdsongs. For example, individuals have a single genome, but a bird may sing many different songs. Genomes are comprised of only four different nucleotides, but birdsongs may have more than four different notes, and in principle entirely new notes can arise. Furthermore, because changes between related birdsongs are more common than genetic changes, aligning birdsongs for study is difficult, and inferences may need to be drawn from multiple possible alignments. Novel approaches are needed to overcome these challenges.

The student on this PhD will develop new models to predict birdsong evolution. These models will help explain how animal cultures evolve, and will have applications for in situ and ex situ conservation. Students with strong backgrounds in maths, physics, computer science, or mathematical and computational approaches in their own fields are particularly encouraged to apply.

The project will be advised by Tucker Gilman (Earth and Environmental Science), Mark Muldoon (Mathematics), and Pat Strycharczuk (Linguistics) at the University of Manchester, and Masayo Soma (Biology) at the University of Hokkaido.

Applicants must be eligible to live and work in the UK/EU. Please contact tucker.gilman@manchester.ac.uk

with questions, or for information on how to apply.

But, if there is a particular format I should use for this, I am happy to edit accordingly!

Tucker

R. Tucker Gilman

Department of Earth and Environmental Science University of Manchester Office: C.1249a Michael Smith Building Tel: +44 (0)161 275 1544 Twitter: @Gilman-Tucker

Tucker Gilman <tucker.gilman@manchester.ac.uk>

UMuenster Genetic Basis Adaptive Plasticity

The Institute of Plant Biology and Biotechnology, University of Muenster, Germany, invites applications for a

PhD Position: The Genetic Basis of Adaptive Plasticity
Wissenschaftliche/r Mitarbeiter/in

Salary level: TV-L E13 (50%)

in the Plant Defense Evolution group, headed by Dr Meret Huber (https://www.uni-muenster.de/Biologie.IBBP/aghuber/members/meret_huber.html).

The position is available for three years and will start in July 2020, or as soon as possible thereafter.

In the Plant Defense Evolution group, we study the molecular mechanism, ecological function and evolution of plant defenses using interdisciplinary approaches. In this collaborative project, we will investigate the biological importance and underlying genetic basis of adaptive plasticity by combining field and laboratory experiments as well as high-throughput sequencing approaches. This project is in collaboration with Prof Shuqing Xu (<https://www.uni-muenster.de/Evolution/plantadapt/people/shuqingxu.html>), who will also supervise the PhD candidate.

What we offer: The PhD candidate can expect a stimulating and international research environment. The position provides the opportunity to acquire a PhD and aims to facilitate successful career development. The candidate will be part of the Muenster Graduate School of Evolution (MGSE, <https://www.uni-muenster.de/Evolution/mgse/>), which offers both a stimulating studying environment and opportunities to connect with ex-

cellent research 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 Master's of Science in biology, evolutionary genetics or computer sciences. The successful candidate is expected to analyze a large amount of next generation sequencing data (e.g. RNA-seq and whole genome re-sequencing) with a high degree of independence. Thus, a background in bioinformatics, biology and genetics is required. Applicants must demonstrate their skill in computer programming, statistics and large-scale data analysis. Experience analyzing next generation sequencing data is therefore an advantage. The new PhD student will work together with people from different 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 of 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. We also welcome applications from candidates with severe disabilities. Disabled candidates with equivalent qualifications will be preferentially considered provided they are able to carrying out the necessary project-related work.

Applications must be in English and include (1) a motivation letter outlining your research interests with reference to the stated requirements in a maximum of 2 pages, (2) a detailed CV including academic and extracurricular achievements, as well as all research experience, (3) abstracts of both the Bachelor's of Science and Master's of Science thesis, and (4) contact details of at least two referees. Applicants should send their documents in one single PDF file to Dr Meret Huber (huberm@uni-muenster.de) before 30 April 2020. The reviewing process will start at the end of April 2020 and the position will remain open until filled.

Shuqing Xu <shuqing.xu@uni-muenster.de>

UMunich Evolutionary Epigenetics

PhD Position in Evolutionary Epigenetics

A PhD position investigating the relevance of epigenetic variation in natural populations to evolution is available in the research group of Jochen Wolf at Munich University, Germany. This project is part of a collaborative effort involving several avian research groups in Europe.

Background

Since the merger of Darwinian evolution and Mendelian hereditary principles at the onset of the 20th century, genetic variation has been at the core of evolutionary research. Genome-wide scrutiny of genetic variation segregating in natural populations has provided fundamental insights into the evolutionary processes underlying adaptation and speciation. Yet, calls for incorporating epigenetic modifications of the DNA blueprint into an extended evolutionary synthesis have repeatedly been made. And indeed, epigenetic variation constitutes an important modifier of phenotypic variation and may promote plastic responses allowing populations to explore novel niche space. Evolutionary relevance of epigenetic modification, however, will depend on the relationship between environmental inducibility and trans-generational stability independent of the underlying genetic variation. Comprehensive data on both of these aspects are scarce.

The Project

The research program run by the successful candidate proposes to fill this knowledge gap using a broad geographic sampling regime of over 2,400 individuals from pedigree-informed natural populations of two avian species as a model: the great tit, *Parus major*, and the blue tit, *Cyanistes caeruleus*. Specifically, we will use this setup to characterize the intrinsic and external forces shaping diversity in 5mC DNA methylation across various scales of integration. First, we will quantify the inheritance patterns of these epigenetic marks within families (broods) leveraging additional power from extra pair young. Second, we will determine the extent of population-level epigenetic variability across diverse environments. Third, by adding populations of the European crow, *Corvus (corone) spp.* we will assess the degree of genetic and epigenetic divergence across 44 million years of evolution.

Qualifications The successful applicant holds a master

degree in a relevant subject, has experience in population genetics and/or comparative genomics and is skilled in bioinformatic analyses of large genome-wide data sets. Previous experience with epigenetic work is an asset.

Research environment of the host lab The Wolf lab applies an integrative approach to explore micro-evolutionary processes and genetic mechanisms underlying species divergence, adaptation and genome evolution (1, 2). Using large-scale genetic approaches, as well as field based experiments, we characterize genomic divergence across populations and (sub-)species and assess its relationship to phenotypic divergence (3) - sometimes with an applied angle (4, 5). In addition, we explore methodological aspects of data analyses (6, 7) and engage in comparative approaches to study evolution across larger timescales (8, 9). Empirical systems currently include natural populations of birds (swallows, cuckoos and corvids (10-14)), marine mammals (pinnipeds and killer whales) (15, 16) and, recently added, the European hemiclinal water frog system and fission yeast (17, 18). More information on the research activities in the lab can be found at http://www.evol.bio.lmu.de/research/j_wolf/index.html. The University of Munich is consistently ranked among the top Universities worldwide, in particular the life science branch with its newly inaugurated campus offering excellent technical facilities and many interaction possibilities including the gene center, several Max-Planck-Institutes and the Helmholtz Centre (<http://www.campusmartinsried.de/en/336-2/#>). With the highest concentration of supercomputing in Germany the Leibniz Supercomputing Centre and its local partners provide access to state-of-the-art computing facilities (<https://www.lrz.de/english/>). Munich, Bavaria's capital, is a vibrant, yet relaxed city with many traditions still alive, a high quality of living and the Alps nearby.

How to apply Applications including a CV, a statement of motivation and the contact details of at least two references in a single .pdf should be sent to evolution@bio.lmu.de. Please use 'epigenetic position' as subject header. The position remains open until filled, starting date is flexible.

Literature reflecting lab interests

1. J. B. W. Wolf, H. Ellegren, *Nat. Rev. Genet.* 18, 87-100 (2017). 2. J. V. Peñalba, J. B. W. Wolf, *Nat. Rev. Genet.*, in press. 3. A. B. A. Shafer, J. B. W. Wolf, *Ecol. Lett.* 16, 940-950 (2013). 4. A. B. A. Shafer, J. M. Northrup, M. Wikelski, G. Wittemyer, J. B. W.

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

UNaples 2 PlantEvolution ExtDeadline

TWO PHD POSITIONS IN PLANT EVOLUTIONARY BIOLOGY AT THE UNIVERSITY OF NAPLES

1. PROJECT DESCRIPTION: The selected student will work with Dr. Salvatore Cozzolino (<https://www.docenti.unina.it/salvatore.cozzolino>) on a research project entitled "The contribution of plastic and heritable components in scent emission for shaping species distribution and speciation in sexually deceptive orchids"

We are interested in how diversity evolves and understanding the processes and factors that determine the spatial distribution of species on the planet. By using one of the most evolutionary successful families of flowering plants, the orchids, as a study system, we are addressing a set of inter-related questions about species sorting/species coexistence and competition. In particular, by focusing on sexually orchids, floral scent traits modulating adaptations to pollinators as well as their molecular bases will be studied using selection analysis, phenotyping (particularly for floral volatiles) and segregation analyses. We are particularly interested in how plasticity and heritability of scent emission in sexually deceptive Ophrys allows the potential for rapid adaptation to local pollinator. This is a central issue for species radiation but also for rapid adaptive response to climate changes. POSITION CHARACTERISTICS: The Department of Biology in Naples (<http://www.dipartimentodibiologia.unina.it/>) offers excellent research facilities and a stimulating working environment for graduate students in plant ecology and evolution. The project will also involve strict collaboration with orchid researchers in Germany (Prof. Philipp Schlueter) and Switzerland (Prof. Florian Schiestl). Salary is according to the University of Naples PhD guidelines. Funding, including for laboratory and field costs, is available for 3 years.

REQUIREMENTS: Applicants should hold a Master degree in plant systematics, biodiversity, plant ecology or evolutionary biology. Prior experience with plants and/or pollinators is an advantage, expertise in profiling scent emission by GC-MS and solid preparation

in biostatistics are highly appreciated. Proficiency in English both orally and written is a must; for a project including field work a driver license is desirable.

PhD candidate should apply to the 2020 Doctoral Program in Biology. As pre-application

: i) PhD candidate should apply to the 2020 Doctoral Program in Biology. As pre-submission a two-page application letter describing your research interests, clearly stating why are you interested in a Ph.D. position in evolutionary botany and your career goals; ii) your CV, including a list of publications (if applicable); iii) a copy of your undergraduate and graduate academic record; iv) names and contact details of at least two referees selected from your academic advisors. HOW TO APPLY: Send the following documents by email AS A SINGLE PDF FILE to Dr. SALVATORE COZZOLINO (cozzolin@unina.it). DEADLINE FOR APPLICATION: Applications will be screened from APRIL 15th 2020 to MAY 15th until the position is filled

STARTING DATE: 1st november 2020.

2. PROJECT DESCRIPTION: The selected student will work with Dr. Salvatore Cozzolino (<https://www.docenti.unina.it/salvatore.cozzolino>) on a research project entitled “ The potential for rapid pollinator niche diversification is fueled by ancestral lineage hybridization”

We are interested in how diversity evolves and understanding the processes and factors that determine the rapid sorting of species in some radiating clades. By using one of the faster flowering plant radiating group, as the Mediterranean sexually deceptive Ophrys, we are addressing a set of inter-related questions about species sorting/radiation by ancestral hybridization. In particular, we focus on two recent species groups that presumable sorted out and quickly radiated following hybridization of ancestral lineages. The PhD project will focus on testing the tempo and mode of origin by hybridization of the these radiating Ophrys lineages by using genomic tools and in-depth phylo-/population-/pan-genomics analytical approaches.

POSITION CHARACTERISTICS: The Department of Biology in Naples (<http://www.dipartimentodibiologia.unina.it/>) offers excellent research facilities and a stimulating working environment for graduate students in plant genomics and evolution. The project will also involve strict collaboration with orchid researchers in Germany (Prof. Philipp Schlueter) and Switzerland (Prof. Alex Widmer). Salary is according to the University of Naples PhD guidelines. Funding, including for laboratory and travelling, is available for 3 years. REQUIREMENTS:

Applicants should hold a Master degree in evolutionary

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USorbone Paris SexualEvolution

Université Sorbonne Paris Nord, Laboratoire d’Ethologie Expérimentale et Comparée, France

Open PhD position Sexual signals in hermaphroditic worms and their evolution during the transition between hermaphroditism and separate sexes

Application deadline: May 31st 2020

Applications are invited for a PhD candidate position funded by the University of Sorbonne Paris Nord for the research project: “ Sexual signals in hermaphroditic worms and their evolution during the transition between hermaphroditism and separate sexes”. The position is funded for 3 years, starting on September 2020.

Project background Sexual selection is a central topic in behavioral ecology and is usually associated with male and female reproductive success. Communication between the two sexes is crucial at the moment of reproduction; a huge amount of research has focused on sexual signals, such as sexual pheromones, visual displays and bodily parades that males and females use in the context of mating. Although the majority of animals have separate sexes, hermaphroditism is almost ubiquitous among animal taxa and more than 65000 hermaphroditic species exist. Hermaphroditic organisms have the two sexual functions tied together in the same body, and produce female and male gametes either at the same time (simultaneous hermaphrodites), or at different times during their life (sequential hermaphrodites).

How does communication between sexes work in hermaphroditic species where individuals need to mate with partners to fertilize their eggs? What implications the hermaphroditic lifestyle has on signals and cues used to attract mates? What quality are hermaphrodites advertising to their partners? Given their two sexual functions, what information are hermaphrodites signaling to attract mates, and what sex are they advertising the most? At what extent do sexual signals produced by hermaphrodites convey honest information as opposed

to manipulative substances to force partners into over expressing the less preferred sex? These questions have been rarely addressed in sexual selection research. This timely PhD project plans to meet these goals using the polychaete worms of the genus *Ophryotrocha* as biological models. This genus includes simultaneously and sequentially hermaphroditic species (all strictly unable to self), as well as species with separate sexes, making it possible to explore the evolution of sexual signals as sexual systems diversify.

References

Picchi L., Lorenzi M.C. 2019.

Gender-related behaviors: evidence for a trade-off between sexual functions in a hermaphrodite. *Behavioral Ecology* 30: 770-784.

Santi M., Picchi L. Lorenzi M.C. 2018. Dynamic modulation of reproductive strategies in a simultaneous hermaphrodite and the preference for the male role. *Animal Behaviour* 146: 87-96.

Picchi L., Cabanes G., Ricci-Bonot C., Lorenzi M.C. 2018. Quantitative matching of clutch size in reciprocating hermaphroditic worms. *Current Biology* 28: 3254-3259.e3.

Lorenzi M.C., Sella G. 2013. In between breeding systems: Neither dioecy nor androdioecy explains sexual polymorphism in functionally dioecious worms. *Integrative and Comparative Biology* 53: 689-700.

The research will be conducted at the LEEC - Laboratoire d'Ethologie Expérimentale et Comparée U.R. 4443, Villetaneuse, France (<http://leec.univ-paris13.fr>);

French language skills are not needed.

Requirements A completed University Master's degree in biology.

Desirable: we welcome applications from enthusiastic and highly motivated students with

- a background/strong interest in behavioral ecology
- good basic knowledge of statistics and experimental design
- proficient in spoken and written English
- good team-working and communication skills
- ability to work independently
- completed projects/internships on topics relevant to the research area are advantageous

How to apply Applications should be sent to Prof. Maria-Cristina Lorenzi (lorenzi@univ-paris13.fr and in cc to mariacristinalorenzi@gmail.com) by May 31, 2020, including: letter of interest, CV, a short research plan proposal and recommendation letters from previous supervisors.

Applicants are strongly encouraged to make an infor-

mal enquiry beforehand by contacting Maria-Cristina Lorenzi via email ASAP.

Maria

Cristina

Lorenzi

<mariacristinalorenzi@gmail.com>

USouthBohemia NeoSexChromosomes LastCall

PhD position in Molecular Biology & Genetics

We are looking for excellent & highly motivated candidate for a PhD position in the* Laboratory of Comparative Cytogenetics and Genomics* (<http://bit.ly/-2Vvhc50>) lead by *Petr Nguyen*.

Project:* Neo-sex chromosome evolution in Lepidoptera* Sex chromosomes, their differentiation, and role in speciation belong to the most intriguing questions of evolutionary genetics. It was proposed that comparison of patterns in sex chromosome evolution between male and female heterogametic taxa could be informative for identification of general features of this process. Moths and butterflies (Lepidoptera) represent the most speciose lineage with female heterogamety (WZ/ZZ). Unlike in other WZ/ZZ taxa, sex chromosome-autosome fusions are common in Lepidoptera, which makes them ideal model system for investigations into establishment and differentiation of neo-sex chromosomes. The project aims at investigating drivers of lepidopteran neo-sex chromosome evolution and a role of sex chromosome turnover in species divergence. It will encompass generating genomic resources, expression profiling, and cytogenetic and population genetic analyses in several non-model taxa such as ghost moth chromosome races and butterflies of the tribe Danaini.

Offer:* > PhD study for 4 years 2020-2024 (possible start in Aug/Sep 2020; <http://bit.ly/2TrFSK1>) > research campus with a strong tradition in biosciences > professional career development in science & soft skills > access to the state-of-the-art research infrastructure & equipment > focus on activity, creativity & innovativeness > international collaboration & visibility, international short-term research visits > English speaking, stimulating and friendly environment > PhD fellowship & part-time job employment on research grants > administration support with relocation & settlement in the Czech Republic > participation in annual PhD retreat > meals allowance, full health insurance, student benefits > work-life balance in a middle-sized university city offering options for outdoor, sport & cultural activities

Requirements: > MSc in Molecular Biology, Genetics or similar > proficiency in English oral and written > openness to learn new techniques, active attitude to problem-solving > ability to work in a team > independent thinking & passion for science

How to apply: Please submit your structured CV including list of publications, motivation letter, name & contacts of two academic referees via e-mail to [*jobs@prf.jcu.cz*](mailto:jobs@prf.jcu.cz) by *Wed 15 Apr 2020*. Interviews with selected applicants will be held in April 2020.

For more information, contact Petr Nguyen Assistant Professor Department of Molecular Biology and Genetics Faculty of Science, University of South Bohemia Ceske Budejovice, Czech Republic petr.nguyen@prf.jcu.cz; <http://bit.ly/2Tq4uSn> PS. Covid-19 situation in the Czech Republic Thanks to early lockdown, social distancing, and wearing masks, we stopped uncontrolled spread of the virus in the Czech Republic. We should get back to work "soon" with protective measures still in place. I believe that travelling from/to the Czech Republic will be allowed with two week follow-up quarantine in summer.

petr.nguyen@prf.jcu.cz

UTurku AvianMicrobiome

NOTE - The deadline of the call is extended due to COVID, until 20.4.2020

A funded PhD position in host-microbiome associations in wild birds (University of Turku, Finland)

We are seeking an outstanding PhD (graduate) student to lead an exciting project exploring the causes and consequences of variation in gut microbiome in a wild bird populations.

All organisms on our planet carry microorganisms in their gut. Human and animal model studies show that gut microbiome is strongly linked to health. Host and its full microbial community have been suggested to form an inseparable entity 'V the holobiont, yet the importance of gut microbiome is poorly understood in wild populations, for example in birds. The project goals are to understand the causes and consequences of variation in microbiome composition in wild populations, and whether microbiome can contribute to local adaptation and allow animals to respond to changing environment. The study system is the wild populations of the passerine great tit (*Parus major*), a well-known

ecological model system.

The work will include (1) collecting and coordinating microbiome data collection at large spatial scale across European populations, (2) conducting experimental microbiome manipulations in wild populations of great tits and common-garden experimental designs (3) laboratory analyses of microbiome and physiological biomarkers (4) statistics and bioinformatics of microbial data (5) dissemination of project results via high-quality journal publications and conference presentations.

Requirements - MSc degree in ecology, evolutionary biology, physiology, genetics or microbiology. - Background knowledge in ecology, physiology and microbial ecology. - High motivation to learn molecular, statistical and bioinformatic skills is essential. - Experience laboratory work/ experimental designs and working in wild populations/ knowledge on avian ecology is a bonus. - Excellent English writing and verbal communication skills are essential.

We offer - Funding for 3 years (25000pounds /year, partly tax-free). A further grant for the 4th year can be applied (high success). - Resources for travel to conferences or workshops abroad. - Well equipped labs and state-of-the-art scientific equipment, software, access to journals and scientific databases - Supervision in all aspects of the work (from field to lab to computational skills), possibility to join workshops to cement the skills in e.g. bioinformatics - International, enthusiastic working environment (the working language is English), large collaborator network. - Starting date: Sept-Nov 2020 The PhD student will be positioned at the University of Turku, Finland, and supervised by Dr. Suvi Ruuskanen (Turku), and Dr. Kirsten Grond (University of Alaska Anchorage, USA).

Application deadline is 20th April 2020. Please email your applications as a single merged PDF (up to 10 MB) to Suvi Ruuskanen (skruus@utu.fi). The .pdf should contain:

- 1) A cover letter summarizing your motivation, research interests, experiences and qualifications
- 2) Curriculum vitae, including an account of relevant technical skills/prior experience.
- 3) Information for three references;
- 4) Proof of completion of the master's degree (diploma) + list of grades received in the master's program (diploma supplement / transcript of records).

If pending, please provide the expected date of graduation 'V before the start of this position 'V with an explanation of the current status.

After reviewing all applicants, I will ask for reference letters from top candidates.

More information on the Ruuskanen Group: <https://->

sites.utu.fi/ruuskanengroup/ Suvi Ruuskanen, Academy research fellow Department of Biology 20014 University of Turku, FINLAND

Mobile +358503256547

Suvi Ruuskanen <skruus@utu.fi>

Vienna PopulationGenetics

Call for PhD students in Population Genetics is open: apply by May 31, 2020

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:

- Temperature adaptation in Drosophila: phenotypic adaptation. - Understanding polygenic adaptation. - Inference of selection signatures from time-series data.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by May 31, 2020 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 EUR 2.205,60 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

T +43 1 25077 4338 F +43 1 25077 4390

<http://www.vetmeduni.ac.at/en/population-genetics/> <https://twitter.com/PopGenVienna>
julia.hosp@gmail.com

Jobs

BinghamtonU EvolGenetics	33	UCDavis LabManager GenomicVariation	38
Heidelberg ShortTerm Bioinformatics	34	UFribourg Switzerland PlantEvolution May31	39
IPMB Taiwan PlantEvolution	35	UGeorgia ResTech Sticklebacks	39
MuseumFuerNaturkunde Berlin 2 Biodiversity	35	UHawaii LabAssist FruitFlyEvolution	39
OakRidgeNatlLab StaffFellowship	36	UMainz EvolutionaryPlantSciences DeadlineExt May1	40
QMULondon 2 EvolutionaryGenetics	37	UMarburg PlantBiodiversity	41
Seattle LabTech MarinePopGen	37	UMiami EvolutionaryBiology	41
TrinityU VisitingProf TeachingEvolution	38		

UMichigan FungusCollectionManager 42 UToronto Mississauga BehaviouralEvolution44
 USaoPaulo EvolutionaryVertZoology 43
 USDA HiloHawaii EvolutionaryEntomology 44

BinghamtonU EvolGenetics

Ecological Genetics Research Assistant Professor 'V Job Description

The First-year Research Immersion (FRI) program at Binghamton University will hire a Research Assistant Professor (also known as the Research Educator), to begin mid August. This full-time position is for a two to three-year duration and candidates must have graduate degree before starting. This is a 10 month non-tenure track faculty position, with additional extra service commitment for two-summer weeks. This position is for Ecological Genetics (open to Ph.D.s with appropriate background in genetics, evolution, ecology and physiology).

In the FRI Ecological Genetics research stream of the FRI program, a Research Assistant Professor guides first-year and second-year students in innovative research that advances the field of ecological genetics. Research projects in this research stream focus on how species adapt to new environments, how populations at a genetic and phenotypic level have changed through time and space, and how specific changes in the genome affect the phenotype and ultimately the fitness of populations. The Research Assistant Professor shapes the research theme. For example, past FRI cohorts have employed sophisticated techniques in genomics, transcriptomics, ecophysiology, field ecology and bioinformatics. under the guidance of the Research Assistant Professor conducting research in that stream's area. This position will entail guiding student cohorts (~30 per cohort) through authentic research experiences and, in doing so, will help students develop the professional skills desired by graduate schools and employers. Within that process and working with faculty stream collaborators, the Research Assistant Professor maintains and/or expands their own research program.

The Research Assistant Professor reports to the FRI Director, and also works closely with the faculty stream collaborators of this research stream. Overall, FRI provides an excellent training program for new PhDs and, thus, is an exceptional transition that positions the Research Assistant Professors for a wider array of future STEM positions (from full range of higher education

institutions to STEM education research).

Information about the FRI program and this research stream, including the faculty collaborators and examples of student research projects, please visit: <https://www.binghamton.edu/first-year-research-immersion/research/ecological-genetics/> Responsibilities:

- Overseedaily research activities of the research stream
- Design and implement course materials for the research stream (e.g., lab manual, lab protocols, videos for procedures, and so forth)
- Deliver mini-lectures for the research stream courses
- Overseethe operation of the research stream laboratory (e.g., with undergraduate peer mentors)
- HelpFRI students with their projects
- Serveas a mentor to the FRI students
- Facilitateformative and summative assessments of the research stream and FRI students
- Participatein a weekly FRI training and preparatory sessions
- Assistwith administrative work of the FRI program (e.g., tracking student progress and completion in the FRI)
- Co-teach FRI Research Methods Seminar with other FRI faculty
- Additional summer responsibilities may be contracted for extra payment (e.g., conducting NSF-REU-type program, working on grant research)

Requirements:

Strong candidates must have:

- Graduate degree in a discipline that matches the research stream goals
- Advanced experimental design, wet lab, field, data analysis and computational skills that align with the research stream goals
- Minimum of two yearsof experience as a teaching assistant in higher education
- Ability to train undergraduate researchers and evaluate their work
- Ability to train, evaluate and supervise graduate teaching assistants and undergraduate peer mentor assistants

Ability to manage a research laboratory

Effective communication skills

Proficiency with Microsoft Office suite and web access software

Ability to manage multiple projects and timelines simultaneously with a high degree of accuracy and efficiency

Ability to work both autonomously and collaboratively

Strong professional, organizational and interpersonal skills

Ability to speak, write and communicate in an articulate and successful manner

Ability to problem solve, prioritize, and manage multiple tasks

Ability to analyze and organize information and materials for a variety of research projects

Please submit as separate documents:

Cover letter (1 page maximum) telling us why you are interested in the position, why you feel you are qualified, and your contact information

Curriculum vita

Contact information for three references, then letters of recommendation will be requested upon application submission via <http://binghamton.interviewexchange.com>

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Heidelberg ShortTerm Bioinformatics

Bioinformatics Analyst - EvoCELL Short term Early Stage Researcher (MSCA)

About the team/job

The EvoCELL network comprises 11 European partner laboratories joining forces to elucidate the evolution of animal cell types by comparative whole-body single-cell RNA-seq approaches. We are looking for a skilled bioinformatician to set up and coordinate the bioinformatic work, which is key to the success of this innovative and exciting project.

Your role

The successful candidate will help analyse and build tools for the analysis and integration of single cell RNAseq data collected from diverse marine animals by laboratories of the EvoCELL network. The researcher will be hosted in the Arendt lab at EMBL (Heidelberg, Germany) and cooperate with all EvoCELL labs across Europe. The project will entail testing and developing bioinformatic tools that allow tracking cell types and cell type families across animal phylogeny.

The network, coordinated by EMBL Heidelberg, brings together 8 academic and 2 non-academic organizations from 6 European countries, including a company and a museum. Partners have complementary expertise in evolutionary developmental biology (EvoDevo), bioinformatics, functional neurobiology, and palaeontology. In this unique environment the researcher will also have the opportunity to take part in the network training activities and benefit from established collaborations.

You have

The 24 months position is part of the EvoCELL Marie Skłodowska-Curie Innovative Training Network started in 2018 (www.evocell-itn.eu). The ideal candidate should have experience writing code in Python and R, as well as basic experience with Linux environments and web development frameworks (e.g. MySQL, Javascript, Django, D3, etc.). Prior experience with phylogenetics, particularly working with resources such as ETE Toolkit and the eggNOG database, or analyzing RNAseq data in an evolutionary context is strongly preferred.

Working language is English, therefore proficiency in this language is required.

Eligibility Criteria - In order to be eligible to apply for this position, candidates should have completed their Master studies (or the degree that allows them to embark in a PhD in their country of origin or in the hosting country), not longer than 4 years from the start of the fellowship.

At the time of recruitment, the candidate must not have resided or carried out their main activity (work, studies, etc.) in the country of their recruiting organisation for more than 12 months in the 3 years immediately prior to start of the project. Short stays such as holidays and/or compulsory national service are not taken into account. Candidates can be of any nationality, but are required to undertake transnational mobility. Candidates should ideally possess a Master's degree in a relevant academic field, or a degree that allows them to embark in a PhD. Candidates must be within the first four years of their research career. Applications

from candidates who already possess a doctoral degree will not be considered. Furthermore, this short term position does not lead to a PhD at EMBL.

Why join us

EMBL is an inclusive, equal opportunity employer offering attractive conditions and benefits appropriate to an international research organisation with a very collegial and family friendly working environment. The remuneration package comprises from a competitive salary, a comprehensive pension scheme, medical, educational and other social benefits, as well as financial support for relocation and installation, including your family and the availability of an excellent child care facility on campus.

What else you need to know

We are Europe's flagship research laboratory for the life sciences an intergovernmental organisation performing scientific research in disciplines including molecular biology, physics, chemistry and computer science. We are an international, innovative and interdisciplinary laboratory with more than 1600 employees from many nations, operating across six sites, in Heidelberg (HQ), Barcelona, Hinxton near Cambridge, Hamburg, Grenoble and Rome.

Our mission is to offer vital services in training scientists, students and visitors at all levels; to develop new instruments and methods in the life sciences and actively engage in technology transfer activities, and to integrate European life science research.

Please note that appointments on fixed term contracts can be renewed, depending on circumstances at the time of the review.

Detlev Arendt Group Leader and Senior Scientist
ERC Investigator European Molecular Biology Laboratory
69012 Heidelberg Germany +49-6221-3878624
arendt@embl.de

Detlev Arendt <arendt@embl.de>

IPMB Taiwan PlantEvolution

TENURE-TRACK FACULTY POSITIONS AVAILABLE IN INSTITUTE OF PLANT AND MICROBIAL BIOLOGY, ACADEMIA SINICA, TAIWAN

The Institute of Plant and Microbial Biology (IPMB), Academia Sinica, Taipei, Taiwan (<http://ipmb.sinica.edu.tw/>), is inviting applications for tenure-

track research-oriented faculty positions. IPMB aims to address key questions in the areas of chromosome biology and genomics, plant-environment interactions, plant and environmental microbiology, and cell and developmental biology. The candidates are expected to have complementary or synergetic expertise to the current IPMB research capacities or have the potential to launch a new research direction for IPMB. An applicant should hold a Ph.D. degree with postdoctoral training. Preference will be given to applicants at the Assistant Research Fellow level (equivalent to Assistant Professor). Successful candidate will receive generous startup funds and annual intramural support.

The application file should include 1) a cover letter, 2) a curriculum vita, 3) a statement of research accomplishments, 4) future research plans, and 5) reprints of five representative publications. The application file (in PDF format) and, separately, three letters of recommendation should be sent via email to:

Dr. Guang-Yuh Jauh, Chair of Search Committee c/o Ms. Hsiao-Yun Wang (email: ipmb-search@gate.sinica.edu.tw) Institute of Plant and Microbial Biology, Academia Sinica 128, Sec 2, Academia Rd, Nankang, Taipei, Taiwan 11529

The review of applications will begin on July 31st, 2020 and continue until the positions are filled.

“chuanku@gate.sinica.edu.tw”
<chuanku@gate.sinica.edu.tw>

Museum fuer Naturkunde Berlin 2 Biodiversity

Museum für Naturkunde Berlin invites applications for the position of

Researcher in Applied Biodiversity of Soil Fauna / Parasites (f/m/d)

Work schedule: full-time Duration: initially for 2 years; tenure after successful evaluation within the first 2 years (tenure-track)

Salary level: E13 TV-L, this translates to a monthly gross salary level ranging from 4.002,26 euro - 5.798,14 euro, depending on the qualification and experience of the candidate.. In addition to the salary, the contract includes health care and social security benefits.

Our Mission: We study life and planet Earth, maintaining a dialogue with people.

The Museum für Naturkunde - Leibniz Institute for Evolution and Biodiversity Science is an excellent and integrated research museum within the Leibniz Association. Its activities cover and tightly link the fields of collection-based research, development of collections and public engagement with science

Responsibilities: Museum für Naturkunde Berlin is currently establishing an internationally visible “Center for Integrative Biodiversity Discovery”. It will meet the scientific and societal challenges arising from rapid worldwide ecosystem change, not least the global biodiversity crisis, and capitalise on the chances and innovations from biodiversity. The center will develop new scientific approaches to the study of biodiversity that will contribute to a more efficient and significantly faster global biodiversity inventory. At the same time it will enable high-quality taxonomic research on extinct and recent organisms and develop targeted knowledge products for various user groups.

We are seeking a talented and motivated taxonomist/biodiversity researcher (f/m) to develop and support the new “Center for Integrative Biodiversity Discovery” at the Museum für Naturkunde Berlin - Leibniz Institute for Evolution and Biodiversity Science. The jobholder is expected to take a leading role in the development of concepts for accelerating the process of biodiversity discovery and taxonomic workflows in order to overcome the ‘taxonomic impediment’ for the Center, to co-ordinate research activities across working groups, and to conduct own respective research in this field. To this purpose, she/he will bring her/his own research agenda in the field of integrative biodiversity discovery of soil fauna and/or parasites, which should be embedded in the research program of the Center for Integrative Biodiversity Discovery. Both tasks involve engagement in grant applications as well as training and supervision of students and junior researchers. We also expect active participation in public outreach activities of the museum about biodiversity and biodiversity discovery.

The Museum für Naturkunde Berlin provides an excellent research environment. It houses state-of-the-art laboratories for morphology (including histology, imaging, SEM, and μ CT labs), molecular genetics/genomics and computation. Numerous research groups are working in a wide range of research fields including population genetics, phylogenetics, developmental and evolutionary genetics, and taxonomy. Our world-class zoological collections provide unique access to specimens collected over the last 200+ years.

Requirements: PhD in biology/zoology and proven record of postdoctoral experience as a taxonomist in

collection-based biodiversity research on a species-rich group of soil fauna and/or parasites. Strong experience in and strong general knowledge of integrative biodiversity discovery and taxonomic research as well as experience in taxonomy related workflows (proven by a strong publication record, which must include taxonomic studies). Demonstrated success in obtaining third party funding and experience in leading a research group, ideally experience in leading international collaborative research projects. Field work experience, preferably also in larger collaborative projects, is required; willingness to participate in research in one of MfN’s geographic focus regions (Southeast Asia, Africa) is desirable. Successful candidates will be expected to work in a highly collaborative, interdisciplinary environment at Germany’s largest natural history museum. The development of research-based taxonomic knowledge products for applied disciplines (e.g. agriculture and/ or medicine) is expected. Excellent team player, proven communication skills and intercultural competence. Professional written and verbal communication in English.

Special notes: In support of equal rights, applications from qualified women are particularly welcome. Handicapped individuals will be given preference in case of identical qualifications.

We look forward to receiving your application with the usual documents (cover letter, curriculum vitae, certificates) as well as a research plan for the taxonomic group of interest and a concept for applications in other disciplines (max. 2 pages in

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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>

OakRidgeNatlLab StaffFellowship

Applications to the Oak Ridge National Laboratory Distinguished Staff Fellowship (<https://www.ornl.gov/-careers/distinguished-fellowships>) program are being accepted through Friday, May 29, 2020 (5:00 p.m. EST). The program includes the Liane B. Russell Fellowships, focusing on broad areas of biological sciences, biomolecular chemistry, computational biology, and environmental and ecosystem sciences. The program cultivates future

scientific leaders by awarding outstanding early-career scientists and engineers—who demonstrate success within their academic, professional, and technical— areas—with resources and enriching research opportunities.

Interested candidates may apply via this link: <https://career4.successfactors.com/sfcareer/jobreqcareer?jobId=3090&company=utbattelleP&username=ORNL> (ORNL (<https://www.ornl.gov/>) is the largest and most diverse science and energy laboratory in the US Department of Energy (DOE) system. Distinguished Fellows represent a broad range of disciplines and are expected to establish the foundation for a long-term career at ORNL, while program mentors facilitate each Fellow's integration into ORNL's scientific community and alignment of their research activities with Laboratory and DOE missions.

Russell Fellowship candidates must demonstrate their ability to contribute to DOE missions in one (or more) of the following research areas: . Artificial intelligence and machine learning . Complexity in biological and environmental systems . Quantitative biology and genome security

Applicants must have received their PhD in a STEM field before they begin their fellowship and can be no more than 5 years beyond receiving their highest technical degree when they apply. Current ORNL postdoctoral researchers and ORNL staff members are not eligible to apply. ORNL's DSF program continues to play a vital role in ensuring the accomplishment of the Laboratory's mission of delivering scientific discoveries and technological breakthroughs needed to realize solutions in energy and national security and provide economic benefit to the nation.

For more details, please visit the program website at <https://www.ornl.gov/careers/distinguished-fellowships>. Potential fellows are strongly encouraged to contact current ORNL staff to discuss alignment between their research interests and DOE/ORNL research priorities.

Josh Michener Staff Scientist, Biosciences Division Oak Ridge National Laboratory michenerjk@ornl.gov michenerlab.org

QMULondon 2 EvolutionaryGenetics

Evolutionary biologists: two 'permanent' positions now open, very short turnaround (starting July-Sept). One post is more research oriented (T&R), the other more teaching (T&S). If you do exciting science that will be much more important than an exact fit to the job description. (E.g. In the past we have appointed a botanist to a post that mentioned human genetics). You will have amazing colleagues (IMO): <https://bit.ly/2w2DhgV>. Formal adverts here, which include application details: <https://bit.ly/3dF3nrc>, <https://bit.ly/2UwD9j5> . I am happy to field questions.

Richard Nichols Professor of Genetics
<https://www.qmul.ac.uk/sbcs/staff/-richardnichols.html> Richard Nichols
<richard.alan.nichols@googlemail.com>

Seattle LabTech MarinePopGen

Molecular Genetic Research Lab Tech - Marine Population Genetics.

The North Gulf Oceanic Society (<http://www.whalesalaska.org/>) has an opportunity for a molecular genetic lab technician to support our research on marine mammal genetic stock assessment, prey metabarcoding and environmental DNA (eDNA). NGOS conducts research on the behavioral and molecular ecology of cetaceans throughout Alaska and the North Pacific. Research on the population genetics and genomics of cetaceans is conducted in collaboration with NOAA Fisheries science centers located in Seattle, WA (USA).

We are looking to hire a full-time research technician with an advanced degree (Msc or PhD) with a start date of approximately June 1, 2020, for a period of at least 1 year, with the possibility of longer term work depending on external funding.

Responsibilities include molecular genetic bench work (including DNA extractions, library prep, amplicon sequencing, NGS sequencing), bioinformatic processing

and report writing. Possible opportunities for fieldwork and sample collection exist.

Candidates for this position must have (1) a Master's or PhD in Molecular Biology, Genetics, or a related field, (2) demonstrated experience with population genetics/genomics (3) experience with next generation sequencing, (4) excellent analytical skills, including experience with R and command line programming, (5) the ability and desire to work as a productive member of a large collaborative team, (6) excellent problem solving, organizational and critical thinking skills.

The position will be located in Seattle, WA. The value of the contract will be dependent on the ideal candidate's relevant professional experience and education qualifications (4132 - 5500/month).

TO APPLY - Interested applicants should submit a brief cover letter, CV and contact details for two professional references to Dr. Kim Parsons (kim.parsons@mail.com).

Kim M. Parsons, Ph.D.

North Gulf Oceanic Society

kim.parsons <kim.parsons@mail.com>

TrinityU VisitingProf TeachingEvolution

Trinity University Visiting Ecology and/or Evolution Faculty in Biology Search Continues

Trinity University Department of Biology invites applications for a full-time, Visiting Assistant Professor to begin in August 2020. Candidates must possess a Ph.D. Responsibilities include teaching in the Biology major curricular sequence and departmental service. Applicants with the ability to teach introductory and advanced undergraduate lecture and lab courses on topics such as Ecology and/or Evolution will be highly competitive.

Trinity University is a top-ranked, small, private liberal arts and sciences university that values high quality undergraduate teaching and supports high impact undergraduate research. The Department of Biology (<https://new.trinity.edu/academics/departments/biology>), located in Trinity's state-of-the-art Center for Sciences and Innovation, has 13 highly collaborative faculty and serves majors in Biology, Neuroscience, Biochemistry and Molecular Biology, and Environmental Studies. Trinity is located in San Antonio, a large, vibrant, cos-

metropolitan city located in south central Texas. San Antonio's cost of living is relatively low for a major metropolitan area. More information on the city of San Antonio can be found at <http://visitsanantonio.com/>. Applicants should electronically submit a cover letter, curriculum vitae, statement of teaching philosophy and contact information for three references to Prof. James Shinkle, Chair of Search Committee, Department of Biology, Trinity University, One Trinity Place, San Antonio, TX 78212. Email applications are welcomed at [Biology@trinity.edu](mailto:biology@trinity.edu). Review of applications will begin April 7th, 2020 and continue until position is filled. Women and minority candidates are strongly encouraged to apply. Trinity University is an Equal Opportunity/Affirmative Action Employer.

Jim Shinkle

James Shinkle <jshinkle@trinity.edu>

UCDavis LabManager GenomicVariation

Due to an error in the original job posting, we are re-flying this position. *The candidate's salary will be covered by extramural funding of GVL PIs.*

The Genomic Variation Laboratory (GVL) is looking to hire a new laboratory manager to start in June or July 2020. The GVL is a large and dynamic group of PIs, students, and technicians who are passionate about using genetic and genomic tools to advance the management and conservation of wild populations. The GVL provides a supportive, inclusive environment that values both rigorous science and work-life balance.

The laboratory manager is integral to the structure of the GVL; the candidate chosen for this position will manage supply budgets and inventories, maintain equipment, and work with vendors. As a scientist, the laboratory manager will have opportunities to innovate methods, steer experimental design, and produce & analyze data for funded research projects. As a mentor to students and technicians, the GVL lab manager will be able to participate in a wide range of conservation genetics studies focused on various fish and wildlife species.

The ideal candidate will have a Masters or PhD in genetics, genomics, or a related field and have demonstrated proficiency in molecular techniques, including preparation of high throughput sequencing libraries. Strong written and verbal communications skills, and the ability

to manage multiple projects at a time are a must.

For more information or to apply for the position, visit <https://recruit.ucdavis.edu/JPF03506> . Best,

Andrea

Andrea Schreier, PhD Adjunct Assistant Professor Director, Genomic Variation Lab Meyer Hall 2235 University of California Davis Office (530) 752-0664 Lab (530) 752-6351 <https://gvl.ucdavis.edu/> < <http://genome-lab.ucdavis.edu/People/Drauch/index.htm> >

Andrea Schreier <amdrauch@ucdavis.edu>

UFribourg Switzerland PlantEvolution May31

The Faculty of Science and Medicine of the University of Fribourg (Switzerland) and the Department of Biology (<https://www3.unifr.ch/bio/en/>) invite applications for an open-rank position of a Professor in Plant Science.

Qualified applicants must have an outstanding track record of research in molecular and/or cellular aspects of plant development, physiology, or interaction with other organisms.

Potential areas of interest include, but are not limited to, plant disease, crop evolution, pest control, stress resistance, and food security. The candidate is expected to use modern approaches such as state-of-the-art genetics, high-throughput -omics, and/or bioinformatic approaches.

The candidate will teach at the Bachelor level and contribute to the future master program “Environmental Biology” and/or the master program “Bioinformatics and Computational Biology”. Teaching experience at university level is expected.

The successful candidate will develop an internationally recognized competitive research program sustained by external funding.

The closing date for applications is 31 May 2020.

More information about the open position on: <https://www3.unifr.ch/scimed/positions> . Prof. Thomas Flatt Department of Biology University of Fribourg Chemin du Musée 10 CH-1700 Fribourg Switzerland e-mail: thomas.flatt@unifr.ch

FLATT Thomas <thomas.flatt@unifr.ch>

UGeorgia ResTech Sticklebacks

The laboratory of Mike White in the Department of Genetics at the University of Georgia is seeking applicants for a technician to support research on the genetics and genomics of sex chromosomes in the three-spine stickleback fish. The successful candidate will have the opportunity to work on a number of exciting evolutionary and developmental biology projects using a combination of molecular and bioinformatic techniques. This position is ideal for recent biology graduates who are seeking additional research experience.

Duties and responsibilities: -Manage a small fish facility. -Assist with lab research projects. -Purchase, inventory, and organize lab supplies. -Participate in lab meetings. -Help train new lab members.

Qualifications: - Bachelor’s degree in biology or a related field. - Experience with general molecular biology techniques (e.g. PCR, DNA extraction, RNA extraction, and running gels). - Proficiency with computers. - Highly organized and detail-oriented.

Interested candidates should apply at <https://www.uga.jobsearch.com/postings/search> using the job posting number: S04891P

Please include a cover letter explaining qualifications and interest in the position, a CV, and contact information for three references.

For additional information about research in our lab, visit our website: <https://mikewhitelab.org> Any questions can be sent to: whitem@uga.edu.

Mike White Assistant Professor Department of Genetics University of Georgia whitem@uga.edu mikewhitelab.org

whitem@uga.edu

UHawaii LabAssist FruitFlyEvolution

Aloha friends!

There is a great job opportunity open currently (and

closing soon) with the Research Corporation of the University of Hawaii (RCUH) for a biological sciences laboratory assistant position studying fruit fly biology, genetics, physiology, and toxicology.

The position is posted through RCUH and the duty station will be in Hilo, Hawaii at the USDA Agricultural Research Service.

Minimum qualifications:

* Bachelor's degree in biological science or a related field
 * Experience with insect rearing * Practical knowledge of insect development and biology * Experience with biological research

Desired qualifications:

* Strong written and verbal communication skills * Ability to independently prepare materials for insect studies
 * Ability to write scientific reports

Please distribute widely. For inquiries about the position, please contact Dr. Sheina Sim sheina[dot]sim[at]usda[dot]gov.

Details about the application process are included below.

Thank you!

ID# 220117 CTAHR Melon Fly Lab Assistant Research Corporation of the University of Hawaii CTAHR/Almeida

We would like to invite you to visit our careers site to complete your application.

DIRECTIONS: 1. Click the link to access our careers site. 2. Review the job description and select the Apply button to begin your application.

https://hcmweb.rcuh.com/psp/-hcmprd_exapp/EMPLOYEE/HRMS/c/-HRS_HRAM.HRS_APP_SCHJOB.GBL?Page=-HRS_APP_JBPST&Action=U&FOCUS=-Applicant&SiteId=3&JobOpeningId=-220117&PostingSeq=1 If you are a current employee of RCUH please use the following link instead: https://hcmweb.rcuh.com/psp/hcmprd_exapp/EMPLOYEE/HRMS/c/-HRS_HRAM_EMP.HRS_APP_SCHJOB.GBL?Page=-HRS_APP_JBPST&Action=U&SiteId=3&FOCUS=-Employee&JobOpeningId=220117&PostingSeq=1

**Disclaimer: Please note that any views or opinions presented in this email are solely those of the sender and do not necessarily represent those of the company.

Sheina B. Sim, Ph.D. Research Biologist USDA-ARS
 Daniel K. Inouye US PBARC

sheina.sim@usda.gov

UMainz Evolutionary Plant Sciences DeadlineExt May1

The Faculty of Biology - Institute of Organismic and Molecular Evolution (iomE) - invites applications for a Professorship in Evolutionary Plant Sciences (Bes.Gr. W 3 LBesG)

available at the earliest opportunity.

We are seeking an internationally renowned scientist in the field of plant organismic and molecular evolution, focusing on processes of evolutionary adaptation and/or speciation. Research foci may include genomics, gene regulation, epigenetics, biotic interactions and aging, in an evolutionary context.

The successful candidate is expected to develop an independent and internationally visible research program, supported by sustained extramural funding. She/he will be embedded in a highly collaborative environment including the three institutes of the Faculty of Biology (http://www.bio.uni-mainz.de/-33_ENG_HTML.php), the Institute of Molecular Biology (IMB; www.imb-mainz.de), the Institute of Biotechnology and Drug Research (IBWF; www.ibwf.de), and other faculties of the natural sciences at Johannes Gutenberg University, as well as the Rhine Main Universities alliance (RMU) with Frankfurt and Darmstadt. Participation in the research training group GenEvo ("Gene Regulation in Evolution: From Molecular to Extended Phenotypes"; <https://www.bio.uni-mainz.de/-koordinierte-forschungsprojekte>), the CRC1361 ("Regulation of DNA Repair and Genome Stability" <https://www.sfb1361.de/>) and in the State's strategic research initiative ReALity ("Resilience, Adaptation and Longevity") is encouraged. Teaching in botany and evolutionary biology in the Bachelor and Master programs is expected with the ability to teach basic classes in German within five years.

Applicants must meet the general requirements according to public services law and the Higher Education Act of Rhineland-Palatinate ("49 Hochschulgesetz 'V Higher Education Act) including the relevant university and doctoral degrees, and an outstanding scientific track record. The State of Rhineland-Palatinate and JGU put particular emphasis on intensive student support. We expect the University's faculty to reflect this in their presence at the University.

JGU aims at increasing the number of female faculty members and therefore explicitly encourages applications by female scientists. Disabled applicants with adequate qualification will be favored.

Applications including the usual documents (e.g. CV; copies of certificates; lists of publications and teaching activities; funding record; current research and future research plans; teaching concept) as a single PDF file and separately the form available at www.bio.uni-mainz.de/-1517_ENG_HTML.php should be submitted in electronic form not later than May 1st 2020 to the

Dean, Faculty of Biology (biologie@uni-mainz.de)

Informal requests can be directed to Prof. Dr. Susanne Foitzik (foitzik@uni-mainz.de) or Prof. Dr. Andreas Wachter (wachter@uni-mainz.de).

The information on data protection in handling your application can be found at: <https://www.verwaltung.personal.uni-mainz.de/files/2019/10/Datenschutz-Bewerber.pdf> Job offers and further information also on the Internet: www.verwaltung.uni-mainz.de "Foitzik, Susanne" <foitzik@uni-mainz.de>

UMarburg PlantBiodiversity

Dear EvolDir members

we have an open call for a tenure track professorship in Plant Biodiversity / Molecular Plant Systematics aimed at talented early career scientists. The successful applicant is expected to strengthen the research priorities of the Faculty of Biology by establishing an independent research group and to actively participate in research alliances and existing collaborative research initiatives of the Faculty of Biology such as in high mountain and forest research, as well as in the overall research priorities of the Philipps-Universität Marburg, especially in the areas of biodiversity and climate research. He/she is expected to have a research focus on the biodiversity of vascular plants with a scientific profile in the field of speciation, systematics, and phylogeny. Attached pdf contains more details. Closing date for the call is the 24th of April.

Best

Lars

Dr. Lars Opgenoorth

www.opgenoorth.org | www.sensing-biodiversity.org De-

partment of Ecology | Philipps-Universität Marburg | Karl-von-Frisch Strasse 8 | 35043 Marburg | 06421 2822080 | opgenoorth@uni-marburg.de Swiss Federal Research Institute WSL | Biodiversity and Conservation Biology | Ecological Genetics | Zürcherstrasse 111 | 8903 Birmensdorf | +41 44 739 25 90 | lars.opgenoorth@wsl.ch

Lars Opgenoorth <opgenoor@staff.uni-marburg.de>

UMiami EvolutionaryBiology

Professor - Aresty Endowed Chair in Tropical Biology
https://careers.insidehighered.com/job/1968150/a-and-s_bil.associate-professor-professor-aresty-endowed-chair-in-tropical-biology/ Job description

*Job location: *Coral Gables, FL

Employment Type: Full-time *Posted data:* 2020-03-16 *Req:* R100039301 *Current Employees:* If you are a current Staff, Faculty or Temporary employee at the University of Miami, please click here < [https://www.myworkday.com/umiami/d/task/-1422\\$7248.html](https://www.myworkday.com/umiami/d/task/-1422$7248.html) > to log in to Workday to use the internal application process. To learn how to apply for a faculty or staff position using the Career worklet, please review this tip sheet < https://my.it.miami.edu/wda/-erpsec/tipsheets/ER_eRecruiting_ApplyforaJob.pdf >

. *Transforming Lives* The University of Miami is among the top research universities and academic medical centers in the nation, and one of the largest private employers in South Florida. With more than 16,000 faculty and staff, the University strives for excellence, and is driven by a powerful mission to transform and impact the lives of its students, patients, members of the community, and people across the globe. The University is committed to fostering a culture of belonging, where everyone feels valued and has the opportunity to add value. Through values of Diversity, Integrity, Responsibility, Excellence, Compassion, Creativity, and Teamwork (DIRECCT) the U community works together to create an environment driven by purpose, excellence, community, and service.

The University of Miami's Department of Biology invites outstanding tropical ecologists to apply for the Aresty Endowed Chair in Tropical Ecology. The ideal candidate will contribute to the Department's research strengths investigating the ecology and evolution of tropical systems. In addition to being outstanding, internationally recognized scientists, applicants must be excellent teachers with strong commitments to undergraduate education. Tropical fieldwork must be an integral component of

an applicant's research program. This prestigious chair includes a discretionary annual budget to support research. Applications will be considered at the Associate and Full Professor ranks.

Interested applicants must apply online:

<https://umiami.wd1.myworkdayjobs.com/UMFaculty> .
Inquiries should be directed to the Search Chairs at:
arestyfacultysearch@miami.edu.

We welcome applications from candidates who would enhance and complement our existing departmental programs in Biodiversity & Global Change, Development & Disease, Neuroscience & Behavior, and Microbiome Biology & Species Interactions. To be eligible for this tenure-track appointment, candidates must hold a Ph.D., and have a strong record of research accomplishments and research funding. The successful candidate will be expected to maintain a vigorous, externally funded research program, to teach at both the undergraduate and graduate level, to regularly teach an off-campus undergraduate field course in the tropics, and be committed to mentoring that supports diversity and inclusion. Applicants should submit a cover letter describing the interactions they foresee with existing research programs in the Department of Biology or other units at the University of Miami and a curriculum vitae online using the above link. More information about the Department and University can be found at <https://www.biology.as.miami.edu>. To receive full attention, application materials must be received by August 15th, 2020.

The University of Miami is an Equal Opportunity Employer - Females/Minorities/Protected Veterans/Individuals with Disabilities are encouraged to apply. Applicants and employees are protected from discrimination based on certain categories protected by Federal law. Click here < <https://www.hr.miami.edu/careers/eo-ada/index.html> > for additional information.
*Job Status:*Full time*Employee Type:*Faculty*Pay Grade:*50 Job description

*Job location: *Coral Gables, FL *Employment Type:* Full-time *Posted data:* 2020-03-16 *Req:* R100039301 *Current Employees:*If you are a current Staff, Faculty or Temporary employee at the University of Miami, please click here < [https://www.myworkday.com/umiami/d/task/1422\\$7248.html](https://www.myworkday.com/umiami/d/task/1422$7248.html) > to log in to Workday to use the internal application process. To learn how to apply for a faculty or staff

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mcmaster.ca/~brian/evoldir.html

UMichigan FungusCollectionManager

Research Museum Collection Manager 'V Fungi

For questions, please contact: tyjames@umich.edu

Note: Because this position may be appointed as a Research Scientist with a proportion of time available for research, we strongly encourage persons with a PhD in mycology to apply.

Considerations due to the current COVID-19 pandemic We realize that due to the current outbreak of COVID-19 that travel to and from Ann Arbor may be a limitation. We will utilize virtual interviews when necessary and will be closely monitoring the situation to provide flexibility to applicants.

How to Apply A cover letter is required for consideration for this position and should be attached as the first page of your CV. The cover letter should address your specific interest in the position and outline skills and experience in the context of the Responsibilities and Qualifications listed below. Applications should be submitted online at: https://careers.umich.edu/job_detail/185446/-research_museum_collection_manager_-_fungi Job Summary The Department of Ecology and Evolutionary Biology (EEB) is seeking a Collection Manager of Fungi. The fungarium is part of the larger MICH Herbarium (<https://lsa.umich.edu/herbarium>), located at the new state of the art Research Museums Center (RMC) in Ann Arbor, Michigan. The MICH fungarium develops and maintains fungal collections explicitly for use in research and education and facilitates specimen-based research on campus and at other institutions. EEB has an outstanding, diverse and collaborative group of researchers in evolutionary biology, ecology, and biodiversity science.

The MICH fungarium contains ~280K preserved fungal specimens, which have been largely digitally databased. The fungarium is extraordinarily strong in North American higher fungi, with, among others, the collections of A. H. Smith (agarics, boletes, and gastromycetes), C. H. Kauffman (agarics), D. Baxter (polypores), R. L. Shaffer (agarics), and R. Fogel (hypogeous fungi). The personal herbarium of F. K. Sparrow, which contains mostly specimens of the parasitic genera *Physoderma*

and Urophlyctis as well as a microscope-slide collection of aquatic fungi, is also included. The fungarium has recently developed a cryopreserved collection of living zoosporic true fungi (<https://czeum.herb.lsa.umich.edu>) which represents the largest collection of chytrid fungi, including hundreds of strains of the amphibian pathogen *Batrachochytrium dendrobatidis*. The collection manager will also be responsible for maintenance of use of a collection of ~57K lichen specimens.

We seek candidates with a strong commitment to curation of fungi, facilitation of specimen based research, and promotion of knowledge about fungi. The position offers exciting opportunities for mentoring, and career development, including limited research within the context of the fungarium's curatorial priorities. This position has the potential to be at the Research Scientist level, with a proportion of time available for the collection manager's own research interests.

Responsibilities 1. Growth, maintenance, and digitization of the collection. Activities may include accessioning and collecting new specimens, upkeep and organization of the collection, and improving specimen metadata, such as through photography and georeferencing. 2. Training and supervision of staff volunteers, work-study students, graduate curatorial assistants, and when needed, visiting researchers in all aspects of specimen research and conservation practices, database use, geo-referencing and digital imaging of specimens and routine collections maintenance tasks. 3. Maintenance and growth of the living chytrid collection (CZEUM) in the Liquid Nitrogen Facility. This activity involves the accessioning of new samples, revival and distribution of cultures for research at U. Michigan and other institutions, and developing genetic barcodes of samples. 4. Working with faculty curators to develop and implement policies, standards, and procedures. This involves, as necessary, developing standard operating procedures for acquisition, accessioning, databasing, archival and use of new or emerging genomic, digital resources and other ancillary collections. Reviewing, updating, and enhancing the fungal collections management plan. 5. Support of and coordination with faculty curators, student researchers and visiting collaborating researchers to plan and develop research projects utilizing the research collections and/or enhance collection resources.

— / —

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USaoPaulo EvolutionaryVertZoology

University of Sao Paulo - Brazil: Faculty Position - Vertebrate Zoology

The Department of Zoology of the Institute of Biosciences of the University of Sao Paulo (Brazil) is seeking applications for one tenure-track Assistant Professor faculty position in Vertebrate Zoology (including theory and methods in phylogenetics, biogeography and comparative phylogenetic methods; evolution, phylogeny, diversity, natural history and biology of major vertebrate groups; and comparative anatomy and organogenesis of the different systems in vertebrates). Applicants must hold a Ph.D. degree in a field related to the position and a demonstrated record of research productivity. The successful candidate will be expected to maintain a rigorous research program and contribute to undergraduate and graduate teaching. Applications must be submitted by April 23, 2020.

Further information (including information for foreign applicants and/or holders of a foreign Ph.D.) can be obtained from: Dr. Ricardo Pinto da Rocha, Head of the Department of Zoology, ricrocha@usp.br.

Silvio Shigueo Nihei Professor Associado / Associate Professor Departamento de Zoologia Instituto de Biociências - Universidade de São Paulo Rua do Matão, Trav. 14, n.101 05508-090 - São Paulo/SP - Brasil Phone +55 11 30917511 E-mail: silvionihei@gmail.com, silvionihei@ib.usp.br

URL: <http://www.ib.usp.br/~silvionihei> <https://usp-br.academia.edu/SilvioNihei> https://www.researchgate.net/profile/Silvio_Nihei XXXIII Congresso Brasileiro de Zoologia Águas de Lindoia-SP, 01-06 de março de 2020 www.cbzoo.com.br Editor, Zootaxa (Diptera: Muscoidea) <http://www.mapress.com/j/zt/pages/view/Diptera> Editor, Manual of South American Diptera <http://msadiptera.wix.com/manual> “La duda es uno de los nombres de la inteligencia.” (Jorge Luis Borges)

Silvio Nihei <silvionihei@gmail.com>

USDA HiloHawaii EvolutionaryEntomology

Aloha!

Could the following position be advertised on the evolDir email list?

The USDA Agricultural Research Service is currently accepting applications for a vacant Research Entomologist position to be employed within the Tropical Crop and Commodity Protection Research Unit in Hilo, Hawaii.

The position is permanent and in the federal service, starting at GS-12 to 14, with promotion potential of GS-15.

Interested applicants should apply through this application portal on USAJOBS.

<https://www.usajobs.gov/GetJob/ViewDetails/-565063200> Mahalo!

Sheina B. Sim, Ph.D. Research Biologist USDA-ARS
Daniel K. Inouye US PBARC 64 Nowelo Street Hilo, HI
96720 Phone: 808-932-2175

“sheina.sim@usda.gov” <sheina.sim@usda.gov>

UToronto Mississauga BehaviouralEvolution

2000847 - Assistant Professor - Behavioural Ecology and Entomology

The Department of Biology at the University of Toronto Mississauga (UTM) invites applications for a tenure stream appointment in Behavioural Ecology and Entomology, at the rank of Assistant Professor, expected to commence July 1, 2021.

Applicants must have a Ph.D. in Biology, a minimum of one year of post-doctoral experience, and demonstrated excellence in research and teaching.

We are searching for an outstanding entomologist who addresses fundamental questions in evolutionary biology by employing field and laboratory experiments in non-model insects. Suitable applicants will integrate

comparative, molecular and statistical methods to investigate life-history evolution and sexual selection in both natural and urban environments. We are searching for applicants who work with insects that utilize aquatic or riparian habitats. The successful candidate must demonstrate excellence in research with a record of publications in top ranked and field relevant journals, invited presentations, national and international funding and awards, and strong endorsements by referees of top international stature. Evidence of research excellence must be detailed in a CV and research statement and demonstrated through the application materials (including sample publications, and strong letters of reference). The research statement should include major research accomplishments and future directions.

The candidate must also demonstrate excellence in teaching and research mentorship. Evidence of excellence in teaching will be demonstrated by teaching accomplishments and the teaching dossier, including a teaching statement, sample course materials, and teaching evaluations or other evidence of superior performance in teaching-related activities submitted as part of the application, as well as strong endorsements by referees. Other teaching-related activities can include performance as a teaching assistant or course instructor, experience leading successful workshops or seminars, student mentorship, or excellent conference presentations or posters

We seek applications from individuals whose research program would complement existing departmental research strengths. The successful applicant is expected to develop and maintain an active, independent, innovative and externally funded program of research and to contribute to the education and training of undergraduate and graduate students in the Department of Biology, University of Toronto Mississauga. This individual will also be appointed to the tri-campus graduate Department of Ecology and Evolutionary Biology at the University of Toronto. For more information on the Department of Biology please visit our webpage at www.utm.utoronto.ca/biology. Information on the graduate unit can be found at www.eeb.utoronto.ca. The University of Toronto Mississauga and its affiliated institutions offer a stimulating and supportive environment with a variety of facilities and a highly interactive community of researchers. Excellent opportunities exist for collaboration within the Department of Biology, with other departments at UTM, as well as with faculty at the St. George and Scarborough campuses of the University of Toronto.

Salary will be commensurate with qualifications and experience.

All qualified applicants are invited to apply online by

clicking the link below. Applications must include a cover letter, curriculum vitae, research statement, three representative publications, and a teaching dossier to include a teaching statement, sample course materials, and teaching evaluations or evidence of superior performance in other teaching-related activities as listed above.

Submission guidelines can be found at: <http://uoft.me/how-to-apply>. We recommend combining attached documents into one or two files in PDF/MS Word files in the following format:1) Cover letter, CV, research statement, and the teaching dossier; 2) Publications.

Applicants must arrange for three signed letters of reference from individuals familiar with the candidate's research and teaching to be sent directly to: Dr. Joel Levine, Chair, Department of Biology, University of Toronto Mississauga, by email (letters must be printed on letterhead, signed, dated and scanned) to: biology.utm@utoronto.ca.

ogy.utm@utoronto.ca.

If you have any questions regarding this position please contact Prof. Joel Levine at biology.utm@utoronto.ca. All application materials, including reference letters must be received by the closing date of May 25, 2020 11:59 pm EST.

The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ persons, and others who may contribute



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Other

AustSocSAB StudentResearchGrants	46	SSE IntlEventGrants DeadlineExt Jun1	50
DifferentStats DifferentResults	46	SSE LifetimeAchievementAward DeadlineExtended Apr26	50
EcologyEvolution CallForPapers Telomeres	46	SwedishFellowships TheoreticalBiol	50
EvolutionaryBiology Adaptation CallForPapers	47	Teaching With Online Simulations	51
Evolution board game	47	WestarcticaInc ConsResScholarship FreeApplication Apr25	51
MolEcol TelomereSpecialIssue	48		
OnlineBook PhylogeneticsInTheGenomicEra	48		
Online EvolEcol Seminars	49		
Quantitative Genetics	49		

AustSocSAB StudentResearchGrants

Applications for the Australasian Society for the Study of Animal Behaviour's 2020 student research grants are open. ASSAB is committed to supporting behavioural research within the Australasian region, with an emphasis on providing opportunities for earlier-career scientists. As such, in 2020 ASSAB will support innovative research by providing \$2500 towards research expenses for particularly promising projects and students undertaking research in the Australasian region.

About the awards: - Up to 2 Grant Awardees, each receiving \$2500 (AUD) - Up to 2 Highly Commended applications - Both successful and highly commended applicants will receive \$200 towards registration for the annual ASSAB Conference in the year following their award, at which grant winners will be asked to report on their project via spoken presentation.

How to apply: Applicants are required complete a very brief form detailing the significance, structure, and timeline of the proposed research, which is available to download via the society's website at www.assab.org/student-grants. Once completed, applications should be emailed in PDF format to grants@assab.org. The closing date for applications in 2020 is May 1st. Full details are available at the society's website (www.assab.org/student-grants).

Dr. Thomas E. White Grants Officer Australasian Society for the Study of Animal Behaviour www.assab.org
ASSAB Grants Officer <assabgrants@gmail.com>

DifferentStats DifferentResults

I sent this message yesterday and neglected to include this link to the project: <https://t.co/D48viuKYRm?amp=1> If you're overwhelmed right now (as many of us are) and have no interest in taking on anything extra, stop reading this. However, if you're in a position to play with a bit of data to distract yourself from the troubles of the world, read on.

Have you ever wondered to what extent results in evolutionary biology and ecology vary just because of the choices we make when processing and analyzing data?

If so, we invite you to help us find out by analyzing a

data set that many other evolutionary biologists and ecologists are also analyzing. We estimate that the analysis will take about a day of your time. However, your single analysis (completed sometime in the next three months or so) will earn you co-authorship on our paper titled "Same data, different analysts: variation in effect sizes due to analytical decisions in ecology and evolutionary biology" (this paper is already provisionally accepted at BMC Biology through a new publishing model known as registered reports, where peer review occurs prior to study implementation).

If you think this project is interesting, but you'd rather not take on a data analysis, we're also recruiting people to peer review the contributed analyses. Ideally, each peer reviewer will review four analyses. These internal peer reviewers are also invited to be co-authors (by the way, identities of people conducting specific analyses or peer reviews will not be shared, so even if you join the project as a co-author, your name will not be linked to a particular analysis or review).

We want people from across the spectrum of experience and expertise 'V we would love to include anyone who would analyse ecological or evolutionary data for their work (including grad students).

If you participate, you have a choice between two data sets, each with its own question. The two questions are: 1) "To what extent is the growth of nestling blue tits (*Cyanistes caeruleus*) influenced by competition with siblings?" 2) "How does grass cover influence *Eucalyptus* spp. seedling recruitment?"

Sending warm wishes to your home office, workplace, kitchen table'K wherever you are based as we ride out this pandemic.

-Tim Parker, Hannah Fraser, and other project leaders

Tim Parker <parkerth@whitman.edu>

EcologyEvolution CallForPapers Telomeres

We are pleased to announce that we are compiling a special issue of the journal *Molecular Ecology* focusing on how telomeres can be used to understand aspects of evolution and ecology.

This issue will highlight the insights that telomeres can provide across a diversity of taxa, situations and conceptual areas. We will include empirical studies across as

wide a taxonomic breadth as possible, but also reviews and opinion pieces on key issues and emerging areas that relate to this scope. Technical papers on new methods to measure or analyse telomeres and how these may promote evolutionary or ecological understanding, are also encouraged. We are aiming for a first submission deadline of January 10, 2021.

Some suggestions for conceptual reviews or opinion pieces: The when and where of telomere attrition: is early life attrition everything? Genetic effects on telomere length and attrition. How is telomere length variation maintained? Telomere function and dynamics across taxonomic groups. Telomeres and reproductive success. Anthropogenic effects and telomeres. Environmental pollution and telomeres Telomeres in conservation biology Uncovering life-history trade-offs involving telomeres Environmental variation and telomeres. Telomeres and telomerase. Phylogenetics and understanding of telomere evolution. New methods in measuring telomere length and telomere state Can interstitial repeats tell us interesting things about genome evolution?

Please contact the guest editors with informal enquiries or to discuss review or opinion papers

Kind regards,

David S Richardson (David.Richardson@uea.ac.uk)
Pat Monaghan (Pat.Monaghan@glasgow.ac.uk) Mats
Olsson (mats.olsson@bioenv.gu.se) Simon Verhulst
(s.verhulst@rug.nl)

Note: Please refrain from submitting actual articles until you receive an official invitation from Molecular Ecology. We encourage submissions of articles that fit both the scope of the special issue and meet the guidelines and criteria for Molecular Ecology. Please refer to the official Author Guidelines for detailed information. Of course, submission does not guarantee acceptance and all submitted manuscripts will go through the same rigorous and efficient peer review process as regular articles. We look forward to your submission. Additional questions about the author guidelines? Contact Sean Rogers (srogers@ucalgary.ca) or Ben Sibett (manager.molecol@wiley.com).

EvolutionaryBiology Adaptation CallForPapers

Dear all,

We are currently guest-editing a special issue of the Journal of Evolutionary Biology on the topic “Genetics and Genomics of Adaptation”. You can find more information at

https://onlinelibrary.wiley.com/page/journal/14209101/homepage/call_for_papers_genetics_and_genomics.html

The deadline for the expression of interest (with a title) is quite tight as it is the end of the current week (apologies for the late notice), but there is still some time for the submission of manuscripts.

Best wishes, Carmelo Fruciano, Paolo Franchini and Julia Jones

Carmelo Fruciano School of Biological Sciences University of Portsmouth, UK <http://www.fruciano.org/>
Carmelo Fruciano <c.fruciano@unict.it> Carmelo Fruciano <c.fruciano@unict.it>

Evolution board game

Dear Evoldir members, A few weeks ago, I released a free educational board game about climate change and evolution inspired by the work of the Evolutionary Ecology group at the University of Cambridge (<http://www.eeg.zoo.cam.ac.uk/>).

Everything needed for the game can be freely downloaded at the link <https://michelaleonardi.netsons.org/climate-change-board-game/> The idea is to let the player experience life as a medium/large mammal species in a world where climate changes unexpectedly. Every species has its DNA and collects mutations through time, allowing it to adapt to new habitats. Sometimes evolving is not an option, and the species must migrate or go extinct. It is also possible to integrate human-associated climate changes.

It has been designed as an educational resource for schools (groups of 4-5 people, with an approximate duration of 30 minutes to leave space for discussion and questions): we have used it successfully to do outreach at the Museum of Zoology, University of Cambridge. Still, it can also be played with friends and family.

At the moment it is available in English and Italian, a Portuguese (Brazilian) version of it will be also uploaded shortly.

Please, feel free to use it for educational purposes or for fun, and to get in touch for questions or comments.

Have a lovely day

Michela –

Michela Leonardi, PhD Evolutionary Ecology Group
Department of Zoology, University of Cambridge
<https://michelaleonardi.netsons.org/> < <https://michelaleonardi.netsons.org/climate-change-board-game/> > Twitter: @MikLeonardi

Michela Leonardi <ml897@cam.ac.uk>

MolEcol TelomereSpecialIssue

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This issue will highlight the insights that telomeres can provide across a diversity of taxa, situations and conceptual areas. We will include empirical studies across as wide a taxonomic breadth as possible, but also reviews and opinion pieces on key issues and emerging areas that relate to this scope. Technical papers on new methods to measure or analyse telomeres and how these may promote evolutionary or ecological understanding, are also encouraged. We are aiming for a first submission deadline of January 10, 2021.

Some suggestions for conceptual reviews or opinion pieces: The when and where of telomere attrition: is early life attrition everything? Genetic effects on telomere length and attrition. How is telomere length variation maintained? Telomere function and dynamics across taxonomic groups. Telomeres and reproductive success. Anthropogenic effects and telomeres. Environmental pollution and telomeres Telomeres in conservation biology Uncovering life-history trade-offs involving telomeres Environmental variation and telomeres. Telomeres and telomerase. Phylogenetics and understanding of telomere evolution. New methods in measuring telomere length and telomere state Can interstitial repeats tell us interesting things about genome evolution?

Please contact the guest editors with informal enquiries or to discuss review or opinion papers

Kind regards,

David S Richardson (David.Richardson@uea.ac.uk)
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Olsson (mats.olsson@bioenv.gu.se) Simon Verhulst

(s.verhulst@rug.nl)

Note: Please refrain from submitting actual articles until you receive an official invitation from Molecular Ecology. We encourage submissions of articles that fit both the scope of the special issue and meet the guidelines and criteria for Molecular Ecology. Please refer to the official Author Guidelines for detailed information. Of course, submission does not guarantee acceptance and all submitted manuscripts will go through the same rigorous and efficient peer review process as regular articles. We look forward to your submission. Additional questions about the author guidelines? Contact Sean Rogers (srogers@ucalgary.ca) or Ben Sibett (manager.molecol@wiley.com).

srogers@ucalgary.ca

OnlineBook PhylogeneticsInTheGenomicEra

Dear colleagues,

It is our great pleasure to announce the publication of the Open Access book “Phylogenetics in the Genomic Era”:

<https://hal.inria.fr/PGE/> The book covers various aspects of phylogenomics, from concepts and algorithms to programs and applications.

It is freely available as a pdf, downloadable as a single document or chapter by chapter. We hope to offer a print-on-demand option soon. Profits, if any, will be directly re-invested in the Peer Community In initiative (<https://peercommunityin.org/>).

We’re very proud of the content, and also of the proof of concept that much can be done without the (expensive) services of professional publishers. We would like to thank all the authors for their tremendous contributions to this collaborative effort.

Céline Scornavacca, Frédéric Delsuc, Nicolas Galtier

Institut des Sciences de l’Evolution CNRS - Université
Montpellier - IRD - EPHE Montpellier, France

Nicolas Galtier <nicolas.galtier@umontpellier.fr>

Online EvolEcol Seminars

Dear all,

We are organising an online seminar series in Evolution and Ecology and would like to invite you to join the online community of evolutionary biologists and ecologists for our upcoming talks.

We are a group of postdocs from the research groups of Alexei Maklakov, Simone Immler and Judith Mank at the University of East Anglia and the University of British Columbia.

Now that many departmental seminar talks and conferences have been cancelled or postponed, we believe there is a great opportunity to replace that otherwise missing stimulus, and to keep our international research community connected. To that end, we are inviting some of the most exciting scientists in the community to share their research.

When: 9-10AM PST / 5-6PM BST, first talk next Wed 8 April, up to 3 seminars/week (Mon, Wed, Fri)

Where: talks broadcast on Zoom, live-streamed to our YouTube channel <https://www.youtube.com/channel/UCMsYvoHLNVm4rbcTLj162zQ>, Q&A for 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-cylz6q41-IL4o9EXDEbSKQ4kh5KFvnQ Our upcoming talk schedule: Wed 8 April Prof. Iain Couzin (Max Planck Institute of Animal Behaviour, University of Konstanz, Germany) <http://collectivebehaviour.com/people/couzin-iain/> Mon 13 April Prof. Kayla King (Department of Zoology, University of Oxford, UK) <https://www.zoo.ox.ac.uk/people/dr-kayla-king> Wed 15 April Prof. Molly Przeworski (Department of Biological Sciences, Columbia University, USA) <https://biology.columbia.edu/people/przeworski> Fri 17 April Dr. Harmit Malik (Fred Hutchinson Cancer Research Center, USA) <https://research.fhcrc.org/-malik/en/labmembers/harmitmalik.html> Wed 22 April Prof. Doris Bachtrog (Department of Integrative Biology, UC Berkeley, USA) <https://bachtroglabberkeley.wordpress.com/> With more

speakers to come!

Hope that you can join us!

Best wishes, Iulia Darolti Elizabeth Duxbury Andreas Sutter Wouter van der Bijl

For more information please contact the organizers Elizabeth Duxbury - E.Duxbury@uea.ac.uk Iulia Darolti - darolti@zoology.ubc.ca Andreas Sutter - A.Sutter@uea.ac.uk Wouter van der Bijl - wouter@zoology.ubc.ca

Benjamin Furman <benjamin.ls.furman@gmail.com>

Quantitative Genetics

ANNOUNCEMENT:

Quantitative Genetics - Cambridge University Press

Armando Caballero

Quantitative genetics is the study of continuously varying traits, which make up the majority of biological attributes of evolutionary and commercial interest. This book provides a much-needed up-to-date, in-depth yet accessible text for this field. In lucid language, the author guides readers through the main concepts of population and quantitative genetics, and their applications. Written to be approachable to even those without a strong mathematical background, applied examples, a glossary of key terms, and problems and solutions, support students in grasping important theoretical developments and their relevance to real-world biology. An engaging, must-have textbook for advanced undergraduate and postgraduate students. Given its applied focus, it also equips researchers in genetics, genomics, evolutionary biology, animal and plant breeding, and conservation genetics, with the understanding and tools for genetic improvement, comprehension of the genetic bases of human diseases, and conservation of biological resources.

Quantitative Genetics Hardcover - 30 April 2020
<https://www.amazon.co.uk/Quantitative-Genetics-Armando-Caballero/dp/1108481418> Armando Caballero <armando@uvigo.es> Armando Caballero <armando@uvigo.es>

SSE IntlEventGrants DeadlineExt Jun1

In light of the uncertainties around event planning for the next few months, the Society for the Study of Evolution (SSE) International Committee has extended the deadline for two of their grants.

A message from the International Committee:

“Due to uncertainties concerning the COVID-19 pandemic, its potential impact on scientific events, and its distressing effects on our communities, we are extending the application deadline for these grants to June 1, leaving more time for organizers to adjust to the current situation and have a better vision about the future. We are also happy to consider applications at any time as long as our budget for the year has not been entirely spent. We will also consider applications for virtual conferences and remote events. If an event has been approved for funding and needs to be postponed, we can arrange to reimburse the organizers once the meeting has actually taken place.”

1. “Co-sponsorship of symposia organized by non-US evolution societies” The goal of this award is to foster communication between scientists from different countries by stimulating scientific dialogue through co-sponsored symposia. Evolution societies with limited financial resources will have the opportunity to invite speakers who are SSE members to their meeting. This will provide growth opportunities for both societies, since it will not only benefit the hosting society but also create opportunities for new collaborations for the invited speakers.

New deadline: June 1, 2020

More information: <https://bit.ly/2RgjTV3> 2. “Evolution International Events Award” These events are aimed at furthering the purpose of SSE by fostering international collaborations amongst evolution oriented societies and scientists. Eligible events would include specialized symposia, workshops and short courses in any aspect of evolutionary biology. The events could be hosted either in the US or abroad and preference should be given to events that specifically include participants from countries other than the USA.

New deadline: June 1, 2020

More information: <https://bit.ly/3aJ92ut> –

*Kati Moore*she/her/hers *Communications Manager*
Society for the Study of Evolution communica-
tions@evolutionsociety.org www.evolutionsociety.org
communications@evolutionsociety.org

SSE LifetimeAchievementAward DeadlineExtended Apr26

The deadline to submit a nomination for the SSE Lifetime Achievement Award has been extended to April 26.

This award recognizes individuals who have made substantial contributions to the study of evolution, who have demonstrated outstanding mentorship of trainees, and/or who have provided noteworthy service to the evolution community. The awardee will be chosen this summer and will be presented at the 2021 Evolution meeting in Albuquerque, NM. SSE values the contributions of diverse researchers and encourages nominators to consider all potential mentors and colleagues. Self-nominations are welcome.

<http://www.evolutionsociety.org/society-awards-and-prizes/lifetime-achievement-award.html> *Kati Moore*she/her/hers *Communications Manager*
Society for the Study of Evolution communica-
tions@evolutionsociety.org www.evolutionsociety.org
communications@evolutionsociety.org

SwedishFellowships TheoreticalBiol

The Swedish Collegium for Advanced Study (SCAS) has a new call to the program in the Natural Sciences, including the theme THEORETICAL BIOLOGY, see:

http://www.swedishcollegium.se/subfolders/-Fellowships/natsci_theoretical%20biology.html
SCAS offers fellowships to provide 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 application may be for the entire academic year or alternatively for one academic semester. In previous years, shorter stays have also been funded.

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 is arranged by the Collegium.

Please feel free to contact Hans Ellegren (hans.ellegren@ebc.uu.se) or me if you have any questions!

Best wishes,

Claus Rueffler Associate Professor

Department of Animal Ecology Evolutionary Biology
Centre Uppsala University Norbyvägen 18D 752 36 Uppsala Sweden

Phone: +46-(0)18-471 2639

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

Teaching With Online Simulations

Dear friends

Our students are at home and I would like to teach variation, gene flow, genetic drift and natural selection using online tools like games or Apps. Suggestions?

Thanks for any help?

Voltolini

VOLTOLINI <jcvoltol@uol.com.br>

WestarcticaInc ConsResScholarship FreeApplication Apr25

DUE TO THE ECONOMIC SITUATION RESULTING FROM COVID19, WE ARE WAVING THE APPLICATION FEE THIS YEAR. THE APPLICATION FOR

THE RESEARCH SCHOLARSHIP IS NOW FREE.

Westarctica, Inc announces the first annual Westarctica Conservation Scholarship, a \$500 graduate research grant for the study of climate change. The goal of this research scholarship is to invest in early-career researchers who are pursuing a career in climate-change science. The topic is intentionally vague, and can include research into range-changes, evolution of adaptive characteristics, etc. Be creative!

Who we are: Westarctica, Inc is a non-profit organization focused on advocating for global conservation, framing conversations around Western Antarctica, an uninhabited ecosystem with no political advocates. Conserving our polar ecosystems means many things reducing carbon use to halt warming and melting of polar ice, learning to talk to people who deny the problem, and researching better alternatives to virtually every aspect of modern living.

Qualification: This research scholarship is available to anyone who meets the following criteria: * pursuing a graduate (Master PhD) in any nationally-accredited university or organization (i.e. zoo, field station) in the world. * researching a topic aligned with climate-change or global conservation issues. * planning a research project for the summer of 2020.

Application Procedure: Please fill out the form here (<https://www.westarctica.info/scholarship>). You will be asked to answer five questions, each in 200 words or less (unless otherwise specified): * In 20 words or less, describe the research question you are addressing. * What is the broad problem this question is addressing? * Why should the public care about your question/the problem/your research? * What possible solutions to climate-change might your work propose? * How will this money improve your research or the proposed solutions?

These applications will be reviewed by a panel of scientifically trained people from a variety of research and conservation backgrounds, as well as Westarctica, Inc board members. Finalists will be chosen, and the above answers will be submitted to the active members of the organization for a final vote.

Important Dates: April 25, 2020 (5pm EST): Applications Close May 4-8, 2020: Finalists responses will be shared with the Members May 9-13, 2020: Member Voting May 15, 2020 Winner Announced

Requirements: In accepting the award, you agree to do one follow-up interview at the end of the research period, and complete one online short-course on talking about climate change to non-believers.

If there are any questions, please feel free to email conserve@westarctica.info

Sincerely, Sheri Sanders Director of Conservation West-

arctica, Inc. conserve@westarctica.info

conserve@westarctica.info

PostDocs

AMU Poznan EvolutionaryImmunogeneticsBorrelia	52	UCalifornia Merced ComparativePopulationGenomics	60
Arizona ComputationalPopulationGenomics	53	UConnecticut HostMicrobiomeEvolution	60
ClemsonU FacialEvoDevo	53	UFerrara UTrieste Italy PopConsGenomics Bioinformatics	61
CornellU GenomicsEducationInitiative	54	UIllinois UrbanaChampaign EvolutionaryBiomechanics	62
CzechRepublic PopulationGenetics	55	UKonstanz 2 ExperimentalEvolutionOfSymbiosis	62
DFO Halifax FishGenomics	55	ULausanne ComputationalBiology	63
ETH Zurich MicrobialEvolution	56	UManitoba SturgeonEvolution	64
Heidelberg LungMicrobiomeEvolution	56	UPittsburgh HostMicrobeInteractions	64
IBENS Paris EvolutionaryGenomicPrimates	57	UppsalaU TheoreticalPopulationGenetics	65
JagiellonianU TardigradeEvolution	57	UWisconsinMadison PopulationGenomics	66
Norway Bioinformatics	58	WSL Zurich AshGenomics	67
SaoPaulo EvolEffectDefaunation	58		
SouthKorea EcoEvolutionaryDynamics	58		
StLouisU FungalEvolGenomics	59		
Stockholm Phylogenomics	59		

AMU Poznan EvolutionaryImmunogeneticsBorrelia

Postdoc:AMU_Poznan.EvolutionaryImmunogeneticsBorrelia

Evolutionary Biology Group of Professor Jacek Radwan (<http://evobio.home.amu.edu.pl>) at Adam Mickiewicz University, Poznan, is offering a Post-Doc in an NCN-funded project aiming to investigate coevolution between Lime disease agent, *Borrelia afzelli*, and its rodent host at the level of genes. The candidate should hold PhD degree in biological sciences or bioinformatics

and should have significant achievements in the area of evolutionary biology, molecular genetics or bioinformatics, published in international scientific journals. The employment is offered for up to four years, starting ideally in July 2020, but it is negotiable. Please apply before 30 May 2020. Further information about the project and application procedure can be obtained from the project leader via email: jradwan@amu.edu.pl

Prof. Jacek Radwan Evolutionary Biology Group Adam Mickiewicz University ul. Uniwersytetu Poznanskiego 6 61-614 Poznan Poland <http://evobio.home.amu.edu.pl/> j.w.radwan@gmail.com

Arizona Computational Population Genomics

A postdoctoral research associate position is available in the Gutenkunst group, in the Department of Molecular and Cellular Biology at the University of Arizona. The group focuses on computational population genomics, with an emphasis on methods development. For more information, see <http://gutengroup.mcb.arizona.edu> or contact Dr. Ryan Gutenkunst at rgutenk@email.arizona.edu.

The postdoc will contribute to an NIH-funded project to develop and apply methods for inferring novel models of natural selection from population genomic data. In particular, the postdoc will work on two-locus methods for inferring the distribution of fitness effects of new mutations, potentially including epistasis. The new methods will be applied to data from humans, *Drosophila*, and other model organisms. The postdoc will also have the freedom to contribute to other ongoing projects and to develop their own projects that mesh with the group's interests.

Applicants should have a Ph.D. in computational biology, bioinformatics, statistics, evolutionary biology, or a related field. Applicants should have prior computational experience and be motivated, creative, and collegial. Experience with statistical inference for complex models is advantageous. The University of Arizona has great strength in population and evolutionary genetics, offering potential interactions with Drs. Joanna Masel, David Enard, Joseph Watkins, Mike Barker, and others. Computational resources are similarly excellent. The campus is highly interdisciplinary and very collegial. The University of Arizona is an EEO/AA - M/W/D/V Employer.

At 2,500 feet above sea level, culturally diverse Tucson, Arizona is nestled among five mountain ranges in the beautiful Sonoran Desert and is surrounded by Saguaro National Park. Housing is affordable, quality of life is high, and outdoor recreation opportunities include the southernmost ski area in the United States and over 100 miles of bike trails. The area receives over 350 days of sunshine per year and enjoys average high/low temperatures of 82/54 degrees F.

Applications should include a C.V., cover letter, and contact information for three references. Please sub-

mit applications by emailed Dr. Gutenkunst at rgutenk@email.arizona.edu. Application review begins April 30, 2020 and will continue until the position is filled.

“Gutenkunst, Ryan N - (rgutenk)”
<rgutenk@arizona.edu>

ClemsonU FacialEvoDevo

The Powder lab in the Department of Biological Sciences at Clemson University is seeking a motivated postdoctoral fellow to work on the evolution of transcriptional enhancers in facial development. This project aims to understand the functional and morphological impact of genetic variation in *cis*-*regulation. Supported by an NSF-CAREER grant, this work will utilize ATAC-seq, RNA-seq, *in vivo** reporter assays, and CRISPR/cas9-mediated embryological manipulations to identify and assess how non-coding variation underlies facial development and evolution using cichlid fishes and zebrafish. Support is for two years with potential for renewal beginning 1 June 2020, or at a mutually-agreed upon date.

Clemson University is located in the beautiful upstate area of South Carolina, with proximity to mountains, lakes, and larger urban areas. The university hosts excellent facilities to conduct the advertised research. We have access to AALAC-accredited animal facilities, the Clemson Light Imaging Facility, and the Clemson University Genomics and Bioinformatics Facility, all of which offer excellent training to assist planned research. The PI is committed to providing mentorship that facilitates diverse career options going forward.

*Qualifications: *

Applicants should have a PhD in evolution, genetics, development, bioinformatics, or a related field; peer-reviewed publications; and enthusiasm and drive to progress specified research.

Preference will be given to candidates with demonstrated experience with ATAC-seq, RNA-seq, and/or zebrafish embryology.

Strong candidates will also be creative and independent thinkers, have effective oral and written communication skills, and possess the ability to collaborate with and mentor a diversity of colleagues including graduate and undergraduate students.

*Application Instructions: *

Applicants must submit the following: (1) cover letter, (2) a curriculum vitae, (3) a description of relevant research experience and motivation/interest in the current position (1 page maximum), and (4) contact information (including telephone numbers and e-mail addresses) for three professional references.

All application materials must be submitted online at <https://apply.interfolio.com/75339>. Review of applications will begin 1 May 2020 and continue until the position is filled.

Questions regarding the search and position may be sent to Kara Powder (kpowder@clemsun.edu).

Kara E. Powder Assistant Professor of Biological Sciences Clemson University www.karapowder.wordpress.com *

Kara Powder <kpowder@clemsun.edu>

CornellU GenomicsEducationInitiative

Postdoctoral Associate: Exploring how undergraduate learning of multifactorial genetics affects belief in genetic determinism

Applications are invited for a fulltime post-doctoral researcher in the Department of Ecology and Evolutionary Biology (EEB) at Cornell University. The successful candidate will explore undergraduate thinking about genetic determinism, develop and implement several undergraduate genetics education interventions, measure the ability of these interventions to influence belief in genetic determinism, and work with instructors to create an updated curriculum that honors the complexity of twenty-first century genetics. This project is part of a collaboration that includes Dr. Brian Donovan (BSCS Science Learning) and Dr. Gregory Radick (BSCS Research Affiliate and Professor of History and Philosophy of Science at the University of Leeds).

This project will involve developing and revising educational interventions that teach undergraduates concepts about multifactorial genetics (e.g., GxE, GWAS). The primary duties and responsibilities include developing these interventions, using surveys to measure thinking about genetic determinism in undergraduate students from several institutions, deploying these interventions in multiple classrooms using randomized controlled trials, conducting think-aloud interviews with undergraduate students, analyzing data from the interventions,

and helping to develop curricular materials that address findings in the study. The successful candidate will also disseminate the results through publications and presentations at meetings.

Discipline-based education research is growing at Cornell, with faculty and collaborators in physics, biology, and other STEM fields, as well as a number of new post-docs, graduate and undergraduate student researchers. The successful candidate will have an opportunity to mentor and work with many individuals and participate in weekly education journal clubs and research meetings with the larger EEB and Cornell community.

Preferred qualifications include:

- Ph.D. in biology, genetics, biology education research, or closely related field
- Experience with relevant literature and education research methods, expertise in quantitative research methods and statistics (proficiency in multilevel statistical modeling using R, STATA, SAS, or HLM), and experience with qualitative research approaches such as conducting interviews with students using think-aloud protocols
- Knowledge of and experience with the field of genetics (e.g., GxE, GWAS)
- Ability and desire to work collaboratively, mentor graduate and undergraduate students, and to also work independently
- Project leadership, time management, communication, and writing skills

The Postdoctoral Associate will be appointed for a one-year period with the possibility of extension for two additional years based on satisfactory performance.

To apply:

Applicants should submit a cover letter, CV, and 2-3 page research statement including relevant background and experiences, as well as the names and email or phone contacts of three professional references to: <https://academicjobsonline.org/ajo/jobs/15915>. Review of applications will begin on May 15, 2020.

Please contact Dr. Smith (mks274@cornell.edu) with any questions.

Diversity and Inclusion are a part of Cornell University's heritage. The College of Arts and Sciences at Cornell embraces diversity and seeks candidates who will create a climate that attracts students and faculty of all races, nationalities, and genders. We strongly encourage women and underrepresented minorities to apply. Cornell University is a recognized EEO/AA employer and educator, valuing AA/EEO, Protected Veterans,

and Individuals with Disabilities. –

Michelle Smith, Ph.D. Associate Professor Cornell University Department of Ecology and Evolutionary Biology
 mks274@cornell.edu 607-254-7081 <https://ecologyandevolution.cornell.edu/michelle-k-smith>
 Irby Lovette <ijl2@cornell.edu>

Czech Republic Population Genetics

Postdoc in Population Genetics and Community Ecology

A three-year Postdoc position is available for a highly motivated candidate to help explore the interface between population genetics and community ecology. The processes that maintain genetic variation in populations and allow species to coexist in diverse communities are likely to interact, but are typically addressed separately. However, genetic variation is likely to have a key role in determining species coexistence. Similarly, species diversity may improve maintenance of genetic variation within interacting populations.

The postdoc position is part of a frontier, high-level funding from 2020 to 2025 (ERC-CZ grant). The candidate will lead the population genomics aspect of the project, which includes laboratory microcosm experiments, experimental evolution, field surveys and ecological modelling. This collaborative project utilizes a novel experimental community model system of wild *Drosophila* species and their parasitoids from tropical Australia. We will sequence genomes of five *Drosophila* and five parasitoid species and use whole genome genotyping to quantify changes in genetic variation and link host resistance phenotypes to their associated genotype. There will also be opportunities to develop the project in a direction of the candidate's own choosing.

The successful applicant will join the Laboratory of Experimental Ecology [<http://lab.hrcek.net>] at the Biology Centre, Czech Academy of Sciences, Ceske Budejovice, Czech Republic, under the supervision of Dr Jan Hrcek. The laboratory is a multinational team of PhD students, postdocs and technicians and the applicant will have the opportunity to work extensively with other team members. The laboratory can provide substantial resources and support for exceptional research. The laboratory is part of the Department of Ecology, a dynamic international centre for research on interaction networks, with regular publications in leading journals. Further,

the candidate will collaborate within a wide network of the PI's collaborations and establish new links for this project.

The review of applications will begin on 10th June 2020 and will continue until the position is filled. The salary of 50.000-60.000CZK/month gross + benefits more than comfortably covers living expenses in Ceske Budejovice and international holiday travel. Further, there will be opportunity to apply for fellowships. The working language is English and applicants from all countries are eligible.

Required: - A PhD degree in Biology with a strong track record - Experience with population genetics or genomics - Experience in bioinformatics or population genetic modelling

Desirable: - Research experience with laboratory experiments or insect ecology

To apply please send one document with your CV, contact details for three references, and cover letter stating qualifications, previous work and motivation to Jan Hrcek [janhrcek@gmail.com].

Jan Hrcek <janhrcek@gmail.com>

DFO Halifax Fish Genomics

NEW POSTDOC POSITIONS FOR 2020 'V Postdoctoral Fellow positions with Fisheries and Oceans Canada on fisheries genomics in Halifax, NS, Canada.

Positions: Several postdoctoral fellow positions (2) are available at Fisheries and Oceans Canada (Halifax, NS) with the Bradbury Lab. Species of primary interest are Atlantic Salmon, Arctic Charr, Atlantic Cod, and Common Lumpfish but current projects include other anadromous fish and species of marine invertebrates as well. The lab's research is broadly concerned with the application of genomic tools to inform marine management and conservation

Candidates must have a PhD in fisheries science, population genetics, or genomics

Application: Please email Ian Bradbury (ibradbur@me.com) with (1) a letter describing your interests in this position and your previous research experience, and (2) a recent CV. Formal applications must be submitted through the Postdoctoral Research Program through Fisheries and Oceans Canada. Review of will applications begin right away with several po-

sitions available as soon as possible, and will continue throughout 2020.

Ian Bradbury <ibradbur@me.com>

ETH Zurich MicrobialEvolution

Postdoc Position in Microbial Evolution at ETH Zürich

The Pathogen Ecology group at ETH Zürich seeks a postdoctoral researcher to join our team for a project investigating antibiotic-resistance plasmids in microbial communities. The project is funded by the Swiss National Science Foundation.

Our group studies microbial ecology and evolution in the context of infectious disease. Current topics include the evolution of antibiotic resistance and bacteria-virus interactions. The group is collaborative, international and includes researchers from a range of backgrounds. For more information, see our webpage: <https://pe.ethz.ch>. The group is part of the Institute of Integrative Biology at ETH Zürich (<https://ibz.ethz.ch>).

We are looking for a highly motivated researcher who can develop projects, carry out experiments, analyze and communicate the results, and interact with other scientists with a high degree of independence. Applicants must have a PhD in a relevant discipline and excellent communication skills in English. Advanced knowledge of microbiology, molecular biology, bioinformatics, genomics or evolution will also be advantageous. The position is for two years. ETH Zürich is an equal opportunities employer.

Research topic: The overall aim is to gain new insights into the spread of naturally occurring plasmids in multi-species microbial communities, such as those in the human gastrointestinal tract. We plan to do this by measuring parameters that drive the spread of clinical resistance plasmids in experimentally assembled communities, and by tracking plasmids in species-rich communities sampled from human gut microbiomes. By doing so, we hope to learn something new about the role of interspecific interactions in the spread of mobile genetic elements, and to identify reservoir species/strains for clinically important plasmids. The postdoc will work on some of these objectives, collaborate with other group members, and potentially develop other related projects.

Further information about being employed at ETH Zürich is available here: <https://ethz.ch/en/the-eth-zurich/working-teaching-and-research.html>. Further en-

quiries about this position can be sent by email to alex.hall@env.ethz.ch.

To apply send a single pdf to alex.hall@env.ethz.ch including (1) cover letter, (2) CV and list of publications, (3) contact details for 2-3 referees. We will start reviewing applications after 15 May and then until the position is filled, with a likely start date toward the end of 2020.

Hall Alex <alex.hall@env.ethz.ch>

Heidelberg LungMicrobiomeEvolution

In the group of Dr. Sébastien Boutin, at the Translational Lung Research Center Heidelberg (Germany), a PostDoc position is available from 01/07/2020, funded for 1 year and renewable until end 2023 by the German Center for Lung Diseases.

The project centers on microbiome of the human airways in the context of chronic lung disease. The candidate will be involve in the microbiome analysis of ongoing clinical trial (Cystic fibrosis, COPD, Idiopathic pulmonary fibrosis) as well as translational research focusing on the influence of the microbiome in the different disease to pinpoint differences and common evolution patterns of the microbiome in chronic pulmonary diseases.

Candidates must hold a PhD and should have specific knowledge in microbiome analysis using next generation sequencing, microbial ecology and evolution and bioinformatics. Independent and self-reliant work is expected.

The lab offers full technical equipment allowing state-of-the art microbiology, in house sequencing facility. We are an interdisciplinary, highly motivated team working in the field of microbiome and microbial genomic.

Please send your application as one pdf file to : sebastien.boutin@med.uni-heidelberg.

Best regards,

Dr. Sébastien Boutin Junior Group Leader “Microbiome” | Translational Lung Research Center Heidelberg (TLRC) | German Center for Lung Research (DZL)

Department of Infectious Diseases, Medical Microbiology and Hygiene | Heidelberg University Hospital | Im Neuenheimer Feld 324 | 69120 Heidelberg Tel. +49 6221 56-34746 | Fax. +49 6221 56-5857 | E-Mail:

sebastien.boutin@med.uni-heidelberg.de

“Boutin, Sébastien” <Sebastien.Boutin@med.uni-heidelberg.de>

IBENS Paris Evolutionary Genomic Primates

Applications are invited for an ERC-funded postdoctoral research position at the Institute of Biology of the Ecole Normale Supérieure (IBENS) in Paris, France. Position is for two years, with possibilities for extension. Start date: from July 1st 2020, flexible.

We are hiring an enthusiastic postdoc to work with Dr Camille Berthelot on ERC Starting Grant EVOMENS, which seeks to understand how menstruation evolved in the primate uterus. Menstruation is a recent evolutionary innovation in primates: the trait is present in some species (humans, baboons) but not in closely related others (vervets). The molecular and genetic bases of menstruation are not fully understood, despite its involvement in critical gynecological conditions. EVOMENS aims to profile cellular populations, gene expression and gene regulation in the uterine lining of several primates across the female hormonal cycle to characterize how menstruation evolved at the functional level. The postdoc will be in charge of functional genomics experiments (single-cell transcriptomics, cell sorting, cell population RNA-seq and ATAC-seq) and data analysis.

Applicants must have a PhD degree or equivalent, or have submitted their thesis at the time of application. The applicant should have wet-lab experience relevant to the project such as functional genomics experiments, transcriptomics, experimental genetics, cell sorting and/or cell culture. Computational experience is appreciated, but not required - however, the successful candidate will be expected to develop that skillset and will receive appropriate support. The postdoc will also be expected to write manuscripts, deliver research presentations and be involved in the daily life and management of the laboratory.

The postdoc will join the Dynamics and Organisation of Genomes laboratory, located at the Institute of Biology of the ENS. ENS is a prestigious university with a vibrant academic life and is part of the Paris Sciences et Lettres (PSL) network of universities and research centers, ranking 1st in France according to the Times Higher Education's World University Ranking. The

institute is located in the heart of Paris, in the Quartier Latin known for its lively student life, restaurants and bars.

Salary: euro 30,000 to euro 48,000/year depending on experience; includes extensive healthcare and benefits. Position is full-time and funded for two years, with opportunities for extensions.

Application deadline: May 1st 2020 Start date: from July 1st 2020 (negotiable)

Application: Please send your cover letter and detailed CV, with the names of two referees and your relationship to them to camille.berthelot@bio.ens.psl.eu

Informal inquiries welcome.

– Camille Berthelot, PhD Laboratoire Dynamique et Organisation des Génomes (Dyogen) Institut de Biologie de l'ENS, CNRS, INSERM, Université PSL 4 rue de l'Ulm, 75230 Paris Cedex 05, France – mail : cberthel@biologie.ens.fr tel : +33(0)144322375

Camille Berthelot <camille.berthelot@bio.ens.psl.eu>

Jagiellonian University Tardigrade Evolution

PostDoc position in tardigrade evolution

A 3-year postdoctoral position in tardigrade evolution at the Jagiellonian University in Krakow (Poland) in the team of Dr. ukasz Michalczyk.

The main goal of the project is to test how reproductive mode and cryptobiotic abilities affect dispersal and, in consequence, speciation and extinction rates in tardigrades. Tardigrades are a phylum of microinvertebrates that dwell a wide variety of habitats throughout the globe. They are famous for their cryptobiotic abilities that allow them to withstand extreme conditions (including outer space) and are also thought to aid dispersal of individual species. Moreover, tardigrades exhibit various reproductive modes, including dioecy and parthenogenesis. Theory predicts that both asexual reproduction and cryptobiotic survival should increase dispersal potential. On the other hand, both reproductive mode and dispersal abilities are hypothesised to affect speciation and lineage extinction rates. Thus, tardigrades are an interesting model to address some of the fundamental questions of modern evolutionary biology, biogeography and taxonomy such as mechanisms underlying the evolution of biodiversity or evolution of sex.

The successful candidate will be involved in laboratory work (extraction of tardigrades from moss samples, slide preparation, morphometrics and imaging in light microscope, processing specimens for scanning electron microscope, karyotyping, DNA extraction, amplification and multilocus sequencing (NGS), species identification, testing cryptobiotic abilities, and taking care of tardigrade cultures) and in data analysis (mostly phylogenetic and phylogeographic analyses) as well as in preparation of manuscript drafts and in the promotion of results at seminars and conferences.

The salary is ca. 4 —500 —PLN per month after tax (typically, cost of life in Krakow for a single young person is ca. 3 —500 PLN/month).

Deadline for applications: 20th May 2020.

Detailed information on the project, university, our team and the application procedure is available at <http://tardigrada.edu.pl/PostDoc.htm> Dr. ukasz Michalczyk LM@tardigrada.net

ukasz Michalczyk <LM@tardigrada.net>

Norway Bioinformatics

#Postdoc #research #position in my lab :) Postdoc position in rapid diagnostics of #AntimicrobialResistance : #Bioinformatics and #MachineLearning https://www.jobbnorge.no/en/available-jobs/job/185050/-postdoc-position-in-rapid-diagnostics-of-antimicrobial-resistance-bioinformatics-and-machine-learning?fbclid=IwAR1hpG7fpEO2rb26X_XDA3r1aVZpW4n52FN05Xn5Z6iNKqG2Cv_KEcVpIhI yusuf.zhc@gmail.com

SaoPaulo EvolEffectDefaunation

POST-DOC POSITION IN BRAZIL One post-doctoral position with fellowship funded by the São Paulo Research Foundation (FAPESP) is available to work on the project entitled “Mammal diversity in the fragmented landscape of northeastern Atlantic Forest, Brazil”. The project aims to: 1. Using seed traps, investigate the composition, richness and abundance of the seed rain in fragments of Atlantic Forest in the state of Alagoas; 2. Assess recruitment limitation and its components (i.e.,

dispersal and establishment limitation) from seed rain and seedling establishment; 3. Evaluate the effect of environmental factors (fragment size, degree of degradation and isolation) and inherent plant factors (seed size, dispersal syndrome) on patterns of recruitment limitation; 4. Analyze a seed rain database already available for Atlantic Forest areas.

Applicants may have completed a PhD in Life Sciences (Ecology, Botany, Zoology or Biology). Applicants must present a CV that attests the capacity to publish papers on high-quality journals. Knowledge on landscape ecology (GIS), statistics (R), and collection and preservation of plants and seeds are highly desirable. Also, applicants must be available to live in São Paulo and Alagoas states, Brazil; have a driver license; speak English fluently; be available for fieldwork (in the first 2 years) at forest remnants of northeastern Atlantic Forest (Alagoas state, Brazil).

How to apply: Deadline for submission is May 15, 2020. Applications exclusively by email (Marco A. Pizo - marco.pizo@unesp.br) with the following documentation (PDF files only):

1. An essay written in English, up to three pages long, describing your motivations and previous experience to work on the project;
2. Short CV (three pages maximum), including previously published works attesting the candidate’s capacity to carry out the project;

This opportunity is open to candidates of any nationalities. More info at <http://fapesp.br/oportunidades/-3525/> Marco Aurélio Pizo

Departamento de Biodiversidade Instituto de Biociências - UNESP Av. 24-A, no. 1515 13506-900, Rio Claro - SP, BRASIL Fone: (19) 3526 4294

Marco Aurelio Pizo Ferreira <marco.pizo@unesp.br>

SouthKorea EcoEvolutionaryDynamics

Title: Postdoc Position in Statistical physics of ecology and evolution group

The research group led by Dr. Hye Jin Park (homepage: hjpark.me) at Asia Pacific Center for Theoretical Physics (in South Korea) invites applications for a post-doctoral research fellow in eco-evolutionary modeling from perspective of statistical physics. The research will

focus on evolving ecosystems with novel mutations. Particularly, identifying characteristics of ecological communities shaped by eco-evolutionary dynamics and understanding underlying mechanisms are the main subjects. Also, the group has a broad range of research interests, appreciating independent ideas.

The work conditions are 1. One year contract with a possible extension of one year 2. The appointment ideally starts this June but negotiable 3. A monthly salary is 3,300,000 KRW 4. 20 days a year of paid annual leave 5. Part of relocation cost will be supported

Qualified candidates are requested to send a CV with a brief motivation to hyejin.park@apctp.org with a title [Postdoc Application - fullname]. The deadline is April 30th.

If you have any questions, don't hesitate to contact me (hyejin.park@apctp.org).

Sincerely yours, Hye Jin Park

Hye Jin Park <hjpark@evolbio.mpg.de>

StLouisU FungalEvolGenomics

Postdoctoral Researcher Position in evolutionary genomics and genetics of fungi

An NSF-funded postdoctoral researcher position is available in the Lin lab in the Department of Biology at Saint Louis University to study the evolution of transcription initiation mechanisms in fungi. The position is available immediately with a flexible starting date. The initial appointment is for one year, with an option for renewal up to three years based on satisfactory performance reviews. Starting salary is \$47k/year plus excellent benefits. All applications will be considered until a selection of the appropriate candidate is made.

The postdoctoral researcher will participate in the generation and analyses of quantitative maps of transcription start sites for a large number of fungal species. This includes CAGE sequencing library preparation and sequencing data analysis, molecular genetic analysis, etc. Candidates should have a PhD in molecular biology, genetics, genomics, or related topics. Experience with sequencing library preparation, fungal molecular genetics, or bioinformatics would be greatly valued. Interested applicants should send a CV, brief summary of research experience, and contact information for at least three references by email to Dr. Zhenguo Lin, zhenguo.lin@slu.edu.

More information about the Lin lab can be found at zlinlab.org.

About Saint Louis University Founded in 1818, Saint Louis University is one of the nation's oldest and most prestigious Catholic institutions dedicated to student learning, research, healthcare and service. It is an Affirmative Action, Equal Opportunity Employer and encourages nominations of and application from women and minorities. For more information, please visit slu.edu.

Zhenguo Lin <zhenguo.lin@slu.edu>

Stockholm Phylogenomics

In view of the current situation we have extended the closing date for applications and delayed the starting date for this position.

Postdoctoral position in phylogenomics

A two-year postdoctoral position is available in the Department of Zoology, Swedish Museum of Natural History, Stockholm. The position is supervised by Prof. Ulf Jondelius, as a part of the project "Evolution of Xenacoelomorpha, an ancient animal group" funded by the Swedish Research Council. The goal of this project is to perform an analysis of phylogeny, evolutionary rates and gene content of the marine animal group Xenacoelomorpha using transcriptomic and genomic data. The successful candidate will manage and analyse transcriptome and genome sequencing data, perform phylogenomic analyses and write papers. There will be opportunities to participate in undergraduate teaching and supervision of students.

Qualifications Postdoctoral positions are appointed primarily for purposes of research. Applicants are expected to hold a Swedish doctoral degree or an equivalent degree from another country. The degree should have been completed no more than three years before the deadline for applications. In the appointment process, special attention will be given to research skills. We are looking for candidates with primarily dry-lab skills in the fields of genomics, transcriptomics and phylogenomics including experience with managing, processing and analysing next-generation sequencing data. Specific experience with metazoan evolution and microscopic invertebrates constitutes an advantage, but is not strictly necessary. The candidate must be highly motivated, creatively thinking with a collaborative attitude, have strong writing skills and a record of high-quality scien-

tific publications. Excellent English language skills both written and spoken, are a requisite.

Terms of employment The position involves full-time employment for a maximum of two years, Start date 2020-08-01 or as per agreement. The Swedish Museum of Natural History strives to be a workplace free from discrimination and with equal opportunities for all.

Application deadline 1 May 2020

Informal queries may be directed to ulf.jondelius@nrm.se

FURTHER INFORMATION AND HOW TO APPLY (in English): <https://www.nrm.se/en/ommuseet/-jobbahososs/ledigatjanster.9005019.html> Ulf Jondelius, PhD Professor of Invertebrate Zoology, Swedish Museum of Natural History Box 50007 SE-104 05 Stockholm, Sweden

Ulf Jondelius <Ulf.Jondelius@nrm.se>

UCalifornia Merced ComparativePopulationGenomics

We are looking for a highly motivated Postdoctoral Scholar to join our lab to lead comparative genomic analyses among species of sea stars with the goal of understanding their varying susceptibilities to sea star wasting disease and related population dynamics and differentiation.

The sea star wasting disease outbreak of 2013-2014 was one of the largest marine mass mortality events on record, affecting up to ~20 species of sea stars in the northeastern Pacific. Mortality rates varied greatly across species. Population-level sampling before and after the outbreak in several species is providing insight into the genomic signatures of resistance. Our goal here is to integrate this population-level perspective with comparisons across multiple species. Your principle role will be in bioinformatics 'X curating and using multiple reference quality genomes and population genomics datasets to understand between and within species differences in response to wasting disease 'X but there is potential for some benchwork and fieldwork if such interests you.

A full description of the position and how to apply is available at <https://aprecruit.ucmerced.edu/JPF00986> This research builds on an NSF-funded project < https://www.nsf.gov/awardsearch/showAward?AWD_ID=1737381 > in collaboration with the Earth BioGenome

Project < https://www.pacb.com/press_releases/pacific-biosciences-to-support-sequencing-of-california-species-for-the-earth-biogenome-project/> and Revive & Restore < <https://reviverestore.org/> >.

Deadline for applications is Monday, 01 June 2020 (Pacific Time).

Enquiries to Mike Dawson at mdawson@ucmerced.edu

Michael Dawson <mdawson@ucmerced.edu>

UConnecticut HostMicrobiomeEvolution

University of Connecticut: Postdoctoral researcher studying microbiota / host gut interactions and co-evolution.

A postdoctoral researcher position is available in Dr. Daniel Bolnick's research group (<https://bolnicklab.wordpress.com>), in the Department of Ecology and Evolution at the University of Connecticut. We seek a successful researcher with experience in cell/tissue culture or mechanistic study of host-microbiome interactions.

Tasks: Thanks to funding from the Gordon and Betty Moore Foundation's Symbiosis in Aquatic Systems Initiative, the Bolnick lab is embarking on a collaboration with Dr. Rebecca Carrier and Dr. Sam Scarpino at Northeastern University, Dr. Natalie Steinel at the University of Massachusetts Lowell, and Dr. Katherine Milligan-Myhre at the University of Alaska Anchorage. We will develop a microfluidics gut-on-a-chip system to enable mechanistic study of the interactions between a small fish, threespine stickleback (*Gasterosteus aculeatus*), and its native gut microbiota. The postdoc will work primarily in the Bolnick Lab at the University of Connecticut, but will frequently collaborate with and visit the other research groups on the team, and work closely with a second postdoc based at the University of Massachusetts Lowell. The postdoc will work on improving methods to maintain primary cell cultures of stickleback gut epithelium and immune cells, kept alive on microfluidic gut-on-a-chip system developed in the Carrier Lab. These cells will be observed during interaction with sticklebacks' gut microbiota (form the Milligan-Myhre lab), and assayed for cell activity using methods developed with the Steinel Lab, and statistical approaches developed in the Scarpino Lab. This platform for experimental study of host-

microbiome interactions can ultimately facilitate studies of host-microbiome coevolution. The postdoc's tasks will include experiments to evaluate cell culture methods, manuscript preparation, presentations at scientific conferences, and some limited animal care.

Duration: The position is available for 27 months with current funding, with possible extensions contingent on additional grant support. The postdoc should be able to start in late summer or early fall 2020, exact dates to be negotiated with the PI.

Compensation: Starting salary will be \$52,700 plus health benefits.

Minimum Qualifications: Applicants should have a PhD in evolution, genetics, immunology, cell biology, or a closely related field. Prior experience with cell or tissue culture is strongly preferred. Previous research experience and publications should demonstrated a commitment to basic research, good work ethic, lab skills, organizational ability, and publication productivity.

Preferred Qualifications: Expertise in molecular genetics (particularly RNAseq), CRISPR/cas9 gene editing, RNAi, or other experimental genetic manipulations is a strong plus, as is experience with flow cytometry.

Applications should electronically submit a single pdf file containing the following, in order: 1) A statement of past research achievements, including relevant skills. This should not exceed two single-spaced pages.

2) A statement of what you can contribute to the Bolnick Lab's research, and how this fits into your career goals. This should not exceed one single-spaced page.

3) CV 4) A copy of two publications or submitted manuscripts.

3) A list of three references, with contact information (email, telephone, and mailing address). We will request letters directly from these references, after identifying top candidates.

The application file should be submitted by applying online at <https://hr.uconn.edu/jobs>, Staff Positions, Search # 494463. You may independently contact Dr. Daniel Bolnick (daniel.bolnick@uconn.edu). Include the subject line "Fish-on-Chips Postdoc: <YOUR NAME>". Applications must be received by May 1, 2020 for full consideration, though the position is open until filled.

For questions about this position, please email Dr. Bolnick (daniel.bolnick@uconn.edu). For information about the Bolnick Lab visit the lab website (<https://bolnicklab.wordpress.com>), lab photostream (<https://www.flickr.com/photos/98765823@N08/-albums>), and Dr. Bolnick's Google Scholar

page (<https://scholar.google.com/citations?user=-cfwxm0AAAAAJ&hl=en>).

The University of Connecticut is an Equal Opportunity Employer. Applicants with questions about disability services can privately discuss their application with the University of Texas Disability Services Office (<http://sites.utexas.edu/disability/>).

Dr. Daniel I. Bolnick

— / —

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>

UFerrara UTrieste Italy PopConsGenomics Bioinformatics

We are seeking expressions of interest for 2 Post Doc positions to be recruited for a project led by the University of Ferrara (Italy).

This three-year project was selected in 2019 by the Italian Ministry for Education and Research, but funding was delayed until February 2020.

Using five iconic endangered Italian endemics as model species, we plan to obtain chromosome-scale, fully-annotated genome assemblies and whole-genome resequencing data to investigate the dynamics of the accumulation of deleterious mutations in small populations, and their impact on individual fitness.

One postdoc position will be based at the University of Ferrara under the supervision of Giorgio Bertorelle, and will focus on population genomics analyses. The second postdoc position will be based at the University of Trieste under the supervision of Marco Gerdol, and will focus on the de novo assembly and annotation of the genomes of the five target species.

Additional details can be found at www.endemics.it. Interested candidates should contact Giorgio Bertorelle (ggb@unife.it), or Marco Gerdol (mgerdol@units.it). The starting date can be negotiated, depending also of course on the evolution of the Covid-19 situation.

"ggb@unife.it" <ggb@unife.it>

Uillinois UrbanaChampaign EvolutionaryBiomechanics

A Postdoctoral researcher position is available in the Anderson lab in the Department of Evolution, Ecology and Behavior at the University of Illinois, Urbana-Champaign. The Anderson lab seeks a post-doctoral scholar with strong experience in some combination of the following: biomechanics, energetics, experimental fracture mechanics, Impact dynamics, and/or dynamic fracture modeling. The applicant will work alongside the PI and lab members to assess how physical principles underlying functional performance influence evolutionary processes in the context of energy flow through biological puncture systems (e.g. teeth, spines and stingers).

The research goals are to 1) execute a comprehensive series of controlled puncture experiments at variable dynamic scales, 2) establish a set of energy balance equations that model how shape, material and kinematic variables influence the energetics of puncture, and 3) use these models to examine the evolution of puncture systems across several lineages.

The expectations of the position include the quasi-independent execution of puncture experiments and energetics modeling, willingness to apply engineering knowledge to evolutionary biology problems (including learning basic comparative evolutionary techniques), and active engagement in mentoring students and disseminating scientific results.

The ideal candidate will have experience in fracture mechanics/impact dynamics, a strong publication record, and a PhD in a relevant Biology or Engineering-related discipline.

The Anderson lab is an evolutionary biomechanics lab focused on examining questions of how physical and mechanical principles influence evolution. The lab is equipped with an Instron materials testing device, tabletop gas gun for impact experiments, a high-speed video camera capable of filming 24000 fps at full resolution (2 million fps maximum), and other resources. The lab also has active collaborations with several engineers in the UIUC College of Engineering, offering lab members access to further resources.

The University of Illinois at Urbana-Champaign, located 120 miles south of Chicago, offers a variety of cultural opportunities that showcase the area's diverse

ethnic population, superb public and private schools, quality public transportation, and a rapidly expanding community of high-tech businesses.

The UIUC College of Liberal Arts and Sciences is a world leader in research, teaching, and public engagement. Faculty in the College create knowledge, address critical societal needs through the transfer and application of knowledge, and prepare students for lives of impact in the state, nation, and globally. To meet these objectives, the College embraces and values diversity and difference through hiring faculty candidates who can contribute through their research, teaching, and/or service to the diversity and excellence of the Illinois community.

The start date for this position is negotiable. Evaluation of applications will begin immediately and priority will be given to applications that are complete by May 1st. The position will remain open until a suitable candidate is found. Initial support is for two years with additional time contingent upon performance. The University of Illinois conducts criminal background checks on all job candidates upon acceptance of a contingent offer. As a qualifying federal contractor, the University of Illinois System uses E-Verify < <https://go.uillinois.edu/EVerifyParticipation> > to verify employment eligibility < <https://go.uillinois.edu/EVerifyRightToWork> >.

Applications must include a CV, a cover letter describing research interests and career goals (2 pages max), and the names and emails of 3 references. Application materials should be emailed to Dr. Phil Anderson (andersps@uillinois.edu) with the subject line "Puncture Postdoc."

The University of Illinois is an Equal Opportunity, Affirmative Action employer. Minorities, women, veterans and individuals with disabilities are encouraged to apply. For more information, visit <http://go.uillinois.edu/EEO>

Phil Anderson
andersps@uillinois.edu

UKonstanz 2 ExperimentalEvolutionOfSymbiosis

Two postdoctoral positions: experimental evolution of symbiosis

Two postdoc positions available in the Aquatic Ecology and Evolution Group (Becks group) at the University of Konstanz. Join us for a project to work on the

evolutionary process and ecological conditions favoring the evolution of symbiosis. We are looking for two highly motivated postdocs that will join us to gain new insights into the biologically relevant conditions, evolutionary pathways and mechanisms that lead to evolution of obligate symbiotic interactions between algal cells and ciliates. The project “Will you kindly cooperate” aims to combine experimental evolution, genomic and cell-biological analysis, automated and high throughput microscopy approaches. There is the opportunity to develop additional projects, as long as they fall under the umbrella of the research interests of the project. Both successful candidates will be responsible for planning and running experimental evolution studies. Position 1 will focus on genomics and transcriptomics analyses of isolates from the experimental evolution studies. Position 2 will focus on the cellular and molecular analyses of isolates from the experimental evolution studies using imaging techniques and high throughput approaches.

Qualifications: Candidates are required to hold a Ph.D. and a background in evolutionary biology or ecology. For position 1, you should have strong programming and bioinformatics skills. For position 2, you should have relevant experience in imaging of microorganisms or plankton organisms and in image analyses. Candidates should also have an ability to conduct independent research, take initiative, and interact with other scientists. Excellent English communication and writing skills are expected. The position is funded through the “Symbiosis in Aquatic Systems Initiative” by Gordon and Betty Moore Foundation Funding is available for 2 - 3 years. Starting date is negotiable, ideally no later than summer 2020.

The collaborative research environment in the lab is highly integrative, very international, and operates in English. Further information on researchers and research in the Becks lab can be obtained from our homepage (<https://www.limnologie.uni-konstanz.de/becks>). Konstanz is a very beautiful and pleasant place to live as it borders the third largest lake in Central Europe and lies at the foothills of the Alps. The University of Konstanz is an equal opportunity employer.

Interested candidates should send a CV, a brief cover letter and contacts of 2 professional references to

lutz.becks@uni-konstanz.de. Review of applications will begin immediately and continue until the position is filled. More information on the

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 <lutz.becks@uni-konstanz.de>

ULausanne ComputationalBiology

Postdoctoral associate in computational biology Expected start date: 01.06.2020 or to be agreed Contract length: 1 year, renewable Activity rate: 100/% Workplace: University of Lausanne, Genopode, 1015 Lausanne

The group of Prof Christophe Dessimoz is seeking candidates for a Postdoctoral (Premier Assistant) position at the Departments of Computational Biology, University of Lausanne, Switzerland. Working at the interface between biology and computer science, the Dessimoz Lab (<https://lab.dessimoz.org/>) seeks to better understand evolutionary and functional relationships between genes, genomes, and species. The group is also a member of the SIB Swiss Institute of Bioinformatics.

The ideal applicant will have research interests generally aligned with the interests of the Dessimoz Lab. We have ongoing projects that would benefit from a skilled and motivated postdoc working in the areas of phylogenetic methods, in semantic data integration (e.g. RDF/SPARQL), and in bioinformatic algorithmic development. However, this is a broad search, and we expect the successful applicant to develop her or his own research direction in collaboration with the lab.

There will also be opportunities to gain teaching experience (e.g. via student project supervision and contribution to undergraduate or graduate teaching).

Working conditions in Lausanne are extremely competitive, and include access to state-of-the-art computing and sequencing facilities. The environment is highly international, and all activities are conducted in English.

Profile Sought

We are seeking to recruit candidates with either a PhD degree in biology with solid computational and quantitative skills, or with a PhD in a quantitative area (mathematics, computer science, physics, engineering, ...) with prior research activity in biological sciences.

Prior experience in publishing papers in peer-reviewed journals is required, but note that we support the principles of the San Francisco Declaration on Research Assessment (DORA) principles.

Candidates need to have demonstrated programming skills ideally in the areas of bioinformatics, computa-

tional biology, and comparative genomics. Experience with evolutionary and comparative genomics analyses would be an advantage. The applicants should have a strong ability to work in a team.

A requirement from the funder (Swiss National Science Foundation) is that postdocs can only be employed up to 5 years after obtaining their PhD (6 in case of maternity leave).

How to apply

The application should fill in the form linked below and provide the following elements:

Curriculum vitae including list of publications Reference to best paper accompanied by a brief supporting statement (approx. 200 words) The names and contact details of 2-3 references Copy of official PhD certificate (or, if you will be graduating shortly, the expected graduation date)

Applications should be submitted via the UNIL HR system using this following link: <http://bit.ly/postdoc3>

Committed to promoting equal employment opportunities among its staff members, the University of Lausanne particularly encourages applications by women.

To ensure full consideration, applications should be received by 30 April 2020.

SNSF Prof, UNIL Dept of Comp Bio & UNIL Center for Integrative Genomics Associate Prof, UCL Genetics Evolution and Environment & UCL Computer Science Group Leader, Swiss Institute of Bioinformatics

<http://lab.dessimoz.org> - Tel: +41 21 692 4155 - Twitter: @cdessimoz

christophe.dessimoz@unil.ch

UManitoba SturgeonEvolution

Postdoctoral Position in Sturgeon genomics and transcriptomics

Under the Canadian Species At Risk Act the Committee on the Status of Endangered Wildlife in Canada (COSEWIC) recently reaffirmed their recommendation that Lake Sturgeon be listed as endangered or of special concern across Canada. Three of the four designatable units of Lake Sturgeon populations in Canada are found in Manitoba and an intensive research effort supported by NSERC and Manitoba Hydro in partnership with indigenous stakeholders, conservation groups, and provin-

cial and federal legislative bodies has been ongoing for at least the last five years forming part of a long-term commitment to augment, conserve and sustain populations of Lake Sturgeon throughout the province and North America. Understanding underlying genetic variation within these populations is key to the success of this research effort. In collaboration with colleagues from UC Davis this research will develop tools to sequence, assemble and annotate the polyploid genome of Lake Sturgeon providing a valuable resource for understanding phenotypic development during early life history and therefore development of appropriate rearing practices for stock enhancement programs.

A maximum of four years of funding is available for a post-doctoral salary commensurate with NSERC guidelines. This position will be responsible for directing genome sequencing, assembly and annotation of the lake Sturgeon genome. Additionally, existing transcriptomic datasets will be available for assessment of transcriptomic responses to environmental factors in Lake Sturgeon related to growth and regulation of pH balance. The successful candidate will join a multidisciplinary research team examining environment phenotype interactions during early life history and developing tools for improving our use of eDNA and elemental signatures to understand effectiveness of stock enhancement strategies in the conservation of this ancient species. Extensive knowledge and experience in the use of bioinformatic tools is an essential for this position, prior experience in working with polyploid datasets is a distinct asset. Interested candidates should email a cover letter and CV to Dr. W. Gary Anderson Gary.Anderson@umanitoba.ca.

Dr. W. Gary Anderson,

Professor, Dept. Biological Sciences, Room 475 Duff Roblin Building, University of Manitoba, Winnipeg, MB Canada, R3T 2N2 Tel: (204) 474-7496

Gary Anderson <Gary.Anderson@umanitoba.ca>

UPittsburgh HostMicrobeInteractions

University of Pittsburgh - Postdoc in Host-Micobe Interactions

The lab of Dr. Kevin Kohl (University of Pittsburgh) is looking to recruit a postdoctoral researcher focused on the ecology/evolution of host-microbe interactions, using approaches of integrative and systems biology.

The concept of phenotypic plasticity, or the ability of a single genotype to produce varying phenotypes depending on the environment, is a central focus of biology. However, animals are not a “single genome” in that they also maintain intimate associations with complex communities of microbes. It has been proposed that the genomes of hosts and associated microbes should be combined into a wholistic “holobiont” and “hologenome”, upon which natural selection acts. Yet, our knowledge of how the microbiome contributes to host plasticity remains poorly understood.

This critical gap will be addressed by experimentally determining how the microbiome and rodent host species interactively influence animals’ physiological responses to variation in diet. This project will test whether gut microbial communities contribute to phenotypic traits and differential host phenotypic plasticity across organisms by conducting microbial transplants into germ-free mice and inventorying aspects of host and microbial physiology at numerous levels of biological organization (gene expression, enzyme activities, whole-system performance metrics). Data integration will be a crucial aspect of this project, and so applicants experienced in systems biology or computational approaches are especially encouraged to apply.

This position will also provide opportunities for mentoring undergraduates, conducting scientific outreach, and designing and implementing allied side projects tailored to the skills and interests of the postdoctoral researcher.

This position is for one year, with renewal for a second year given sufficient progress. Start date is negotiable but expected to be late summer/fall 2020.

TO APPLY: Please go to www.tinyurl.com/-KohlPostDoc. This form has a few short writing prompts, as well as areas to upload a Cover Letter, CV, and contact information for 3 references. Review of applications will begin on May 1st.

Kevin Kohl <kevin.d.kohl@gmail.com>

UppsalaU Theoretical Population Genetics

A position as a postdoctoral researcher/fellow in theoretical population genetics is available at the Evolutionary Biology program, Department of Ecology and Genetics, Uppsala University, Sweden.

Further information about the position and details about application are available at: <https://www.uu.se/en/about-uu/join-us/details/?positionId=3D322453> You are welcome to submit your application no later than 2020-04-30.

For inquiries please contact: Carina Farah Mugal, carina.mugal@ebc.uu.se

Project description: Stochastic models have a strong tradition in population genetics. Diffusion and branching processes are frequently used to describe evolution forward-in-time. At the same time, birth-death processes such as the coalescent are used to track evolution backward-in-time. Duality relationships between forward-in-time and backward-in-time models have been established and analysed. Together, such mathematical treatment has led to a large body of theoretical population genetics and promoted our general understanding of evolution.

Building on concepts of theoretical population genetics, we have formulated a time-dependent Poisson random field model that permits describing allele frequency trajectories in nonstationary populations (doi: 10.1016/j.tpb.2016.06.003). This has, for example, enabled us to formulate an analytical description of the joint allele frequency spectrum of two populations during the process of speciation, and investigate the impact of incomplete lineage sorting on genomic signatures of natural selection.

The project profits from an interdisciplinary collaboration between the Department of Ecology and Genetics and the Department of Mathematics at Uppsala University.

Duties: Several extensions of the basic model of allele frequency evolution are of interest, such as dependence among allele frequency trajectories due to physical linkage and recombination. A relevant body of population genetics models that address recombination exists the sequential Markovian coalescent, the ancestral recombination graph and diverse branching process models.

The Postdoc project will start by investigating possibilities of integrating such models of recombination into the forward-in-time model of allele frequency evolution, which has been formulated by our group. In particular, analytical results on the allele frequency spectrum (AFS) in the presence of physical linkage are of interest. Ultimately, the derivation of such an AFS shall form the basis to analytically investigate the relationship between the recombination rate and measures of natural selection, which is a central question in evolutionary biology.

Qualifications required: For this position, the candidate must hold a PhD degree within mathematics, evolutionary biology, bioinformatics or another relevant field. The Postdoc candidate must have experience in mathematical biology and interest in population genetics. The candidate must be able to express themselves fluently in spoken as well as written English. In addition, the applicant must be able to work independently, have good collaborative skills and be able to communicate (both spoken as well as written). The applicant must have integrity and personal maturity, be able to take initiative and to handle setbacks.

To be eligible the candidate must have a PhD degree, or a foreign degree equivalent to this, completed less than three years before the application deadline. The three year period can be extended due to circumstances such as sick leave, parental leave, duties in labour unions, etc.

Carina Farah Mugal Department of Ecology and Genetics Evolutionary Biology Centre Uppsala University Norbyvägen 18D 752 36 Uppsala Sweden

<http://katalog.uu.se/profile/?id=3DN8-1504> När du har kontakt med oss på Uppsala universitet med e-post innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här: <http://www.uu.se/om-uu/dataskydd-personuppgifter/> E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: <http://www.uu.se/en/about-uu/data-protection-policy> “carina.mugal@ebc.uu.se” <carina.mugal@ebc.uu.se>

UWisconsinMadison PopulationGenomics

In light of the past month’s upheaval, I would like to clarify that: * This position described below remains open through May 1. * Start date is still flexible. * It should be possible to start work on a remote basis for the first few months if travel is not yet possible.

The research group of John Pool at the University of Wisconsin - Madison invites applications for a postdoctoral research position. There are multiple potential project areas, with an overarching theme of addressing big questions in population/evolutionary genetics. I’d like to give the successful candidate for this position a strong voice in shaping their research direction in the lab.

Potential research areas could include (but are not limited to):

* Model Inference for the Genetic Architecture of Adaptive Evolution When traits evolve in nature, we’d like to understand things like how many genes are involved, whether selection acts on standing variation or new mutations, whether it ultimately fixes the causative variants. We focus on local adaptation among *Drosophila melanogaster* populations from contrasting natural environments, which provides a powerful and efficient system for investigating these questions. One particular opportunity is to make statistical inferences about the genetic architecture of adaptation, in part from existing QTL mapping data.

* Fundamental Population Genetics We are interested in leveraging big data (such the >1000 genomes from our *Drosophila* Genome Nexus) to ask basic population genetic questions. Our lab is especially interested in leveraging genetic differentiation between populations to address classic but unresolved questions about the influence of natural selection on genomic diversity.

* Quantifying Adaptive Potential It is widely recognized that genetic diversity is a primary determinant of whether populations can rapidly adapt to new challenges. Yet in spite of its relevance to basic evolutionary biology and conservation, our understanding of adaptive potential is still quite lacking. Our lab is interested in which types of genetic diversity are most important for adaptive potential (e.g. within vs. between population) and how best to quantitatively estimate adaptive

potential within and among populations.

Our research group was founded 8 years ago and currently includes 1 postdoc and 6 graduate students. I have also advised 5 former postdocs, and the publication records of Amir Yassin and Justin Lack show what a productive environment our lab can be. I also welcome postdocs taking important components of our research with them when they found their own labs. Further lab info: <http://www.johnpool.net> UW-Madison offers a superb scientific environment with a supportive, collaborative, and egalitarian culture. Many labs focus on population genetics, evolutionary genomics, and Drosophila research: <https://evolution.wisc.edu/people/faculty/> <https://genetics.wisc.edu/drosophila-and-other-insects/> Madison offers an exceptional quality of life in a beautiful landscape, and has been ranked as the best US city for young adults. Downtown and campus are bordered by lakes, and Madison features diverse art, music, cultural, and culinary offerings. <http://www.visitmadison.com/media/rankings/> To apply, send a statement of research interests (up to 1 page) addressing the intersection between your own scientific interests and the Pool lab's research in terms of potential projects, along with a CV and contact info for 3 references.

I am interested in adding to the diversity of our lab in a broad sense, including gender balance, cultural perspectives, and intellectual backgrounds and skill sets.

Start dates are flexible. Salary follows the NIH scale. Individual or family health insurance is offered.

Applications are due May 1. However, earlier applications are welcome, and later applications may still be considered. Informal pre-application inquiries (e.g. to discuss potential research topics) are also welcome at any time.

John Pool Associate Professor Laboratory of Genetics
University of Wisconsin - Madison

"jpool@wisc.edu" <jpool@wisc.edu>

WSL Zurich AshGenomics

Post-Doc position for 1 year available at WSL (Switzerland) in Phytopathology / Fungal Virology (80-100%)

The WSL group Phytopathology is part of the Research Unit Forest Health and Biotic Interactions and investigates fungal diseases of forest trees with particular emphasis on diagnostics, population genetics and biological control. Within the European project HOMED "Holistic Management of Emerging Pests and Diseases", we offer a one-year position, starting on June 1, 2020, or upon agreement, as a Post-Doc in Phytopathology / Fungal Virology (80-100%)

You will analyze next generation sequencing data to detect viruses in the fungal pathogen *Hymenoscyphus fraxineus*, the causal agent of ash dieback in Europe. You will genetically characterize the identified viruses and compare native Asian with invasive European populations. You will also determine the effect of the viruses on the virulence of its fungal host and evaluate their potential for the biological control of ash dieback. Therefore you will intensively collaborate with our project partners and publish your results in international scientific journals.

You have a PhD in Natural Sciences, a strong background in phytopathology and preferably bioinformatics/genomics. Basic knowledge in virology and fungal biology is favorable. You are fluent in written and spoken English and have excellent skills in scientific writing. You are ambitious, proactive, highly motivated and flexible.

Please send your complete application to Michèle Bucher, Human Resources WSL, by uploading the requested documents through our webpage (<https://apply.refline.ch/273855/1035/pub/2/index.html>). Applications via email will not be considered.

Dr. Simone Prospero (<https://www.wsl.ch/de/mitarbeitende/prospiero.html>) Tel. +41 (0)44 739 22 48 and Dr. Daniel Rigling Tel. +41(0)44 739 24 15 will be happy to answer any questions or offer further information.

The WSL strives to increase the proportion of women in its employment, which is why qualified women are particularly called upon to apply for this position. <https://apply.refline.ch/273855/1035/pub/2/index.html> "deborah.leigh@wsl.ch" <deborah.leigh@wsl.ch>

WorkshopsCourses

Crete PythonMachineLearning Jul20-24	68	ONLINE PopulationGenomics May18-22	71
Online AdvancedRProgramming Jul6-10	69	Online R for evolution May20-21	71
ONLINE ComparativeGenomics Sep21-25	69	Videos for EvolutionaryBiology	72
ONLINE IntroMachineLearningInR Jul13-16	70	Vienna MICPhy Postponed	73
ONLINE Metagenomics Jun1-5	70		
Online MorphologicalPhylogenetics Oct19-30	70		

Crete PythonMachineLearning Jul20-24

Dear evoldir members,

Transmitting Science is offering the following courses:

(Please note that due to the COVID-19 outbreak, registration for this course is open, but it does not require payment at this moment. We will only receive payments once the outbreak has calmed down and travel restrictions have been lifted.)

'PYTHON MACHINE LEARNING IN BIOLOGY'

Instructor: Nichole Bennett (The University of Texas at Austin, USA) Dates: July 20th-24th, 2020 Location: Crete, Greece

COURSE OVERVIEW: The field of biological sciences is becoming increasingly information-intensive and data-rich. For example, the growing availability of DNA sequence data or clinical measurements from humans promises a better understanding of the important questions in biology. However, the complexity and high-dimensionality of these biological data make it difficult to pull out mechanisms from the data. Machine Learning techniques promise to be useful tools for resolving such questions in biology because they provide a mathematical framework to analyze complex and vast biological data. In turn, the unique computational and mathematical challenges posed by biological data may ultimately advance the field of machine learning as well. This course will cover basics of the Python programming language as well as the pandas and sklearn Python libraries for data wrangling and machine learning. The course is intended to give participants a conceptual overview of machine learning algorithms and an intuition for the

mathematics underlying them, equipping participants to be able to choose and implement appropriate models for biological datasets

For more information and registration: bit.ly/python-machine-learning-biology

'INTRODUCTION TO PYTHON FOR BIOLOGY'

Instructor: Nichole Bennett (The University of Texas at Austin, USA) Dates: July 13th-17th, 2020 Location: Crete, Greece

COURSE OVERVIEW: Python is a user-friendly and powerful programming language commonly used in scientific computing, from simple scripting to large projects. This workshop will provide hands-on practice in a biological context for beginners, with very limited prior programming experience. This course is designed to be very applied, and we will explore Python tools of immediate help to the working scientist. After completing this course, participants will be able to apply Python programming automation to their own research problems and should be equipped to continue their own Python learning. While this course will focus on data analysis using Python, participants will gain language-agnostic principles of programming, like automation with loops and encapsulation with functions, that will serve as best practices for their scientific computing.

For more information and registration: bit.ly/intro-python-biology

Contact: courses.greece@transmittingscience.com

All the best, Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.org
haris.saslis@gmail.com

Online AdvancedRProgramming Jul6-10

Dear all,

the Physalia course on “Advanced programming in R for biologists” will be held online from the 6th to the 10th of July.

Instructor: Dr. January Weiner 3rd (Staff scientist, Berlin Institute of Health, Germany).

This is a very practical course that aims at giving the students abilities in R programming that go beyond basic R usage. This includes both learning important frameworks as well as tips and tricks and coding style.

Participants will learn: 1) how to import, clean, reshape and visualize their data in R using Tidyverse 2) create complex/customized graphics in R 3) how to code in R (good coding practices and common fails) 4) create their own R packages 5) build reproducible reports with RMarkdown 6) create their Github page to share your code & materials with others.

For more information, please see: (<https://www.physalia-courses.org/courses-workshops>) (<https://www.physalia-courses.org/courses-workshops/course47/>)

Should you have any questions, please feel free to contact us: (<mailto:info@physalia-courses.org>)

Thanks and stay healthy,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org <http://www.physalia-courses.org/> =0A=0ATwitter: @Physacourses mobile: +49 17645230846 <https://groups.google.com/forum/#!forum/physalia-courses> info@physalia-courses.org

ONLINE ComparativeGenomics Sep21-25

Dear all,

the 3rd edition of the Physalia course on Comparative

Genomics will be held ONLINE from the 21nd to the 25th of September: <https://www.physalia-courses.org/courses-workshops/course34/> Instructors: Prof. Ingo Ebersberger (Goethe University Frankfurt, Germany) and Dr. Fritz J. Sedlazeck (Human Genome Sequencing Center at Baylor College of Medicine, USA).

This course will introduce biologists and bioinformaticians into the field of comparative genomics. We will cover a broad range of software and analysis workflows that extend over the spectrum from assembling and annotating small eukaryotic genomes, via the identification of single nucleotide variants (SNVs) and structural variants (SVs) within the population, to the assessment of their likely functional impact of the detected variants in an evolutionary context.

Learning outcomes:

- 1) Identification of SNPs and SVs using de novo genome assembly and read mapping strategies
- 2) Assessment of strengths and weaknesses of the different DNA sequencing technologies, Illumina, Pacific Bioscience, Oxford Nanopore, for the detection of variations
- 3) Strengths and pitfalls of de novo assembly and mapping approaches for comparative genomics
- 4) Hands on experience of state of the art methods to compare multiple genomes
- 5) Annotation of variations and comparative genomics analysis
- 6) Familiarity with biological sequence analysis in an evolutionary context

Programme: (<https://www.physalia-courses.org/courses-workshops/course34/curriculum-34/>)

Other upcoming Physalia courses will be also held online: <https://www.physalia-courses.org/courses-workshops/> Should you have any questions, please feel free to contact us at info@physalia-courses.org

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 17645230846 <https://groups.google.com/forum/#!forum/physalia-courses> info@physalia-courses.org

ONLINE IntroMachineLearningInR Jul13-16

Dear all,

the Physalia course “Machine Learning - a hands-on introduction” will be held online from the 13th to the 16th of July: (<https://www.physalia-courses.org/courses-workshops/course43/>)

The aim of this course is to provide a broad hands-on introduction to the use of multivariate methods and machine learning in R for the analysis of complex biological datasets.

Instructors:

Dr. Pietro Franceschi (Fondazione Edmund Mach, Italy) and Dr. Filippo Biscarini (National Research Council (CNR), Italy)

Programme: (<https://www.physalia-courses.org/-courses-workshops/course43/curriculum43/>)

Our other online courses: (<https://www.physalia-courses.org/courses-workshops/>)

All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR
info@physalia-courses.org <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 17645230846 <https://groups.google.com/forum/#!forum/physalia-courses> “info@physalia-courses.org”
<info@physalia-courses.org>

ONLINE Metagenomics Jun1-5

Dear all,

due to the COVID-19 pandemic the Physalia course on “Metagenomics, metatranscriptomics, and multi’omics for microbial community studies” will be also held online (<https://www.physalia-courses.org/courses-workshops/-course33/>)

Where: Free University Berlin (Germany)

Instructors: Dr. Curtis Huttenhower, Dr. Jeremy E. Wilkinson, Dr. Kelsey N Thompson, Dr. Eric Franzosa

(Department of Biostatistics, Harvard T.H. Chan School of Public Health)

This course will provide a thorough introduction to microbial community data analysis (metagenomics, metatranscriptomics, and other culture-independent molecular data) through a balanced approach of lectures and hands-on lab sessions. Course participants will learn how to process data from raw meta’omic sequencing files through appropriate bioinformatic methods and approaches for subsequent integrative statistical analyses. Participants are invited to bring their own data to the practical session on the final day or can use publicly available data from the Integrative Human Microbiome Project (HMP2).

Programme: (<https://www.physalia-courses.org/-courses-workshops/course33/curriculum-33/>)

All the Physalia courses will be held online until July: (<https://www.physalia-courses.org/courses-workshops/>)

Should you have any questions, please contact us at info@physalia-courses.org

Best, Carlo

Carlo Pecoraro, Ph.D

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Online MorphologicalPhylogenetics Oct19-30

Dear colleagues,

Registration is open for Transmitting Science online course: MORPHOLOGICAL PHYLOGENETICS: PRINCIPLES, APPLICATIONS, AND TECHNIQUES ’V 2nd edition.

Dates: October 19th-30th, 2020

This course will be delivered ONLINE: 35 hours of online live lessons. A good internet connection is required to follow the course.

Max number of students: 18, slots will be allocated in first come, first served basis.

Course Overview: An accurate reconstruction of evolutionary relationships among species is the cornerstone of

evolutionary biology. Building phylogenetic trees thus provides the fundamental framework upon which systematic, biogeographic and evolutionary research operates. Morphological phylogenetics provides a unique toolkit for inferring relationships, considering that the vast majority of the species that have ever lived are now extinct and can only be assessed based on morphological data. Additionally, combining fossils and morphological data with molecular data from extant species is becoming the most comprehensive method of assessing phylogenetic relationships on deep time and the time of origin of major evolutionary lineages. In this course, we will focus on the analysis of morphological data (and combining morphological data with molecular data) using multiple optimality criteria for phylogenetic inference. We will discuss the best available approaches to construct morphological data sets and their impact on phylogenies. We will follow with theory and hands-on practice of phylogenetic programs using maximum parsimony, maximum likelihood and Bayesian inference. Participants will learn how to combine morphological and molecular data for total evidence analyses, how to conduct time-calibrations using tip and node dating, different birth-death models, morphological clocks and combined evidence relaxed clock analyses. Softwares: Mesquite, TNT, RAxML, IQTree, Mr. Bayes and BEAST.

More information and registration: <https://www.transmittingscience.com/courses/-/www.transmittingscience.com/courses/-/evolution/morphological-phylogenetics-principles-applications-techniques/> or writing to courses@transmittingscience.com

With best regards Sole

Soledad De Esteban-Trivigno, PhD Scientific Director Transmitting Science www.transmittingscience.org Soledad De Esteban Trivigno <soledad.esteban@transmittingscience.org>

analysis from SNP data onwards and will cover the key analyses that may be required to successfully analyze a population genetic data set. The course will NOT cover steps prior to generation of a .vcf file or SNP data set such as NGS data demultiplexing, clustering and SNP calling (This is covered in detail in the Introduction to RADseq course). This course will introduce Linux and the command line environment, basic perl and python usage, file conversions and manipulation, population structure and differentiation in R, outlier analysis, landscape / seascape genomics and introgression. The course will use a range of software including the Linux operating system and R.

This course is aimed at postgraduate students and early career researchers who are interested in using population genomic tools in their research. No previous experience of bioinformatics is required, but an underpinning in evolutionary biology and basic population genetics concepts such as Hardy Weinberg Equilibrium and FST are desirable.

Having completed the course, students should have a good understanding of the software and methods available for population genomic analysis and be competent in population genomic analysis.

Programme: (<https://www.physalia-courses.org/-courses-workshops/course9/curriculum9/>)

Other upcoming Physalia courses will be also held online: <https://www.physalia-courses.org/courses-workshops/> Should you have any questions, please feel free to contact us at (<mailto:info@physalia-courses.org>)

All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org <http://www.physalia-courses.org> <https://www.physalia-courses.org/> [@physacourses](https://twitter.com/physacourses) mobile: +49 17645230846 <https://groups.google.com/forum/#!forum/physalia-courses> info@physalia-courses.org

ONLINE PopulationGenomics May18-22

Dear all,

the 5th edition of the Population Genomics course will be held online: <https://www.physalia-courses.org/-courses-workshops/course9/> Instructors: Dr. Martin Taylor and Dr. Lewis Spurgin (University of East Anglia, UK)

The course will cover the basics of population genomic

Online R for evolution May20-21

ONLINE COURSE 'V Introduction to R for ecologists and evolutionary biologists (IRFB03) This course will be delivered live

<https://www.prstatistics.com/course/introduction-to-r-for-ecologists-and-evolutionary-biologists-irfb03/> 20th - 21st May 2020

This is a 'LIVE COURSE' V the instructor will

be delivering lectures and coaching attendees through the accompanying computer practical'As via video link, a good internet connection is essential.

TIME ZONE 'V Western European Time 'V however all sessions will be recorded and made available allowing attendees from different time zones to follow a day behind with an additional 1/2 days support after the official course finish date (please email oliverhooker@prstatistics.com for full details or to discuss how we can accommodate you).

Course overview: The 2 day course will consist of a series of modules designed to build required R skills and statistical understanding to develop yourself or move on to more advanced courses. At its conclusion, participants will have acquired basic skills in coding with R, and will be able to perform and interpret simple analyses, and critically evaluate similar analyses from the scientific literature and technical reports. All example datasets used for practical'As will have an ecological and evolutionary theme.

Wednesday 20th

Morning 09:30 'V 12:30 What is R, why is it perceived as difficult and why its role in reproducible science makes it ideal. How R works: making life easier with Rstudio; how to install packages; and how to set up your workspace to your liking. Rnotebooks as the analogue of field and lab notebooks. Setting up a basic workflow as a template for all your analyses

Afternoon 13:15-17:00 Objects in R and their different classes: data is not just data. Importing basic datasets Basic data visualisation using ggplot Customising ggplots

Thursday 21st

Morning 09:30 'V 12:30 Basic statistics in R: summaries, tables, correlations, t-tests and ANOVA Simple linear regression as the foundations for nearly all statistical models Models are just lines on a page: adding our models to our graphs

Afternoon 13:15-17:00 Understanding linear model statistical outputs Using these outputs to gain insights about the data General linear models: fitting more than one line on a page Introduction to non-gaussian error models: Generalized Linear Models Friday 22nd Half day catch-up for other time zones

Email oliverhooker@prstatistics.com

Other online courses

Python for data science, machine learning, and scientific computing (PDMS02) 4 May 2020 - 8 May 2020 [https://www.prstatistics.com/course/python-for-data-](https://www.prstatistics.com/course/python-for-data-science-machine-learning-and-scientific-computing-pdms02/)

[science-machine-learning-and-scientific-computing-pdms02/](https://www.prstatistics.com/course/introduction-to-spatial-analysis-of-ecological-data-using-r-ispe03/) ONLINE COURSE 'V Introduction to spatial analysis of ecological data using R (ISPE03) 18 May 2020 - 21 May 2020 <https://www.prstatistics.com/course/introduction-to-spatial-analysis-of-ecological-data-using-r-ispe03/> Generalised Linear (MIXED) (GLMM), Nonlinear (NLGLM) And General Additive Models (MIXED) (GAMM) (GNAM01) 25 May 2020 - 28 May 2020 <https://www.prstatistics.com/course/generalised-linear-mixed-glmm-nonlinear-nlglm-and-general-additive-models-mixed-gamm-gnam02/> Stable Isotope Mixing Models using SIBER, SIAR, MixSIAR (SIMM06) 8 June 2020 - 11 June 2020 <https://www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm06/> Reproducible Data Science using RMarkdown, Git, R packages, Docker, Make & Drake, and other tools (RDRP01) 29 June 2020 - 3 July 2020 <https://www.prstatistics.com/course/reproducible-data-science-using-rmarkdown-git-r-packages-docker-make-drake-and-other-tools-rdrp01/> Applied Bayesian modelling for ecologists and epidemiologists (ABME06) 20 July 2020 - 24 July 2020 <https://www.prstatistics.com/course/applied-bayesian-modelling-for-ecologists-and-epidemiologists-abme06/> Species Distribution Modeling using R (SDMR02) 27 July 2020 - 30 July 2020

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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>

Videos for Evolutionary Biology

In this new era of distant engagement, those who tire of Power-Point may find the "Academy" approach of Salman Kahn a refreshing change (<http://www.khanacademy.org>). Students see multicoloured drawings, arrows, numbers and letters, moving across a black background to Khan's melodious vocal accompaniment. With pause and rewind options, they can proceed at their own pace. Each 15 minute video can act as a basis for a subsequent Zoom discussion. The courses have spread worldwide and volunteers have translated them into many languages.

While lacking Kahn's high oratorical skills, I have done my best to emulate his pen-tablet approach with a series of 54 short historically-orientated evolutionary biology

videos, primarily aimed at high school and first year college students.

01-12. Introduction to Evolutionary Principles (no history; <https://www.youtube.com/playlist?list=PL149AF63B4B8B20EC>) 12-24. Natural Selection (the history begins; <https://www.youtube.com/playlist?list=PL59A9C65FB0DCED9E>) 25-36. Blending Evolution (a Victorian hay-day; <https://www.youtube.com/playlist?list=PLCC0362CBEB47B5C0>) 37-54. Introns and Exons (forward to the modern era; https://www.youtube.com/playlist?list=PL378EB17561C23228&feature=edit_ok)

The videos may be found in YouTube or accessed by way of my “Video Lectures and Academy” webpage (<http://post.queensu.ca/~forsdyke/videolectures.htm>). This contains several, more advanced, full lectures. Here you may also access videos 1-36 by way of Vimeo.

Donald R. Forsdyke, Emeritus Professor Department of Biomedical and Molecular Sciences, Queen’s University, Kingston, Ontario, Canada <http://post.queensu.ca/~forsdyke/homepage.htm> [The above “post” URLs are shortly to be replaced by Queen’s IT with an alternative access point. In the interim they may be accessed by way of the Internet Archive: <https://archive-it.org/->

[collections/7641](#)]

Donald Forsdyke <forsdyke@queensu.ca>

Vienna MICPhy Postponed

Dear All,

Due to concerns regarding COVID19, we have decided to postpone MIC-Phy 2020 to a early 2021 date (probably January or February) that is to be determined at a later time.

For updates, please check ou website:<https://www.vetmeduni.ac.at/de/micphy2020/> With best wishes,

Carolin Kosiol and Rui Borges

(Organizing Comittee)

Carolin Kosiol Centre for Biological Diversity University of St Andrews St Andrews, UK ck202@st-andrews.ac.uk

Carolin Kosiol <ck202@st-andrews.ac.uk>

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 \LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be send to me at `Golding@McMaster.CA` and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.