
E v o l D i r

February 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.



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Asilomar ForestGenetics Jun16-18

The NAFGS first biennial meeting will be held June 16-18 in Asilomar, California; the meeting website (link: <https://treegenesdb.org/nafgsconference>) is now available with details on registration, abstract submission, and meeting schedule. We are accepting abstracts for posters and lightning talks which will be presented on the evening of June 16. The deadline for these abstracts is May 1. The meeting will include one day of presentations, a full day field trip to Big Basin Redwood State Park, and a symposium in honor of David Neale's retirement on the last day.

For more information on NAFGS please see the website (link: <https://treegenesdb.org/nafgs>). We hope you will

join our community in participating in NAFGS activities toward the advancement of our discipline.

north american forest genetics society
<noramforgen@gmail.com>

Avignon France ForestGeneticRescue Jan28-29

Lest days to register!

Conference: Genetics to the rescue, Managing forests sustainably in a changing world In Avignon, France, 28-29 January 2020.

The open conference days (28-29 January 2020) are built

around four topical sessions: - Genomes and the environment; - Local adaptation of climate change-related traits; - Conserving and using genetic diversity; - Evolutionary management of forests.

Important dates: - Submit your abstracts and posters: closed. - Early bird registration: closed. - Registration closes January 10, 2020.

Reduced registration fees for students - financial help for registering possible

More info: <https://colloque.inra.fr/confgentree2020>
Twitter: #rescueforest

The week also consists of the partners' annual assembly (Jan 27), a joint stakeholder consultation co-organized by EUFORGEN (Jan 30, upon invitation), a genomics training session (Jan 30) and a Wikipedia editing session (Jan 31). The scientific conference will welcome a maximum of 250 participants while the training and the stakeholder sessions held back to back with the conference will welcome no more than 80 participants each. The Wikipedia session is fully booked already.

The conference is organized by the H2020 project Gen-Tree (<http://www.gentree-h2020.eu/>) (@GentreeProject) and is held at the beautiful University of Avignon, France

Contact: Bruno Fady <bruno.fady@inrae.fr>, INRAE Avignon, France

"bruno.fady@inrae.fr" <bruno.fady@inrae.fr>

Budapest MathStatMolBio Apr18-19

The 30th Workshop on Mathematical and Statistical Aspects of Molecular Biology (MASAMB) will be held in Budapest on April 18 and 19, 2020.

Registration is open until March 10, 2020. For details see <http://masamb2020.elte.hu> and below.

Bioinformatics and statistical genetics, twin themes of the long-running series of annual MASAMB meetings, have gained huge impetus from large-scale genome sequencing projects and development of high-throughput biological assay systems, including gene-expression, proteomic, metabolomic and single-cell genomics technologies. These immense data resources, and the underlying complexities of molecular and cell biology, provide exciting research opportunities for numerate scientists.

With typically around 80-120 participants from mathematics, statistics, computer science, bioinformatics, biology and related fields, the MASAMB meetings provide an intimate setting for exchanging ideas in methodological and applied research. Research students and scientists newly entering the field of genomic research are particularly welcome and encouraged to submit abstracts. Details of previous meetings are available at the MASAMB archive: <https://www.ebi.ac.uk/goldman-srv/masamb/> Gergely J Szöllősi <sszolo@gmail.com>

Guelph Canada EnvironmentalDNA May28-29

Pathwaysto Increase Standards and Competency of Environmental DNA Surveys(PISCeS)International Conference will be held in Guelph, Canada on May 28-29, 2020.

Training eDNA Workshop: Wednesday, May 27, 2020

Registration is now open! Early bird registration deadline: January 31st, 2020.

To register visit <https://confreg.uoguelph.ca/-registration/Register/default.aspx?code=C000063>
Abstract submission deadline:February 14th, 2020.

Submit your abstract following the submission guidelines from https://www.uoguelph.ca/ib/PISCeS_2020
PISCeS 2020 International Conference is envisioned as a conference where academia, regulators, and industry will join in adiscussion on Pathwaysto Increase Standards and competency of Environmental DNA Surveys. Theintent of the conference is to explore and inform public policy, industry strategies and futureresearch on eDNA.For more conference details andkeydates visit:https://www.uoguelph.ca/-ib/PISCeS_2020 If you have any questions please emailpisces@uoguelph.caortloezaqu@uoguelph.ca

Tzitziki Loeza-Quintana, PhD

Postdoctoral Research Fellow Hanner Lab Department of Integrative Biology University of Guelph Guelph, ON, Canada tloezaqu@uoguelph.ca

Tzitziki Loeza Quintana <tloezaqu@uoguelph.ca>

Harvard DrewNodenEvoDevo May18

DO YOU WANT TO BE PART OF MEETING HONORING ONE OF GREATEST & MOST INFLUENTIAL DEVELOPMENTAL BIOLOGISTS OF THE LAST DECADES? Just send me an email to attend for free & let me know if you are also interested in giving short talk & contributing to special issue of journal Devel.Dyn..

Rui Diogo, PhD in Evol.-Funct. Morphol. & PhD in Hominid Paleobiol., Assoc. Prof. at Howard Univ. College Medicine, Dep. Anat., 520 W St. NW, Numa Adams Building, room 1101, Washington DC 20059, USA. | Fellow of American Association Anatomists

Diogo's Lab Website: <http://www.ruidiogolab.com>
 Diogo's books: <http://www.amazon.com/Rui-Diogo/-e/B001JS2K96> Diogo's Wikipedia page: https://en.wikipedia.org/wiki/Rui_Diogo Diogo's researchgate: https://www.researchgate.net/profile/Rui_Diogo
 Diogo's Lab Twitter: @Rui.Diogo.Lab

rui_diogo@hotmail.com

Heidelberg EvolSexualDimorphism Sep20-22

EMBO | EMBL Symposium: The Molecular Basis and Evolution of Sexual Dimorphism

Symposium Overview

Females and males display striking patterns of sexual dimorphism in many animals and other organisms. Differences are documented in morphology, physiology and behaviour. In recent years, advances in genomics technologies have facilitated the discovery of genetic mechanisms underlying sex-specific phenotypes, showing that sex-biased expression of hundreds to thousands of genes across the genome contributes to male and female phenotypic differences. The sex-specific evolutionary forces shaping sexual dimorphisms have also begun to be unravelled, including the interactions between 'master' sex determining genes on the sex chromosomes, and other

genes during development to control sex-biases of other genes.

This symposium will focus on the molecular basis and evolution of sexual dimorphism across animals and other organisms, including the origins, evolution and biology of sex chromosomes. It will cover topics ranging from the evolution of sex determining systems, sex linkage and sex chromosomes, sex-biased gene expression (on autosomes and sex chromosomes) and X chromosome dosage compensation mechanisms, to the evolution of associated dimorphic phenotypes and the underlying selective pressures.

Session Topics

- The diversity of genetic sex determining regions and sex chromosomes - Evolutionary challenges for sex-linked genome regions: Genetic degeneration and dosage compensation - Adaptive evolution: Evolution of sexually dimorphic phenotypes and gene expression, sexual antagonism - Sexual dimorphism in human disease

LOCATION & DATES EMBL Heidelberg, Germany 20 - 22 Sep 2020

DEADLINES Registration - 10 Aug 2020 Abstract - 29 Jun 2020

Website: <https://www.embo-embl-symposia.org/-symposia/2020/EES20-09/> For more information contact: events@embl.de

Carolina Cuadras <carolina.cuadras@embl.de>

Ireland EvolutionaryBiol Apr19-24

26 European Meeting of Students in Evolutionary Biology - recall for the abstract submission !

EMPSEB26 will be held in Killarney, Ireland. We invite all students to present their past or ongoing research, discuss other projects and to take part in plenary talks with our guests. The deadline for abstract submission is on the 24th of January. For more details, check our webpage (<https://sites.google.com/view/empseb26/>) and Twitter account (@EMPSEB26).

If you have any question, feel free to e-mail us: empseb26@gmail.com This Ph.D. meeting is organized by and dedicated to Ph.D. students studying Evolutionary Biology from across Europe although participants from other countries are also welcome. Thus, it provides a platform for students to present their work and meet their peers from different countries. Along

with the participants, 6 key speakers working on influential Evolutionary Biology topics are invited to present their work.

Louise Fouqueau <louisefouqueau@gmail.com>

Istanbul EcoEvolution Jun8-10

Dear colleagues,

We would like to announce the 7th Ecology and Evolutionary Biology Symposium in Turkey (EEBST 2020) which will take place in Istanbul on 8-10 July 2020. EEBST is a symposium organized by the Ecology and Evolutionary Biology Society of Turkey (EkoEvo, eko-evo.org) with the aim of bringing scientists and students together and promote the ecology and evolution studies in Turkey. The symposium is in English and well attended by a diverse body of faculty and students from different parts of the world including Europe, North America, and Asia. This year, Koc University will be hosting the symposium.

We are pleased to invite oral and poster presentations in all the areas of ecology and evolutionary biology. Early registration and abstract submissions are now open and the deadline is April 30th, 2020. Late registration is between May 1st - July 6th. For any additional information, please contact the organizing committee (ik-saglam@ku.edu.tr) or visit <https://eebst.org/> Sessions and keynote speakers:

- Genome Architecture Keynote: Magnus Nordborg <https://www.oeaw.ac.at/gmi/research/research-groups/magnus-nordborg/>
- Evolutionary Ecology Keynote: Hanna Kokko <http://www.kokkonuts.org/>
- Microbiome Ecology Keynote: Sarah Knowles <https://www.zoo.ox.ac.uk/people/dr-sarah-knowles>
- Wildlife Ecology Keynote: Matthew Hayward <https://www.newcastle.edu.au/profile/matthew-hayward>
- Human Evolution Keynote: Andrea Migliano <https://www.ucl.ac.uk/anthropology/people/academic-and-teaching-staff/andrea-migliano>
- Plant Evolution Keynote: Martyn Lysak <http://www.plantcytogenomics.org/>
- Conservation Genomics Keynote: Michael R. Miller <https://animalscience.ucdavis.edu/people/faculty/michael-miller> We hope to see you all in Istanbul.

On behalf of the EEBST 2020 Organizing Committee

Eren Ada erenada@gmail.com

Leipzig MountainBiogeography Mar24-27

Dear colleagues,

we would like to draw your attention to the “Mountain biogeography: new insights, challenges, and future directions” session which will be held during the “European Conference of Tropical Ecology” and the Annual Conference of the Society for Tropical Ecology (Gesellschaft für Tropenökologie, gto) at Leipzig University, Germany (March 24-27, 2020).

The deadline for submission of abstracts and early bird registration is January 16th, 2020.

For further information on the conference programme and abstract submission, please visit: <https://www.soctropecol-conference.eu/index.php?cat=callforpapers> — We hope to see you in Leipzig! — Alexandra Muellner-Riehl with co-chairs Suzette Flantua, Zehao Shen, Adrien Favre, and Carina Hoorn — European Conference of Tropical Ecology

“The future of tropical ecosystems - new insights and innovative methods”

and Annual Conference of the Society for Tropical Ecology

(Gesellschaft für Tropenökologie, gto)

24 - 27 March, 2020, Leipzig University, Germany

Website: <http://www.soctropecol-conference.eu/> e-mail: info@soctropecol-conference.eu/

muellner_alexandra@yahoo.de

Leipzig Tropical Evolution Mar24-27

Dear colleagues,

Don't miss the deadline for early registration and submission of abstracts: January 16, 2020!

Please visit our conference webpage to register online and submit your abstract.

For more detailed information, please also visit <https://www.soctropecol-conference.eu/index.php?cat=>

registration Accommodation

Attention! Make sure you book your accommodation soon, as in March also other conferences take place and rooms are in high demand. Please find more detailed information on our website at

<https://www.soctropecol-conference.eu/index.php?cat=AttrACTIVE+train+ticket>

The best way to travel to Leipzig for the European Conference of Tropical Ecology. Pay as little as €54.90 with the EventTicket (one way, nationwide). Leipzig Tourismus und Marketing GmbH has partnered with Deutsche Bahn to create this exclusive offer. Please check the details on our webpage: https://www.soctropecol-conference.eu/WEBS/SocTrop2020.pages.download/-DB%20Event%20Ticket%202020_%20European%20Conference%20of%20Tropical%20Ecology_%2024.-27.03.2020.pdf Please share the information on the “European Conference of Tropical Ecology” with colleagues, students and all other persons who might have an interest in participating.

In case you have any questions, please don't hesitate to contact us at e-mail: info@soctropecol-conference.eu/

We look forward to welcoming you to Leipzig!

With best regards, Chairs Alexandra MUELLNER-RIEHL, Professor University of Leipzig, Director LZ, Andreas HUTH, Professor Helmholtz Centre for Environmental Research -UFZ, Leipzig

European Conference of Tropical Ecology

“The future of tropical ecosystems - new insights and innovative methods”

and Annual Conference of the Society for Tropical Ecology

(Gesellschaft für Tropenökologie, gto)

24 - 27 March, 2020, Leipzig University, Germany

Website: <http://www.soctropecol-conference.eu/> e-mail: info@soctropecol-conference.eu/

muellner_alexandra@yahoo.de

Marseilles EvolBiol Sep22-25 EarlyDeadLine

Dear all, the early registration dead line, for the next Evolutionary Biology Meeting in Marseilles, is January 31 2020. The congress will take place from September 22nd to 25th (followed by social events 26 and 27) see

<http://aeeb.fr> < <https://t.co/x6FwUOF0ve?amp=1> >
> <https://ebm24.sciencesconf.org> <
< <https://t.co/pYJNQoCYsr?amp=1> >

Best regards Pierre

< <https://twitter.com/pontarotti> >

PONTAROTTI Pierre <pierre.pontarotti@univ-amu.fr>

Marseilles Evolutionary Biol Registration Dead Line Jan 31

<https://t.co/pYJNQoCYsr?amp=1>

Dear all, Evolutionary Biology Meeting in Marseilles: Early registration dead line Friday January 31
<http://aeeb.fr> < <https://t.co/x6FwUOF0ve?amp=1> >
> <https://ebm24.sciencesconf.org> <
< <https://t.co/pYJNQoCYsr?amp=1> > twitter
:EvolBiolMeetingMarseilles < <https://t.co/pYJNQoCYsr?amp=1> >

< <https://t.co/pYJNQoCYsr?amp=1> > <https://www.facebook.com/groups/203530083353767/> Pierre

PONTAROTTI Pierre <pierre.pontarotti@univ-amu.fr>

Montpellier Marine Epigenetics May 13-14

Dear EvolDir lister,

We are pleased to announce that EPIMAR 2020 Epigenetics in Marine Biology Congress (EPIMAR) will be held on May 13th-14th, 2020 in Montpellier, France.

This first edition will explore cutting-edge aspects of epigenetics in marine biology: environmental epigenetics, developmental epigenetics and epigenetics in aquaculture. EPIMAR 2020 aims at gathering scientists with interest in this field which has recently gained an increasing interest among all the scientific communities in biology.

Registration (up to the 1st of April) and abstract submission (up to the 1st of February) are open on the EPIMAR website <http://epimar.univ-perp.fr/>. Do not hesitate to share this message with colleagues.

Looking forward to welcome you in Montpellier,

Celine, Rossana, Guillaume and Jeremie

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IHPE - <http://ihpe.univ-perp.fr/> Labex CEMEB - <http://www.labex-cemeb.org> jvidaldu <Jeremie.Vidal.Dupiol@ifremer.fr>

Netherlands NLSEB 21Apr2020

Dear colleague,

We would like to invite you to the third conference of the Netherlands Society for Evolutionary Biology (NLSEB) on Tuesday 21 April 2020 in Ede.

Registration and call for abstracts are now open: <http://nlseb.nl/meetings/> With this yearly NLSEB conference, we aim to bring together scientists from all disciplines working on evolutionary questions, and build a broad community of evolutionary biologists based in the Netherlands. Therefore, the conference offers a broad overview of the topics and questions within evolutionary biology, reflected in three exciting plenary talks.

- Toby Kiers (VU Amsterdam) "The evolution of symbiotic dependency" - Thijs Ettema (Wageningen UR) "The archaeal origin of the eukaryotic cell" - Mark van Vugt (VU Amsterdam) "Two evolutionary pathways to leadership and hierarchy"

Talks and posters are organised entirely bottom-up: we want to know what YOU are working on, without any subject limitation. We will select 16 oral contributions (15 min. including discussion) and 12 poster pitches (2 min.), and there will be ample room and time for poster viewing. Registration of abstracts for talks and posters is open until 14 February 2020.

See for the provisional program <http://nlseb.nl/nlseb2020/> Registration for the conference is open until 21 March 2020.

The NLSEB 2020 Conference organising committee

Marian Bemer | Jacintha Ellers | Casper van der Kooi | Jeroen Meijer | Katja Peijnenburg | Sijmen Schoustra | Arjan de Visser

e-mail: meeting@nlseb.nl

Katja Peijnenburg <K.T.C.A.Peijnenburg@uva.nl>

OeirasPortugal EvolutionOfReproduction July15-17

Dear Colleagues,

We are happy to invite you to the first Satellite meeting of the Society for Molecular Biology and Evolution (SMBE) dedicated to the Evolution of Reproduction (https://igc.events.idloom.com/smbe_evorepro). This meeting will take place July 15-17 in Oeiras, Portugal, at the Instituto Gulbenkian de Ci ncia.

In this groundbreaking meeting we aim to establish the first cross-disciplinary network dedicated to the Evolution of Reproduction. Our objective is to tackle three outstanding biological questions: i- What are the origins of sexual reproduction? ii- How does evolution constrain the function of reproductive cells? iii- What can evolution teach us about infertility?

Our family-friendly event encourages the interaction between scientists from different backgrounds and at different career stages: all speakers will be given a 30-minute time slot and poster presenters will be able to promote their work in a "1 minute + 1 slide" flash talk. We place particular emphasis on the participation of those at early stages of their career: registration fees are low and we have a travel grant program (limited numbers) to support the attendance of graduate students, postdocs and early career professionals.

Please check the official website (https://igc.events.idloom.com/smbe_evorepro) to know more about our outstanding invited speakers, unique program and commitment to diversity & inclusiveness.

Participant number is limited and registration is required. Please register before March 15th 2020 (https://igc.events.idloom.com/smbe_evorepro/register). Selected applicants will be notified March 31st.

We look forward to welcoming you this summer to the Portuguese Riviera!

On behalf of the organizing committee,

Paulo Navarro-Costa (Instituto Gulbenkian de Ci ncia, Portugal) Antoine Molaro (Fred Hutchinson Cancer Research Center, USA)

For more information regarding this event: smbevorepro20@igc.gulbenkian.pt

"otto@zoology.ubc.ca" <otto@zoology.ubc.ca>

**Padova Italy RECOMB-Genetics
May9**

The 8th RECOMB Satellite on Computational Methods in Genetics will focus on current research at the intersection of population genetics, computer science and statistics: <https://recomb2020.org/recomb-genetics>. The satellite will take place on the 9th of May, immediately prior to the main RECOMB conference in Padova, Italy. Abstracts are due on January 30th. Trainees are highly encouraged to submit.

“Belbin, Gillian” <gillian.belbin@icahn.mssm.edu>

**PortTownsend Washington
EVO-WIBO Apr17-19**

We invite you to attend the 2020 EVO-WIBO Conference, a gathering of evolutionary biologists from across the Pacific Northwest. This meeting is held every other year and typically attracts 120-140 researchers for a fun and lively weekend of presentations and discussions about all aspects of evolutionary biology. The conference will be held April 17th-19th at Fort Worden State Park in beautiful Port Townsend, Washington. For more information on the conference and to register visit <https://www.zoology.ubc.ca/evo-wibo/index.html>. Space is limited, so register early. We look forward to seeing you there!

Alison Scoville, Ph.D.

Associate Professor of Biology

Central Washington University

400 E University Way

Ellensburg, WA 98926

Scoville@cwu.edu

**QuebecCity SMBE Jun28-Jul2
CallForAbstracts**

Dear Colleague,

** The deadline for abstract submission is Monday 20 January 2020, 23:59 (GMT) **

We invite you to submit an abstract for the 2020 annual conference of the Society for Molecular Biology and Evolution (SMBE 2020) at <http://smbe2020.org/abstracts/abstract-submission/>. SMBE 2020 is taking place in Quebec City, Canada, from 28 June – 2 July 2020.

Several awards are available and can be applied for during abstract submission. They require SMBE membership at the time of application (3 years costs \$10 for students and \$30 for others).

Membership can be applied for at <https://www.smbe.org/smbe/MEMBERSHIP.aspx>. Carer awards can also be applied for at registration or by email.

Awards include:

- 1) The Walter M. Fitch Award for current graduate and recent postdoctoral researchers; Extended abstracts are not required, just the conference abstract and a CV. Unsuccessful Fitch Award applicants will automatically be considered for Young Investigator and Registration-only awards.
- 2) The Young Investigator Award substantially funds the cost of attending, is for any graduate student or postdoc, requires a conference abstract and a CV, and will automatically also be considered for Registration-only awards.
- 3) The Undergraduate Travel & Mentoring Award (including Masters students under a 3+2 system) requires title, abstract, a short explanation (250 words) of why you want to attend this meeting, including a mention of whether you fall into a group traditionally underrepresented at SMBE such as enrolling in university later in life or being the first in your family to attend university. A short letter of support (250 words) should also be sent from your academic supervisor to Sarah Schaack and Mary O'Connell (SMBE.contact@gmail.com) confirming that you are undergraduate or a Masters student under 3+2, and that the research to be presented is your own.

4) Carer Travel Awards can be applied for during registration, or by email to smbe2020@mci-group.com if an earlier response is needed. Up to \$2000 may be awarded for members with children or dependent adults (including adult children with a disability or elderly relatives) to spend as to facilitate member's attendance at the annual SMBE meeting. Examples of eligible expenses include (but are not limited to) providing airfare for your child or for your caregiver to accompany you, flying a relative out to help with care at your home while you're at the meeting, or extra help paying for on-site daycare.

And we are delighted to announce that registration is now live. Register before the early bird deadline on April 1st, 2020 in order to secure discounted registration rates.

If interested in sponsorship of the meeting, please contact SMBE2020@mci-group.com. For any queries over abstracts or registration, please contact SMBE2020@mci-group.com.

We look forward to welcoming you in Quebec City.

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

smbe.contact@gmail.com

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

QuebecCity SMBE Jun28-Jul2 EvolutionOfReproductiveSystems

Last few days to submit your proposals to our symposium “Evolution of reproductive systems : beyond the usual suspects” at SMBE (june 28- july 2) in beautiful Québec city !

All details below and at <http://smbe2020.org> Hope to see you there ! Vincent et Christelle.

Organisers

Christelle Fraïsse, Institute of Science and Technology Austria, Austria

Vincent Castric, CNRS - University of Lille, France

Invited Speaker

Melinda Pickup, University of Vienna, Austria The mechanisms by which living organisms reproduce are strikingly diverse, including sexual reproduction w/o sex chromosomes or mating-types, self-fertilisation, self-

incompatibility or asexuality. The recent years have drastically enriched our understanding of the genetic and ecological factors driving the way mating systems evolve and diversify, how species transition from one to another, as well as of the consequences of these transitions for the ecology, demography and genomic diversity of natural populations. Notably, identification of the molecular determinants of a number of reproductive systems contributes to the development of more realistic models of mating system transitions and diversification. In parallel, there is growing recognition that mating systems interact with wider set of life history traits than generally considered, with important consequences on the effective population size and patterns of gene flow. New exciting avenues are also being explored regarding the feedback between genome dynamics and mating system transitions, such as changes in transposable elements regulation or accumulation of the genetic load. These outcomes are now beginning to be better understood thanks to more realistic theoretical expectations and advanced molecular approaches. This symposium will bring new insights into the causes and consequences of reproductive systems evolution, spotlighting the multiple feedback loops between genome evolution and reproductive systems. We encourage contributions illustrating the wide variety of methods employed in the field, such as theoretical population genetics, comparative genomics and expression analyses, field experiments or experimental approaches on diverse study organisms.

Dr. Vincent CASTRIC Directeur de recherche CNRS <http://eep.univ-lille.fr/fr/perso-vincent-castric> Unite Evo-Eco-Paleo (EEP) - UMR 8198 CNRS / Universite de Lille - Sciences et Technologies Batiment SN2, bureau 207 59655 Villeneuve d'Ascq - FRANCE Tel: 33 3 2033 6303 Fax: 33 3 2043 6979

Vincent CASTRIC <vincent.castric@univ-lille.fr>

QuebecCity SMBE Jun28-Jul2 GermlineSomaDistinction

Dear colleagues,

< <https://www.smith.edu/academics/faculty/laura-katz> > Laura Katz, Anne-Marie Dion-Côté, and I are organizing a symposium on “Within-individual genome variation and germline / soma distinction” to be held at SMBE2020 28 June - 2 July 2020 in Quebec city. The summary of the symposium is below and you can submit you abstract here:

group.com/AbstractSubmission/SMBE2020.aspx

Abstract submission deadline is January 20 and we hope that many of you can make it. Our ultimate goal is to make this a productive, stimulating and diverse event!

Cheers, Alex

On behalf of the symposium organizers: Laura Katz (<https://www.smith.edu/academics/faculty/-laura-katz>) Anne-Marie Dion-Côté (<https://amdioncote.weebly.com/>) Alexander Suh (<http://www.ieg.uu.se/evolutionary-biology/suh/>)

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Within-individual genome variation and germline / soma distinction Genomes are typically considered static/fixed across cell types and/or life stages within an organism, with changing transcriptional patterns resulting in cell differentiation and specialization. Yet, various within-individual genomic changes have been observed during development in many species across the tree of life. Such changes include ploidy variation, amplification or elimination of specific parts of the genome, and chromosome rearrangements with potentially important consequences that include cell fate, sex determination and dosage compensation as well as aging. These data demonstrate that 1) genomes are more dynamic than typically envisioned, 2) eukaryotes can distinguish between somatic (i.e. flexible within species) and germline (i.e. heritable) genomes, and 3) Mendelian inheritance is insufficient to explain many patterns observed across lineages. Further, genome conflicts including those involving selfish genetic elements (i.e. transposable elements, viruses, B chromosomes), likely underlie some of these genome processes. Combined with classic approaches such as cytogenetics and histology, emerging technologies such as single-cell and long-read sequencing now allow to study these processes at an unprecedented scale. This symposium will bring together biologists interested in within-individual genome dynamics, with a particular emphasis on germline / soma distinction and how these processes may impact cell fate, sex determination and aging. We hope this will help identify central questions to foster synergy and bring the field forward.

När du har kontakt med oss på Uppsala universitet med e-post så 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> Alexander Suh <[alexander.suh@ebc.uu.se](mailto:alexander.suh@ebc.uu.se)>

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## QuebecCity SMBE Jun28-Jul2 ParallelConvergentEvolution

The SMBE meeting in Quebec in 2020 (June 28 - July 2) will include a symposium on

\*The Molecular Basis of Parallel and Convergent Evolution\*

Abstracts submissions are open at <http://smbe2020.org/> Please think about coming along for this interesting discussion!

– Roger Butlin

Professor of Evolutionary Biology Animal and Plant Sciences The University of Sheffield

Guest Professor Marine Sciences University of Gothenburg

[r.k.butlin@shef.ac.uk](mailto:r.k.butlin@shef.ac.uk)

Roger Butlin <[r.k.butlin@sheffield.ac.uk](mailto:r.k.butlin@sheffield.ac.uk)>

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## QuebecCity SMBE Jun28-Jul2 Registration

We are delighted to announce that registration for SMBE 2020 is now live. SMBE 2020 is taking place in Québec city, QC, Canada on June 28th-July 2nd 2020 at the Québec Convention Center. Full details on the symposia programme and confirmed keynote speakers can be viewed here.

Information on the registration fees can be viewed here. Register before the early bird deadline on April 1st, 2020 in order to secure discounted registration rates. Please note that in order to receive a discounted member-rate registration you will be asked to provide your SMBE member number. Your SMBE member number is: 00023633. You can book your accommodation from a range of city centre properties from inside the registration system. As always SMBE are keen to ensure good international representation. Support will be provided to all delegates that may require additional documentation in order to secure a visa to Canada. Please click here to check if you require a visa for Canada. You can

request support for your Visa application within the registration portal. Select the Visa application support letter and submit the required details. You will then receive a covering letter confirming your attendance at SMBE 2020. Childcare facility will be provided on-site for SMBE 2020 delegates. During the registration process please advise whether you would like to make use of the facility and add details on the age of your child. Further details will be shared on the facility nearer the time.

Attendees can apply for

Carer Awards as part of conference registration rather than abstract submission, or by email to [smbe.contact@gmail.com](mailto:smbe.contact@gmail.com) if an earlier response is needed. SMBE will make available up to \$2000 to SMBE members with children or dependent adults (including adult children with a disability or elderly relatives) to spend as they wish to facilitate the member's attendance at the annual SMBE meeting. Examples of eligible expenses include (but are not limited to) providing airfare for your child or for your caregiver to accompany you, flying a relative out to help with care at your home while you're at the meeting, or extra help paying for on-site daycare. All other awards can be applied for during the Abstract submission portal.

Abstract and Award submission deadline.

The abstract submission deadline is fast approaching. The deadline for abstracts is 20th January 2020 23:59 GMT. Please be aware that the deadline will not be extended. Abstracts should be no longer than 2500 characters (~250 words), with a title no longer than 300 characters. Full details on abstract topics, guidance and the submission portal can be found here.

A range of awards can be applied for during Abstract submission, all of which require SMBE membership (costing only \$10/\$30 for 3 years for students/others at <https://www.smbe.org/smbe/MEMBERSHIP.aspx>) at the time of application. Current graduate students and postdoctoral researchers who received their primary doctoral-level degree no earlier than one year prior to the start of the annual meeting of the society may apply for the Fitch award. Extended abstracts are no longer required this year, just the conference abstract and a cv. Unsuccessful Fitch applicants will automatically be considered for Young Investigator and Registration awards. Any graduate student or postdoc may apply for the Young Investigator Award, which substantially funds the cost of attending. Application materials are the same as for the Fitch, i.e. abstract and cv. Unsuccessful applicants for both will automatically be considered for Registration-only awards. Undergraduates (including Masters students under a 3&#43;2 system) can apply

for the Undergraduate Travel & Mentoring award. In addition to presentation title and abstract, this requires a short explanation of why you want to attend this meeting, including mention of whether you fall into a group traditionally underrepresented at SMBE, such as enrolling in university later in life or being the first in your family to attend university. You also need to arrange to have a short letter of support (250 words) sent from your academic supervisor to Sarah Schaack and Mary O'Connell ([SMBE.contact@gmail.com](mailto:SMBE.contact@gmail.com)) confirming that you are an undergraduate or a Masters student under 3&#43;2, and that the research is your own. A range of sponsorship opportunities have been developed for the meeting, if interested please contact [SMBE2020@mci-group.com](mailto:SMBE2020@mci-group.com). For any queries over abstracts or registration, please contact [SMBE2020@mci-group.com](mailto:SMBE2020@mci-group.com).

Society for Molecular Biology & Evolution  
<[smbe@allenpress.com](mailto:smbe@allenpress.com)>

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## Seattle HumanBrainEvolution Apr1-2

Expanding Minds: Allen Institute Conference on Human Brain Evolution (hyperlink: [https://alleninstitute.org/what-we-do/frontiers-group/events/expanding-minds/?utm\\_source=-Newsletter&utm\\_medium=email&utm\\_campaign=-ExpMindsInvite1&utm\\_content=EventWebsite](https://alleninstitute.org/what-we-do/frontiers-group/events/expanding-minds/?utm_source=-Newsletter&utm_medium=email&utm_campaign=-ExpMindsInvite1&utm_content=EventWebsite))

Hear from experts in human evolution, genomics, and neuroscience discuss theories underlying the evolution of the human brain. Apply to present a talk/poster.

Soha Ashrafi, Ph.D. Department of Neurobiology Harvard Medical School 220 Longwood Avenue Boston, MA 02115 617-432-2527

"Ashrafi, Soha" <[Soha\\_Ashrafi@hms.harvard.edu](mailto:Soha_Ashrafi@hms.harvard.edu)>

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## Snowbird Utah GenesAsEnvironment May31-Jun2

Early Registration is now open for AGA2020: Genes as Environment: Indirect Genetic Effects in Evolution,

Agriculture, and Medicine The American Genetic Association 2020 President's Symposium May 31 through June 2 in Snowbird, Utah

Indirect genetic effects (IGE) are genetic effects of an individual on the trait values of others in the same species. These effects are also known as social or associative genetic effects. 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, providing great opportunities to interact with the best in the field.

AGA members receive significant discounts on symposium registration. Student and postdoc members receive free registration if they submit a poster abstract early, and have the chance to be selected for an oral presentation and travel award.

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 Nora Underwood Michael Wade Alastair Wilson

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

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## Tavira Portugal MarineEvolution Oct12-15

Dear friends,

SESSION PROPOSALS can now be submitted for Marine Evolution 2020 (<https://ccmar.ualg.pt/en/page/-marine-evolution-2>), organized by the Centre of Marine Sciences of Algarve (CCMAR), which will take place from the 12th through 15th of October 2020 in Tavira, Portugal. The deadline for proposals is February 15th, 2019 and should be submitted via the form available on the web portal. Proposals are invited within the field of Marine Evolution addressing major, broadly framed questions or themes. Session proposals should include: A short but descriptive title of the topic, a list of chairs of the session with contact information, a brief abstract (max 200 words), and a tentative list of proposed speakers to invite.

Session chairs are requested to actively invite peers to

register and submit abstracts for presentations. Once registration opens (March 2020) participants will suggest which session they would like to participate in, and these registrations will be forwarded to the session chairs for consideration. Session chairs are free to organize sessions in the manner they see fit, with possibilities for keynote talks, speed talks, oral presentations of posters, etc. All session chairs will have the opportunity to designate poster presentations to applicants who cannot be fitted into the oral presentation time frame. Session chairs are also free to organize publication of presented materials in scientific journals, if deemed of interest by the participants. Sessions will be run three in parallel each day, from 11:00 -14:45 with a 75-minute break for lunch.

We are also pleased to announce that PLENARY presentations by six renowned speakers have been confirmed (see details on the website). If you have further questions about the scientific program, including content questions relative to the sessions, please contact the organizing committee at [marineevolution2020@gmail.com](mailto:marineevolution2020@gmail.com)

Sincerely, the MarineEvolution 2020 Organizing Committee

Gareth Pearson Rita Castilho

Gareth Pearson (Research Associate) Centre of Marine Sciences (CCMAR), Universidade do Algarve, 8005-139 Faro Portugal email: [gpearson@ualg.pt](mailto:gpearson@ualg.pt) website: <https://scholar.google.com/citations?hl=en&user=bO73-WoAAAAJ> [https://www.researchgate.net/profile/Gareth\\_Pearson](https://www.researchgate.net/profile/Gareth_Pearson) Tel: +351 289800928

GARETH ANTHONY PEARSON  
<[gpearson@ualg.pt](mailto:gpearson@ualg.pt)>

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## UCambridge EvolutionaryGeneticsGenomics Mar17

Dear Colleagues,

The annual Evolutionary Genetics and Genomics Symposium (EGGS) will take place on Tuesday 17th March 2020 at the University of Cambridge. This Genetics Society meeting attracts participants from across Europe and is a friendly and informal way to meet researchers in the field and listen to interesting talks. We aim to bring together participants from a range of backgrounds, with a particular focus on genomics and evolutionary biology. EGGS 2020 will feature keynotes from:

Mattias Jacobsson Professor at Department of Organismal Biology, Human Evolution, Uppsala universitet

Claudia Bank Principal Investigator, Gulbenkian Institute

Mark Blaxter Professor & Programme Lead for the Tree of Life Programme, Wellcome Sanger Institute Talk title: Sequence everything: first fruits from the Tree of Life

Registration is now open and costs just 5. Please register at <https://onlinesales.admin.cam.ac.uk/-conferences-and-events/department-of-genetics/-evolutionary-genetics-and-genomics-symposium/-evolutionary-genetics-and-genomics-symposium-2020>

Abstract submission is also open and the deadline is 20/1/2020. If you are interested in presenting a talk, please submit a title and upload your abstracts (250 words) in Word or PDF formats as attachments during registration. Registrations can be cancelled with a full refund until the registration deadline on 10th March 2020.

This meeting coincides with Speciation Genomics 2020 to be held the previous day (16th March 2020) at St John's College, Cambridge and we encourage you to attend both meetings (REGISTER HERE: <http://bit.ly/sp-geno> & ABSTRACTS HERE: <http://bit.ly/2R62lv0>).

With best wishes,

The organising committee.

Arunkumar Ramesh <ar885@cam.ac.uk>

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## UCambridge Speciation Genomics Mar16

We would like to invite you to the one-day Speciation Genomics 2020 meeting at St John's College, Cambridge, on the 16th of March. This meeting is organised by Chris Jiggins, Joana Meier, Hilde Schneemann, and Gabriela Montejó-Kovacevich.

The symposium will include a series of short talks by empiricists and theoreticians at the forefront of speciation research, followed by a discussion round led by senior researchers. There will also be a poster session. Confirmed speakers so far include Sonya Clegg, Oscar Puebla, Konrad Lohse, Christelle Fraisse and Sean Stankowski. Ole Seehausen, Roger Butlin, and Claudia Bank are confirmed attendees and will help lead discussion groups.

To submit an abstract for a talk or poster fill in this form <http://bit.ly/2R62lv0> (by the 01/02/2020).

REGISTER HERE: <http://bit.ly/sp-geno> (by the 01/03/2020).

The registration fee (pounds 40 standard, pounds 25 students) includes lunch, dinner in the evening and all tea and coffee etc. Note that accommodation is not included we recommend that you look for B&B options at the university accommodation site < <https://www.accommodation.cam.ac.uk/> >.

This meeting coincides with our annual Evolutionary Genetics and Genomics Symposium < <http://evolutionarygenetics.heliconius.org/2017/eggs-2018-on-march-20-cambridge/> > (EGGS, <https://evolutionarygeneticsandgenomics.com/>) to be held the following day on the 17th March we encourage you to attend both meetings.

"mgm49@cam.ac.uk" <mgm49@cam.ac.uk>

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## UMuenster Evolution Mar30-Apr2

Conference: 2nd Münster Evolution Meeting (MEM)

Date: 30 March - 2 April 2020

Location: Münster University, Germany

We already received more than 150 registrations (>70 talks and 40 posters) for the 2nd Münster Evolution Meeting on 30 March - 2 April 2020! To accommodate more talks, we decided to offer parallel sessions for the contributed talks but have joined sessions for the invited talks. Abstracts can still be submitted until 31 January 2020, we particularly encourage submissions for poster presentations! Regular registration (participants without talk or poster) will be open until 15 March 2020. The registration fee is 80 EUR.

For registration and detailed information on the meeting visit the MEM website: <https://www.uni-muenster.de/Evolution/MEM/main.shtml> Confirmed speakers: Detlev Arendt (EMBL Heidelberg) Nicholas Barton (IST Austria) Benjamin Bomfleur (Münster University) Juliette de Meaux (University of Cologne) Susanne Dobler (University of Hamburg) Wolfgang Enard (Ludwig Maximilians University Munich) Heike Feldhaar (University of Bayreuth) Thomas Flatt (University of Fribourg) David Garfield (Humboldt University Berlin) Michael Grünstäudl (Freie Universität Berlin) Joachim T. Haug (Ludwig Maximilians University Mu-

nich) Adamandia Kapopoulou (Centre hospitalier universitaire vaudois Lausanne) Hans Kerp (Münster University) Barbara König (University of Zürich) Fyodor Kondrashov (IST Austria) Martin Kuhlwilm (University Pompeu Fabra Barcelona) Camila Mazzoni (Leibniz Institute for Zoo and Wildlife Research Berlin) Axel Meyer (University of Konstanz) Bernhard Misof (Zoological Research Museum Alexander Koenig Bonn) Kai Müller (Münster University) Marlis Reich (University of Bremen) Walter Salzburger (University of Basel) Christian Schlötterer (University of Veterinary Medicine Vienna) Mark Stoneking (Max Planck Institute for Evolutionary Anthropology Leipzig) Anja Widdig (Max Planck Institute for Evolutionary Anthropology Leipzig/University of Leipzig)

Organizers:

Institute for Evolution and Biodiversity, Münster University

Münster Graduate School of Evolution, Münster University

Chairs:

Jürgen Gadau, Münster University

Katja Nowick, Freie Universität Berlin

On behalf of the organizers,

Kristina Wensing

mem@uni-muenster.de

MEM 2020 Congress Bureau Westfälische Wilhelms-Universität Münster Hüfferstr. 1a, D-48149 Münster, Germany +49(0)251 83 21252 mem@uni-muenster.de <http://www.uni-muenster.de/Evolution/-MEM/main.shtml> "Evolution Meeting, Münster" <mem@uni-muenster.de>

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## USussex JohnMaynardSmith May13

This year marks the 100th year since John Maynard Smith was born. To celebrate John's life and legacy we will be holding a symposium at the University of Sussex on Wednesday May 13th 2020. The speakers include those that worked with John alongside younger scientists that have continued to work in the fields that he influenced. The following speakers have so far confirmed their attendance - Deborah and Brian Charlesworth, Ed Feil, Eors Szathmary, Nick Lane, Andrew Pomiankowski, Kayla King and Susan Riechert.

More will be added. We will also have some of John's family in attendance. Attendance is free but please book at <http://www.sussex.ac.uk/lifesci/newsandevents/jms>. The symposium will be followed by a drinks party.

Adam Eyre-Walker Professor of Biology University of Sussex

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

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## Vienna MIC-Phy May25-27

Meeting: Mathematical, inferential and computational phylogenomics (MIC-Phy)

Date: 25-27 May 2020

Location: Vetmeduni Vienna, Austria

Scope: Phylogenomics aims at reconstructing the evolutionary histories of organisms considering whole genomes or large fractions of genomes. The abundance of genomic data for an enormous variety of organisms has enabled phylogenomic inference of many groups, and this has motivated the development of a myriad of models and methods. The MIC-Phy meeting intends to stimulate a larger debate focus on the main advances and challenges of the current phylogenetic models, methods and algorithms that are permitting to make sense of phylogenomic data.

Cost: The meeting is sponsored by WWTF and there is no registration fee.

Workshop: The meeting includes a workshop entitled \*New approaches and methods to phylogeny inference\* that will focus on the polymorphism-aware phylogeny estimation, including practical exercises based on the software IQ-TREE and RevBayes.

Keynote speakers: \* Ziheng Yang (University College of London, UK) \* Tracy Heath (Iowa State University of Science and Technology, USA)

Important dates: \* Deadline for workshop registration and abstract submission: March 31, 2020 \* Notification of oral presentation and/or workshop acceptance: April 15, 2020 \* Registration deadline: May 1, 2020

Registration: Please visit <https://www.vetmeduni.ac.at/de/micphy2020/home/> for more information on how to register, submit your abstract and participate in the workshop.

Local organizers: Carolin Kosiol and Rui Borges

Questions: micmeeting2020@gmail.com

Rui Borges <ruiborges23@gmail.com>

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## YosemiteNatIPark Symbiosis May15-17

Dear Colleagues,

Registration will SOON be open for the 10th Annual Yosemite Symbiosis Workshop!

The TENTH annual Yosemite Symbiosis Workshop will take place on May 15-17, 2020 at the Sierra Nevada Research Institute, Yosemite National Park.

Keynote speaker 2020: TO BE ANNOUNCED SOON  
Information about our meeting:

Why: Our continuing goal is to better integrate the broad groups of scientists that focus on symbiosis and microbiome research. Yosemite serves as an ideal site as it is both beautiful and secluded. This will be our ninth annual meeting and we have been consistently attracting scientists from all over the country and overseas.

Who: The meeting is small by design (~50 participants) and we seek to focus on scientists interested in the microbiome, cooperation, mutualism, and symbiosis. In the past we have covered a range of symbiosis topics

from ecology and evolution to molecular mechanisms in different model and non-model systems. We would like to make room for a diverse group of people so we will initially accept up to 3 lab members per group (including the PI) on a first come first served basis.

When: The talks and formal meeting will be held 16-17, 2020, though we make accommodation arrangements available for attendees to arrive on Friday the 15th to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting.

Past attendees and talks can be found here: <http://www.sachslab.com/symbiosis-2015.php> Where: SNRS has a set of cabins in Wawona and all within a short walk of the conference room. Costs: See details in the registration page (up soon). We will only be able to accept credit card payments this year

\*Joel L. Sachs\* \*Professor & Vice Chair, \*Department of Evolution Ecology & Organismal Biology

\*Director of UCR Microbiome Initiative (<https://microbiome.ucr.edu/>) Department of Botany & Plant Sciences (Cooperating Member) Department of Microbiology & Plant Pathology (Cooperating Member) University of California, Riverside

\*Mailing Address:\* Sachs Lab - UC Riverside 3401 Watkins Dr., 1229 Spieth Hall Riverside, CA 92521

Office (951) 827-6357 / Fax (951) 827-4286  
[www.sachslab.com](http://www.sachslab.com) <http://www.biology.ucr.edu/people/faculty/Sachs.html> Joel Sachs <joels@ucr.edu>

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## GradStudentPositions

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## Auckland BeetleCrypsisEvolution

Two PhD Scholarships: Evolution of Debris-cloaking in Cryptic Beetles

Manaaki Whenua - Landcare Research (MWLR) and the School of Biological Sciences (SBS), The University of Auckland, New Zealand, has funding for two suitably motivated and dedicated applicants to apply for fully funded PhD scholarships to work on the evolution, biomechanics, and function of debris-cloaking in cryptic beetles of New Zealand. By reconstructing the evolution of cuticular morphology over phylogenetic trees, determining the biomechanical properties of beetle surfaces, and testing adaptive hypotheses relating to their function in camouflage, students will explore factors driving the evolution of this complex mechanism of protection. The research will include molecular phylogenetic research, behavioural studies, and training in functional morphology with Stanislav Gorb (University of Kiel, Germany). The exact content of either PhD

project will depend on the research goals and skill of each student. The successful candidates will be highly independent, have research experience, a strong academic record and possess a MSc or Honours research degree in evolutionary biology, morphology and/or behavioural ecology.

The students will work under the supervision of Drs Rich Leschen (MWLR), Greg Holwell (SBS), and Thomas Buckley (SBS and MWLR), and will have access to a range of world-class facilities with the opportunity to travel for both fieldwork and collaboration. This position is funded for 3 years through the Marsden Fund of the Royal Society of New Zealand, and the successful applicant is expected to begin during 2020.

Please submit applications directly to Rich Leschen (leschenr@landcareresearch.co.nz) and provide a CV, academic transcript, contact details for three referees, and a letter detailing your research interests and motivation for considering the project.

Key words: Ultra-conserved elements; adhesive structures, background mimicry

Thomas Buckley <BuckleyT@landcareresearch.co.nz>



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## Belgium PlantPestAdaptation

Impact of climate changes on plant-pest interaction: insights from the rosy apple aphid and its apple host in a context of domestication

Amandine Cornille's group (<http://moulon.inra.fr/index.php/fr/equipes/group-leader-amandine-cornille-young-atip-avenir-team>) and Tim Belien's group (<https://be.linkedin.com/in/tim-beli%C3%ABn-4a41164>) are recruiting a Master student and a bachelor to investigate the adaptation to climate and plant host of aphid pests.

Lab address (supervision): PC-Fruit pcfruit vzw Fruituinweg 1 3800 Sint-Truiden Belgium

Supervisors: Amandine Cornille (amandine.cornille@inrae.fr), Ammar Alhmedi (Ammar.alhmedi@pcfruit.be) and Tim Belien (tim.belien@pcfruit.be)

**Project summary** Understanding the extent of local adaptation in natural populations and the mechanisms enabling individuals to adapt to their native environment is a major avenue in evolutionary ecology research. Host-pathogen coevolution is widely seen as a major driver of local adaptation and has therefore been a study model to dissect the evolutionary processes at work during local adaptation. However, the relative contributions of species interactions (i.e. biotic factor) and abiotic factors to local adaptation are still unclear. Addressing these issues is more than a simple academic exercise. Understanding of local adaptation processes in host-parasite interactions will also help tackling pressing issues, such as the ways in which environmental change alters the emergence of pathogens leading to host extinctions, how to promote sustainability of agroecosystems in the face of emerging crop diseases or in guiding for public health practices as more human pathogens and their vectors expand their ranges.

In this project, we investigate whether local adaptation occurred during the recent rapid colonization of cultivated apple by *Dysaphis plantaginea*, the major aphid pest of cultivated apple orchards, in Europe. We will carry out in April 2020 experimental tests for *D. plantaginea* fitness differences across environments (i.e. host and climate) to investigate whether the aphid is locally adapted to its host and/or climate. This project will generate original results adding to our understanding

of how species interactions and abiotic conditions can shape local adaptation.

**Master project** The project involves the transplant of Belgian, French and Spanish aphid genotypes on Belgian, French and Spanish apple varieties in three locations (Belgian, France and Spain). The candidate will be involved in the assessment of the adaptive capacities at the ecological level of the rosy apple aphid at the BELGIAN site located at PCFruit (Sint-Truiden, Belgium). The project can last two (Bachelor) to six months (Master), and will consist in participating in aphid infestations and rearing on the field, tree measurement, associated statistical analyses, and final report writing.

1) The candidate will lead the launching of the experiment there during Spring 2020 by transplanting aphids on several apple cultivars and will measure several phenotypic traits. The growth rate of each colony will be measured after 12 days of infestation. Various functional traits which are proxies of the condition of the plant (i.e. chlorophyll content, carbon/nitrogen balance, and flavonol and anthocyanin content measured with the Dualex pinel) will also be measured.

2) He/She will analyze the dataset that will be generated.

**Methodology:** Statistical analyses (linear and mixed models, R), ecophysiology, phenotypic measurement, rearing, insect biology, field experiment.

**Profile preferred for the candidate:** Ideally, the candidate will have skills in ecology and evolution or at least will show strong interest in these fields. He/She will have to be highly motivated about field experiment, as this one will be intense the first two months. He/she will not necessarily be familiar with apple or aphid model.

**Deadline for submission:** The sooner the better.

**Duration :** 2 to 6 months, August 2020, starting dates are flexible, contact Amandine CORNILLE for further discussions.

**Supervision:** Amandine CORNILLE - Chargée de Recherche CNRS CRCN Génétique Quantitative et Evolution - Le Moulon Ferme du Moulon 91190, Gif-sur-Yvette, France mail: amandine.cornille[at]gmail.com  
 Google Scholar profile : <https://scholar.google.com/citations?user=EqIE2h8AAAJ&hl=fr> Personal page : <http://moulon.inra.fr/index.php/fr/equipes/dygap/-355> Group page:

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## Canada 2 Freshwater Fish Genomics

M.Sc. M.A., doctorats et postes de postdoctorat entièrement financés : Réseau Génomique Pour l'Identification, le Stress et la Santé des Poissons

Devenez acteurs d'une révolution en conservation des poissons! Notre programme pancanadien de plusieurs millions de dollars changera la donne pour la gestion et la conservation des poissons d'eau douce.

Nous recherchons des étudiants diplômés en sciences naturelles et en sciences sociales intéressés à : \* Entrer de plain-pied dans le domaine en pleine croissance de la recherche sur l'ADN environnemental; \* Faire partie de la plus grande expérience d'ADNe aquatique jamais entreprise; \* Développer le premier réseau transcriptionnel universel pour les poissons d'eau douce; \* Être parmi les premiers à explorer les défis éthiques et juridiques potentiels de la recherche basée sur la génomique aquatique.

Développer un réseau professionnel avec nos partenaires du monde universitaire, de l'industrie et du gouvernement pendant que vous travaillez dans un laboratoire ultramoderne ou que vous effectuez des travaux sur le terrain dans les régions les plus reculées du Canada... ou les deux!

Des opportunités sont présentes pour des postes en Colombie-Britannique, au Manitoba, en Ontario, au Québec et au Nouveau-Brunswick de 2020 à 2024. Les citoyens canadiens et les immigrants reçus seront considérés en premier.

GEN-FISH est un projet de recherche collaboratif mis sur pied par l'Université de Windsor et ses partenaires et financé par Génome Canada et Agriculture et Agroalimentaire Canada.

Pour découvrir ce que GEN-FISH peut faire pour vous, visitez notre site Web à [www.gen-fish.ca](http://www.gen-fish.ca) ou contactez la coordonnatrice de la recherche GEN-FISH à [Sara.Jamieson@gen-fish.ca](mailto:Sara.Jamieson@gen-fish.ca).

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PhD Position - Larval Freshwater Fish Genomics Lovejoy and Mandrak Labs, University of Toronto Scarborough

Join a revolution in freshwater fish conservation! Our Canada-wide, multimillion-dollar GEN-FISH network

(gen-fish.ca) will be a game-changer for freshwater fish management and conservation.

The Lovejoy and Mandrak labs, University of Toronto Scarborough (UTSC), have an opening for a PhD student to conduct genomic research on the direct and indirect identification and quantification of larval freshwater fishes caught in larval traps or entrained in water intakes. This research will be undertaken in collaboration with Indigenous, academic, government, and industry partners within the GEN-FISH network.

Candidates are required to have a sound knowledge of genomic and bioinformatic methods, strong written and oral communication skills, and excellent quantitative and laboratory skills. The position is expected to start September 2020. Applicants are required to send an updated CV, representative reprints or preprints, a cover letter and/or statement describing the candidate's past experience and accomplishments, interests (generally and with respect to the specifics of this position), and the names and e-mails of at least two references. These materials should be combined into a single pdf document and sent to [nathan.lovejoy@utoronto.ca](mailto:nathan.lovejoy@utoronto.ca). We will review applications beginning February 1, 2020.

The University of Toronto Scarborough (UTSC), located on the eastern edge of Toronto, is one of the three campuses of the University of Toronto. The campus is on a forested ravine and is a short commute to the Toronto city centre. UTSC is an exciting place to do research, with a young and active research community and excellent students in Biological Sciences (<http://www.utoronto.ca/biosci/>). Toronto is Canada's largest city and is extremely culturally diverse, full of parks and green areas, and hosts numerous cultural, culinary, and music events.

The Lovejoy and Mandrak labs are committed to increasing gender, ethnic, disciplinary, and cultural diversity. They aim to promote equity, diversity, and inclusion within our field of research in Canada.

Sara Jamieson <[saraj@uwindsor.ca](mailto:saraj@uwindsor.ca)>

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## CIBIO-InBIO Portugal 2 Biodiversity

Dear Colleagues,

We would like to inform you about two open positions at the Research Center in Biodiversity and Genetics Resources (CIBIO-InBIO), Vairão, Portugal. If possible,

we would greatly appreciate to count on your collaboration in the dissemination of these opportunities amongst potential candidates.

Please find below the links to the announcements.

#### OPEN POSITIONS @ CIBIO-InBIO

PhD Holder Position| Biological sciences

CIBIO-InBIO, Portugal

Application deadline: January 31, 2020

< <https://cibio.up.pt/open-positions-careers/details/-iceta-2020-01> > Click here for more information and to know how to apply

PhD Holder Position| Biological sciences

CIBIO-InBIO, Portugal

Application deadline: January 31, 2020

< <https://cibio.up.pt/open-positions-careers/details/-iceta-2020-02> > Click here for more information and to know how to apply

CIBIO-InBIO's Office for Science Communication and Outreach CIBIO - Research Center in Biodiversity and Genetic Resources InBIO Associate Laboratory University of Porto, Vairão Campus Rua Padre Armando Quintas 4485-661 Vairão Portugal

t: +351 252 660 400

e: [divulgacao@cibio.up.pt](mailto:divulgacao@cibio.up.pt)

w: <http://cibio.up.pt> | <http://www.inbio-la.pt>

f: <https://www.facebook.com/cibio.inbio>

CIBIO-InBIO Divulgaçã

netic manipulation, and transcriptomic profiling. There will be multiple opportunities for career development, including mentoring, participating as a guest lecturer in courses taught by the PI, and attending workshops such as the Embryology course at the Marine Biological Laboratories.

Spiralians are a great group of animals to study evolution of body plans in part because many spiralian taxa develop via a stereotypic and likely ancestral cleavage program. Ultimately, this cleavage program results in formation of highly diverse body plans. Research in Dr. Meyer's lab is currently focused on understanding how centralized nervous systems evolved. The research community that studies evolution and development of spiralians is rapidly growing and is very welcoming and collaborative.

The successful applicant will enter Clark University's Biology PhD program with an anticipated start date in late August. Previous experience in molecular biology and working with marine larvae and/or bioinformatics is desirable. Additionally, the Meyer lab is interested in creative, engaged applicants who can contribute to diversity of the academic community, for example via outreach to students from historically underrepresented communities. The successful applicant will be guaranteed funding for five years through a combination of research assistantships and teaching assistantships.

Please email a cover letter explaining your interest in the position and qualifications and a CV to [nmeyer@clarku.edu](mailto:nmeyer@clarku.edu).

[NWebster@clarku.edu](mailto:NWebster@clarku.edu)

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## ClarkU AnnelidNeuralEvoDevo

Come join us! We are accepting applicants after the Clark University Deadline.

A PhD position is available in the laboratory of Néva Meyer at Clark University in Worcester, MA USA beginning in late August 2020 as follows:

The successful applicant will develop a project focused on molecular control of neural specification in the annelid *Capitella teleta*, but this can be expanded to include other spiralian/lophotrochozoans and different avenues of research depending on the applicant's interests and goals. Possible avenues of research include analysis of fate specification via blastomere isolation, ge-

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## Cologne RoundwormEvoDevo2

Dear all,

The previously advertised PhD-position in the newly established Worm Lab at the University of Cologne has now been officially announced. The newly established Worm Lab at the University of Cologne is looking for a PhD-Student to join their team in a project funded by the DFG. The project will analyse evolutionary developmental constraints on the highly conserved nematode Bauplan using DNA and RNA sequencing methods, as well as molecular gene knockout assays. The successful candidate will be focussing on conducting DNA (genome) and RNA (transcriptome) sequencing on single nematode individuals, early developmental stages

(eggs), and blastomeres (individual cells) using established Illumina methods. The student will establish the same techniques on a single molecule level using ONT long read methods in the lab and analyse the obtained data computationally.

At the Worm Lab we are fully committed to diversity and gender equality. Come as you are and bring whom you want. We also know how difficult it is to work in a job like ours when having kids. Thus we offer very flexible working models and regardless of their gender, all parents will be encouraged to take parental leave.

The official job advert can be found here <https://www.stellenwerk-koeln.de/jobboerse/wissenschaftl-stellen-phd-position-worm-lab-ag-schiffer-k-2020-01-24-297369> Looking forward to read your applications

Philipp

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## ETH Zurich Population Genomics Fungi

PhD Position Available at ETH Zurich in the Plant Pathology Group of the Institute of Integrative Biology [in collaboration with the University of Neuchâtel]

Population Genomics of Plant Pathogenic Fungi

We seek applicants with interests and background knowledge in the fields of Population Genomics, Evolutionary Biology, Quantitative Genetics, Microbiology, Molecular Plant-Microbe Interactions, or Fungal Ecology to conduct PhD research oriented around the population genomics of plant pathogenic fungi. Applicants should be able to work independently and to publish their research in excellent peer-reviewed journals. Applicants should have effective communication skills, both oral and written.

Experience with fungi or plant pathogens is desirable, though not required, but applicants who already have experience with plant pathogens and fungi will have an advantage. Experience with population and/or quantitative genetics is also desirable. The applicant should be interested in managing and analyzing extensive phenotype datasets containing millions of data points in addition to generating and analyzing new genome datasets to complement the ~1000 genomes already available in the laboratory.

Our major areas of research are population genetics and genomics, evolutionary biology, evolutionary ecology, ex-

perimental evolution, and phylogeography. Our primary experimental organisms are the plant pathogenic fungi *Zymoseptoria tritici* (aka *Mycosphaerella graminicola*), *Parastagonospora nodorum* (aka *Phaeosphaeria nodorum*), and *Rhynchosporium commune* (aka *Rhynchosporium secalis*). Extensive genome sequence datasets are already available for all three fungi, including multiple finished reference genomes for *Z. tritici* and *P. nodorum*. We have already acquired complete genome sequences for globally distributed field populations for all three fungi (~200-1000 genomes). We have developed and implemented high throughput phenotyping methods oriented around automated image analysis to acquire millions of phenotype data points for a variety of important traits, including virulence, reproduction, fungicide sensitivity, and growth at different temperatures and under different stresses.

As a result of earlier projects centered around QTL mapping, GWAS, RNA seq and population genomics, we have identified many candidate genes that contribute to virulence, fungicide resistance, thermal adaptation, and host responses. Several of these genes have already been functionally validated, with more functional validations underway. The successful candidate will be integrated into a research program that uses knowledge obtained from these genomic and phenomic datasets to understand trade-offs among pathogen traits and identify new candidate genes that play important roles in the evolutionary ecology of these pathogens.

The PhD project will also include an interaction component with the Laboratory of Evolutionary Genetics headed by Prof. Daniel Croll (<http://www.pathogen-genomics.org>) for the analyses and interpretation of genomic sequence datasets.

The ETH and the Institute of Integrative Biology possess advanced infrastructure including the Genetic Diversity Center (<http://www.gdc.ethz.ch/>) and the Functional Genomics Center Zurich (<http://www.fgc.ethz.ch/>). Zurich is consistently rated as one of the most livable cities in the world. The Plant Pathology Group (<http://www.path.ethz.ch/>) is currently composed of ~20 people from 11 countries, and English is the working language of the group. But knowledge of German or French is useful outside of the university.

Applications consisting of a CV, publication list and a detailed statement of research interests (at least 2 single-spaced pages in length), with names and contact information for 3 references should be prepared as a single pdf file and sent by email before 1 March 2020 to Prof. Bruce A. McDonald at [bruce.mcdonald@usys.ethz.ch](mailto:bruce.mcdonald@usys.ethz.ch). Applications will be processed as they are received, so it is possible that the position will be offered to excel-

lent candidates before 1 March 2020. The position will remain open until a suitable candidate has been found.

Bruce McDonald Plant Pathology Institute of Integrative Biology, Zurich (IBZ) ETH Zurich, LFW B16 8092 Zurich Switzerland

Office: +41 44 632 3847 FAX: +41 44 632 1572 Office Manager: +41 44 632 3848 (Janine Gremion) Email: bruce.mcdonald@usys.ethz.ch Web (Group): <http://www.path.ethz.ch> McDonald Bruce <bruce.mcdonald@usys.ethz.ch>

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## Geneva MolecularPopGenetics

Geneva, January 21st, 2020

Open PhD position A PhD position in molecular population and evolutionary genetics is available at the Anthropology Unit of the Department of Genetics and Evolution, University of Geneva, Switzerland, under the supervision of Professor Alicia Sanchez-Mazas (<http://ua.unige.ch/en/personne/aliciasanchezmazas>). The project will consist in the analysis of DNA sequence data of the Human Leukocyte Antigen (HLA) genes in African populations. The main aim is to investigate the molecular diversity and evolution of these immune genes in Africa within an evolutionary framework taking into account demographic history and selective pressures. We are seeking a highly motivated person with a strong interest in human biological evolution, population genetics and genomics, immunogenetics and anthropology.

Requirements: Master degree in biology or equivalent;

Skills in population genetics and bioinformatics; English speaking, reading and writing; Collaboration and communication abilities; Previous experience in DNA sequence data analysis is a plus; French speaking is not mandatory but is an asset. Terms of employment: Duration: 4 years, provided that the first year is successful (trial period);

Start: the position is available from 1st May 2020 or by arrangement. Salary: Swiss National Science Foundation ([www.snf.ch](http://www.snf.ch)) salary scale for a candoc.

Other conditions:

The PhD student will participate to the teaching and other activities of the Laboratory.

About the Anthropology Unit The Anthropology Unit of the Department of Genetics and Evolution at the

University of Geneva, Switzerland, offers a very stimulating scientific environment with several independent groups of research, international collaborations and excellent computer resources. It is located in the Science campus in the heart of the city of Geneva. Both English and French are the working languages in the Lab. More details about the Anthropology Unit may be found at <http://ua.unige.ch/en/> and more information on the Department of Genetics and Evolution at <http://genev.unige.ch>. How to apply Applications should be sent as a single pdf file by email to Professor Alicia Sanchez-Mazas ([alicia.sanchez-mazas@unige.ch](mailto:alicia.sanchez-mazas@unige.ch)) by February 14th, 2020. It should include a cover letter, a detailed CV, at least two letters of recommendation, copies of secondary and university diplomas, and an attestation of B1 competency level (Common European Framework of Reference for Languages) in the English language.

sancheza <[Alicia.Sanchez-Mazas@unige.ch](mailto:Alicia.Sanchez-Mazas@unige.ch)>

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## GoetheU Frankfurt PlantEvolutionaryEcol

The new research group Plant Evolutionary Ecology in the Institute for Ecology, Diversity and Evolution at the Goethe-University Frankfurt am Main, Germany, invites applications for a PhD position in plant evolutionary ecology.

In the project HerbAdapt, the PhD student (m/f/d) will investigate phenotypic variation and local adaptation of selected understorey forbs and grasses in relation to forest management. Common-garden experiments and a large transplant experiment are core to this project. The project will start at the University of Tübingen in March 2020 but will move to the Goethe-University Frankfurt in Summer 2020.

The PhD student will be supervised by Niek Scheepens in collaboration with Pieter De Frenne from Ghent University, Belgium.

The project is part of the Biodiversity Exploratories (<http://www.biodiversity-exploratories.de/>), one of the largest ecology projects in the world, which will allow the PhD student to interact with many other ecological researchers. Sampling of plant material as well as the reciprocal transplant experiment will take place across Germany in the Schwäbische Alb, Hainich-Düden and Schorfheide-Chorin regions.

The HerbAdapt project will be conducted in collaboration with the project ForGenDiv, led by Henri Thomassen (University of Tübingen, Comparative Zoology) and Oliver Bossdorf (University of Tübingen, Plant Evolutionary Ecology). In ForGenDiv the PhD student (already recruited) will sequence DNA of 20 plant and arthropod species from the forest understorey and link genomic data to forest management. The two projects will collaborate during sampling as well as through joint data analysis.

We are looking for candidates with strong interests in ecology and evolutionary biology. The successful candidate should have a MSc in biology (or equivalent), solid statistical skills (preferably in R), a good command of English, and a driving license. Experience with plant ecological experiments is a plus.

The position is funded by the German Research Foundation (DFG) for a period of 3 years. Salary is at the scale 13 TV-L (65%). Starting date should be 1 March 2020 or soon thereafter.

To increase the share of women in academic positions, women are particularly encouraged to apply. Disabled candidates will be given preference over other equally qualified applicants.

If you wish to apply, please send your CV (max. one page), along with a letter of motivation (max. one page) and the contact details of two references as a single PDF to [niek.scheepens@biologie.uni-tuebingen.de](mailto:niek.scheepens@biologie.uni-tuebingen.de). Deadline for applications is 9 February 2020 or until the position is filled. If you have any questions, please use the same email address as above.

“[niek.scheepens@biologie.uni-tuebingen.de](mailto:niek.scheepens@biologie.uni-tuebingen.de)”

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## HarperAdamsU AffectOfNoiseOnFitness

See below a funded PhD opportunity on the impacts of environmental noise on animal welfare. Although this is an applied project, the supervisory team envision a broader remit and are interested how anthropogenic noise may impact individual fitness. The model for this project will be bovine domestic animals but we have expertise in and are interested in impacts on wildlife as well. This would fit someone with a background and interests in evolution, ecology, conservation, animal science, etc).

Short deadline of 12 Jan 2020. Competitive BBSRC

DTP PhD project.

Info: [https://warwick.ac.uk/fac/cross\\_fac/mibtppgstudy/phd\\_opportunities/animal/noise](https://warwick.ac.uk/fac/cross_fac/mibtppgstudy/phd_opportunities/animal/noise) Apply: [https://warwick.ac.uk/fac/cross\\_fac/mibtppgstudy/phd\\_opportunities/application/](https://warwick.ac.uk/fac/cross_fac/mibtppgstudy/phd_opportunities/application/) #####

Evaluating the animal welfare impacts of chronic noise on livestock

Primary Supervisor: Dr Ed Harris, Crop & Environmental Sciences Secondary supervisor: Professor Mark Rutter External supervisors: Selvino De Kort, Sue-Anne Zollinger PhD project title: Evaluating the animal welfare impacts of chronic noise on livestock University of Registration: Harper Adams University

The negative effects of exposure to chronic, low decibel noise are known to impact humans and other animals, increasing stress and associated physiological function such as blood pressure, immune response and chromosomal telomere damage. For example, humans suffer under the effects of urban noise (1) and there is growing evidence that farm animals and wildlife suffer similar impacts. The increase in terrestrial noise associated with transport networks is a global phenomenon but has had the greatest impacts in Europe and the United States (2,3). As part of the European Commission environmental noise directive, the UK government has policy in place to mitigate the growing impact of urban noise on human health, but there is no specific policy at present with respect to the impact of noise on biodiversity. To that end, Defra recently commissioned a study (4) that concluded that current data tentatively suggest that noise likely has measurable, negative impacts on non-human animals, but that information is lacking detail about how, why and to what extent noise interferes with animals behaviour, wellbeing and individual fitness. The increase in the human population and the concurrent increase in urban noise put considerable pressure on animals. The main contributors to noise pollution are recognised to be road, rail and air traffic. In the UK the motor vehicle traffic volume increased tenfold between 1949 and 2013 (5), with similar increases in aviation and rail activity and associated noise. Thus, it is crucial to understand the impact of urban noise on animals, both at an individual level and for populations. This project aims to investigate specific impacts of noise pollution on welfare, stress and productivity in agricultural livestock. One objective will be to analyse the specific large-scale effects of noise on livestock by identifying “noisy” and “quiet” farms using the predictive noise map from the Strategic Noise Mapping exercise in the UK. Terrestrial noise will be ground-truthed and behavioural (measured via haptic data loggers) and physiological (e.g. corticosteroid production) correlates of stress will be measured

to evaluate the degree to which chronic anthropogenic noise (arising from transport networks) directly impacts livestock. Second, the perception of noise in livestock will be measured using in-ear noise pressure sensors. This will aim to distinguish the overlap between the noise map that is measured in the environment, from the actual perceived sound inside the ear. Finally, we will evaluate evidence that chronic noise can negatively impact telomeres, the protective region flanking animal chromosomes that are linked to senescence and ageing. We will do this by measuring relative telomere length in livestock of different ages using quantitative PCR (6)

Ed Harris <EHarris@harper-adams.ac.uk>

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## HolarU Iceland SticklebackEvoDevo

\*A PhD position on ECO-EVO-DEVO dynamics in threespine stickleback of lake MÄ½vatn, Iceland\*

Hólar University, Iceland, seeks a PhD student to participate in research supported by a Grant of Excellence (RANNIS) on the dynamics of \*Ecological (ECO), Evolutionary (EVO) and Developmental (DEVO) processes\* for origin and maintenance of biodiversity.\*

The phenotype is an important determinant of the dynamic interactions between ecological and evolutionary processes (eco-evolutionary dynamics) and the processes that shape biological diversity in face of environmental change. The project aims to understand the interactions between ECO, EVO and DEVO by focusing on 1) the dual role of ecology in evolution (as driver of natural selection and phenotypic plasticity), 2) the molecular mechanisms underlying phenotypic variation, and 3) the feedbacks between phenotypic change and ecosystem function. The model species in the study is threespine stickleback (\*Gasterosteus aculeatus\*) from lake MÄ½vatn, Iceland. The project is led by Prof. Bjarni K. Kristjánsson (lead PI, Hólar University, Iceland) and Dr. Katja Räsänen (Swiss Federal Institute of Aquatic Sciences, Eawag, Switzerland). It is part of international collaboration across Hólar University (Prof. Skölli Sköglason), Eawag, Switzerland (Dr. Blake Matthews), Univ. of Wisconsin-Madison, USA (Prof. Anthony R. Ives), Univ. of Iceland (Prof. Zophonías O. Jónsson) and the MÄ½vatn research station (Dr. Árni Einarsson).

We are looking for an excellent PhD student to work on studying the \*consequences of phenotypic and genetic variation for ecosystem processes. \*The project

will include both mesocosm and field experiments and is an integral part of an ongoing study which includes long-term field data, laboratory experiments, genomics and mathematical modelling. The student will be a part of an international team, and be provided with opportunities to collaborate with post-docs, students and mentors at the collaborative institutions. The student will be provided high quality training.

\*Location\*: The student will be based at the Department of Aquaculture and Fish Biology (DAFB - <http://www.holaraquatic.is/>) at Hólar University (North Iceland) and registered at the University of Iceland (Reykjavik). HU main campus is in the scenic Hjaltadalur (Skagafjörður), with offices and research laboratories for DAFB in the nearby town Sauárkrúkur. DAFB is an active research centre and the students will become part of a dynamic international team of graduate students and faculty. The rural setting and central location of HU in North of Iceland provides opportunities for outdoor activities.

\*Requirements: \*

§MSc degree in a relevant field (e.g. Ecology, Molecular Biology, Evolution, or Developmental Biology).

§Strong interest in \*evolutionary ecology\*

§Ability to work independently as well as in a team

§Experience in work on experiments and in the field

§A valid driving license

§Peer-reviewed publications and experience off work on animal experiments (fish in particular) is of advantage

The working language is English.

This is a 100% position for three years. \*Application deadline is February 24th, 2020.\* Rights and obligations follow the Act 70/1996 on the Rights and Obligations of Civil Servants.

Applications should be sent by email to [ecodevo@holar.is](mailto:ecodevo@holar.is). The application should include application letter, with a statement of research interests and relevant experience (max. 2 pages), \*curriculum vitae\* with a list of publications, copies of academic qualifications and contact information for three referees.

\*For further information\* contact Bjarni K. Kristjánsson (Head of the Dept. of Aquaculture and Fish Biology, Hólar University) ([bjakk@holar.is](mailto:bjakk@holar.is)) or Dr. Katja Räsänen (EAWAG, Switzerland) ([katja.rasanen@eawag.ch](mailto:katja.rasanen@eawag.ch)).

– Dr. Bjarni K. Kristjánsson, Prófessor Hólaskóli - Háskólinn á Hólum/ Hólar University Hólar í Hjaltadal Iceland [bjakk@holar.is](mailto:bjakk@holar.is) Phone: +354 4556300 [holar.is](http://holar.is)

Bjarni Kristófer Kristjánsson <bjakk@holar.is>

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## KULeuven EvolutionSuperorganismalTraits

The Evolution and Inheritance of Superorganismal Traits

A fully funded PhD position is available at the Laboratory of Socioecology & Social Evolution headed by Prof. Tom Wenseleers at KU Leuven 'V Belgium.

We are seeking highly motivated and enthusiastic applicants to work on this exciting project aiming to understand how superorganismal traits evolve, and how they are inherited across generations. This project will have a good mix of experimental work (both in Belgium and Brazil), genomics and theoretical modelling using social insects as model organisms.

The PhD candidate will perform experiments with bumblebees, stingless and bees, paper wasps and leafcutter ants as well as learn state-of-the-art genomic techniques. The work will be carried out in close collaboration with Dr. Ricardo Caliari Oliveira and Prof. Tom Wenseleers.

A successful applicant must have a master's degree in biology or related fields and previous experience working with social insects. The working language in the lab is English but some level of Portuguese and/or Spanish is a plus given that field work will be carried out in Brazil.

KU Leuven is top University located in a vibrant student town in the heart of Europe, close to major cities and with easy access to Brussels international airport.

Applicants should send a CV, a motivation letter with research interests and the full contact of two referees to ricardo.oliveira@kuleuven.be

We expect to fill the position by March 2020, but it will remain open until filled.

More info about the position can be found at: <https://bio.kuleuven.be/ento/vacancies.htm> Kind regards,

Ricardo Oliveira

/Postdoctoral Researcher Laboratory of Socioecology & Social Evolution KU Leuven - Belgium/

Ricardo Oliveira <ricardo.oliveira@evobio.eu>

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## Lisbon PopulationGenomics

Dear colleagues

As part of an agreement between La Caixa Foundation and several European Research Institutes, the Instituto Gulbenkian de Ciência (IGC) in Lisbon, Portugal, proposed a PhD project entitled

“Demographic inference over time and space: fragmented landscapes and population genomics”

The application deadline is February 4.

All information is available on the Caixa Foundation website (<https://obrasociallacaixa.org/en/-investigacion-y-becas/becas-de-la-caixa/doctorado-inphinit/descripcion-del-programa>)

The proposed project is very open and can be seen here: <https://hosts.lacaixafellowships.org/finder#1> To access this project, simply choose IGC in the “RESEARCH CENTER” section because it is the only project submitted by the IGC. Of course you can see if there are other interesting projects for our community.

Sincerely,

Lounes Chikhi

“Lounes Chikhi (Univ Toulouse)” <lounes.chikhi@univ-tlse3.fr>

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## LMU Munich RecombinationRateEvolution

PhD position on “The (in)stability of recombination rates” LMU Munich, Germany starting as soon as possible

A 3 year PhD position is available in the laboratory of Dr. Bart Nieuwenhuis at the division of Evolutionary Biology, Ludwig-Maximilians-University of Munich, Germany. My lab uses the fission yeast *Schizosaccharomyces pombe* to investigate the evolution of sexes and local adaptation, which both depend on the rise and maintenance of beneficial allele combinations. The rate of recombination between loci with such alleles and along the genome in general greatly affect the course



of evolution, however, little is known about the rise of recombination landscapes and their stability.

I seek a self-motivated candidate to conduct studies on the evolution of recombination rates using a combination of phenotyping, genomics, and experimental evolution approaches. Specifically, you will investigate natural variation and heritability of recombination rates between individuals and along the genome. Additionally, you'll study the evolvability of local and global recombination rates using an experimental evolution approach, followed by genomic and functional genetic analyses in collaboration with Dr Alexander Lorenz at the University of Aberdeen, UK. Your results will help understand how recombination landscapes are shaped and can evolve, and which mechanisms might generate variation in recombination rates.

I welcome all applicants with a background in evolutionary biology, molecular biology, genetics or related subjects that have completed a Master course or equivalent. Candidates with experience in using yeast as a model system are especially encouraged to apply. This work takes a multidisciplinary approach, combining methods in genomics, molecular genetics, and microbial experimental evolution; the ideal candidate is interested and committed to working both in the wet lab and on the computer.

At the division of Evolutionary Biology, we take an integrative approach to the study of evolutionary processes (<http://www.evol.bio.lmu.de/>), and apply a wide range of methodologies that include evolutionary theory, population genetics modelling, genomic approaches, experimental evolution and functional characterization. The working language in our lab and division is English. Knowledge in German is not required, but students are encouraged to take free German classes on campus if they want. The student will also spend some time at the University of Aberdeen (UK), in Dr Alexander Lorenz's research group.

This position is funded for 3 three years by a grant from the German Research Foundation DFG.

How to apply? Informal inquiries should be directed to Dr. Bart Nieuwenhuis ([nieuwenhuis@bio.lmu.de](mailto:nieuwenhuis@bio.lmu.de)). Applications, including a CV, a motivation letter, and names and contact information of at least two referees should be sent as a single pdf file before 16 February 2020 to the same address using the subject header "Recombination Rates PhD".

Deadline: 16 February 2020

Bart Nieuwenhuis <[nieuwenhuis@biologie.uni-muenchen.de](mailto:nieuwenhuis@biologie.uni-muenchen.de)>

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## Lund Sweden

### EvoPlantInsectInteractions

PhD positions in the evolutionary ecology of plant-insect interactions

Two PhD positions are currently available in the Evolutionary Ecology of Plant-Insect Interactions research group (EEPII) at Lund University (<https://www.biology.lu.se/research/research-groups/-evolutionary-ecology-of-plant-insect-interactions>).

Research within the EEPII strives to understand the evolutionary forces driving diversification and adaptation in species interactions among plants and plant-feeding insects. We combine genomic, evolutionary and ecological studies to ask and answer questions about the distribution, diversification and conservation of biodiversity within and among species, and in particular how these patterns and processes are affected by the interaction between plants and insects. Our research bridges the gap between zoology and botany by integrating studies of animal- and plant biodiversity.

Position 1: <https://lu.varbi.com/en/what:job/-jobID:302793/> Position 2: <https://lu.varbi.com/en/what:job/jobID:302607/> Deadline for both positions is the 10. January 2020.

Both projects focus on the evolution of fragrance-based pollination systems, are focused on well-established empirical systems (Position 1: *Arabis alpina* + *Lithophragma bolanderi*, Position 2: *Dalechampia*), and will combine field and greenhouse work with macroevolutionary analyses. We strongly encourage interested candidates to apply for both positions. Please note that this requires two separate applications.

Informal inquiries are welcome to Dr. Magne Friberg ([magne.friberg@biol.lu.se](mailto:magne.friberg@biol.lu.se)) and Dr. Åystein Opedal ([oystein.opedal@biol.lu.se](mailto:oystein.opedal@biol.lu.se)).

Åystein Opedal <[oystein.opedal@biol.lu.se](mailto:oystein.opedal@biol.lu.se)>

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## MaxPlanck AnimalMicrobeSymbiosis

The Max Planck Research Group on Mutualisms offers two doctoral positions in microbial symbiosis, evolutionary biology and developmental biology.

### Introduction:

Housed in the Max Planck Institute for Developmental Biology, the research group aims to elucidate the molecular basis behind the establishment of host-microbe symbioses, and to describe the developmental profiles contributing to their persistence. Contextualized through our work on leaf beetles and their pectinolytic mutualists, and by leveraging a broad range of methodologies, our aim is to study these partnerships across multiple biological scales.

### Available projects:

- 1) Functional diversity and evolutionary history of symbioses across leaf beetles (Coleoptera: Chrysomelidae)
- 2) Symbiont role in shaping leaf beetle physiology and ecological range

### Outlook and responsibilities:

Candidates will be trained to combine computational and experimental approaches in order to characterize the molecular underpinnings behind the establishment of specialized symbioses in herbivorous beetles. Specifically, we are interested in how symbionts are integrated into their hosts' developmental cycle, and the regulatory and physiological implications of long-term coevolution between host and microbe. The ideal candidates are expected to apply their expertise and interests in molecular biology, ecology, genomics, proteomics and/or microscopy to formulate hypothesis-driven research and participate in collaborations with other members of the group.

The laboratory is part of a collaborative environment equipped with state-of-the art infrastructure and a highly collegial community. With access to excellent core facilities within the Institute for Developmental Biology (including platforms for microscopy, proteomics, and metabolomics, and sequencing and high-performance computing facilities), the applicant will be in a position to develop and pursue independent multidisciplinary questions, consistent with the dynamic research environment in Tübingen and the International Max Planck

Research School (IMPRS).

Applicants should have a bachelor's or master's degree in biology, entomology, evolutionary biology, bioinformatics, developmental biology, microbiology, chemistry or a related field. Prior research experience in sequence data analysis, physiology, bioinformatics, fieldwork, and/or molecular techniques are desirable. We offer a stimulating environment, a tractable study system, and the opportunity to combine a number of approaches to better understand the intricacies of host-microbe symbioses.

### Application information:

Expected start date in position: Summer/Fall 2020. Funding is available throughout the length of your training. A completed application includes emailing the following to salemh@si.edu:

- 1) A statement of research interests (1-2 pages), describing how your past experiences will inform your future research in the group. Articulating concrete questions, hypotheses and/or approaches is highly encouraged.
- 2) Curriculum vitae (1-2 pages).
- 3) Contact information for two references familiar with your background and training.

Please include all the materials in a single .pdf file. Applications are due on March 15th, 2020.

Additional information: [www.mutualisms.net](http://www.mutualisms.net) Hassan Salem, Ph.D. National Museum of Natural History Department of Entomology 10th St. & Constitution Avenue, Washington D.C. 20560 salemh@si.edu

"Salem, Hassan" <SalemH@si.edu>

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## MaxPlanckInst Cologne PlantGenomics

Phd position in population genomics available at the Max Planck Institute for Plant Biology (MIPBZ), Cologne, Germany in Group Fulgione in collaboration with George Coupland. Title: Evolutionary genomics of flowering behaviour in the perennial model species *Arabis alpina*. An abstract can be found here.

We seek applicants with an interest and background in some of the following fields: population genetics/genomics, evolutionary genomics, evolutionary biology, bioinformatics, computer science, statistics and data science. An interest in plant evolution, physiology and molecular biology is advantageous. A disposition

towards quantitative biology is highly desirable, as are some experience in population genetics and/or bioinformatics and statistics. Experience in managing experiments with plants in greenhouses/growth chamber is an advantage, but not a requirement. Applicants should be able to work independently and have effective communication skills, both oral and written.

The project focuses on some intriguing populations of the perennial model plant *Arabis alpina* under selection for unusual flowering strategies. The project capitalises on phenotypic data collected in the department across years of experiments and field work. The phd candidate will use computational and population genomic approaches to reveal evolutionary and adaptive dynamics in these populations.

The group studies how plant populations adapt to their environment from a population and evolutionary genomics point of view. Our primary model organism is the alpine, perennial herb *Arabis alpina*. The project will make use of the tools we have developed in this species, such as the genome sequence (Willing et al. 2015) and populations collected in diverse environments (Laenen et al. 2018) as well as population genomic approaches as in (Durvasula et al. 2017, Fulgione et al. 2018). The project will be co-supervised by Max Planck director George Coupland.

The phd position is 3 years long and it would start in summer/fall 2020. The position is affiliated to the International Max Planck Research School (IMPRS) on "Understanding Complex Plant Traits using Computational and Evolutionary Approaches". In order to be eligible for this program the deadline is February the 2nd, 2020. Instructions to apply can be found here. If you have specific questions about the position contact me directly at fulgione@mpipz.mpg.de.

The MPIPZ and the Universities in Cologne and Düsseldorf form an outstanding cluster for basic research in the plant sciences. Supported through the Excellence Strategy of the German federal and state governments (see here), we offer a truly interdisciplinary training of young researchers who will work in a supportive international environment designed to harness creativity.

Andrea Fulgione, Ph.D

Max Planck Institute for Plant Breeding Research

Carl-von-Linné-Weg 10 50829 Köln  
email: fulgione@mpipz.mpg.de

Andrea Fulgione <fulgione@mpipz.mpg.de>

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## MaxPlanckInst Cologne PlantPopulationGenomics

Phd position in population genomics available at the Max Planck Institute for Plant Biology (MPIPZ), Cologne, Germany in Group Fulgione in collaboration with George Coupland. Title: Evolutionary genomics of flowering behaviour in the perennial model species *Arabis alpina*\*. An abstract can be found here <<https://www.mpipz.mpg.de/imprs-fulgione>>.

We seek applicants with an interest and background in some of the following fields: population genetics/genomics, evolutionary genomics, evolutionary biology, bioinformatics, computer science, statistics and data science. An interest in plant evolution, physiology and molecular biology is advantageous. A disposition towards quantitative biology is highly desirable, as are some experience in population genetics and/or bioinformatics and statistics. Experience in managing experiments with plants in greenhouses/growth chamber is an advantage, but not a requirement. Applicants should be able to work independently and have effective communication skills, both oral and written.

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The MPIPZ and the Universities in Cologne and Düsseldorf form an outstanding cluster for basic research in the plant sciences. Supported through the Excellence Strategy of the German federal and state governments (see here < <https://www.ceplas.eu/en/home/> >), we offer a truly interdisciplinary training of young researchers who will work in a supportive international environment designed to harness creativity.

Andrea Fulgione, Ph.D Max Planck Institute for Plant Breeding Research Carl-von-Linné-Weg 10 50829 Köln email: fulgione@mpipz.mpg.de

Andrea Fulgione <fulgione@mpipz.mpg.de>

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### MichiganStateU SeaLampreyPopGen

Ph.D. Assistantship in Population Genetics, Department of Fisheries & Wildlife, Michigan State University

Position Description: The Robinson lab in the Department of Fisheries and Wildlife at Michigan State University seeks a Ph.D. student, beginning in Summer 2020, to collect and analyze population genomic data from samples of larval sea lamprey collected from multiple Great Lakes tributaries. This research is part of a large collaborative project to evaluate supplemental control approaches to limit reproduction and metamorphosis of the invasive sea lamprey in the Great Lakes basin. The successful applicant will work collaboratively with scientists at state and federal agencies, faculty at Michigan State University, and members of the Robinson lab. The student will be responsible for curating and archiving samples received from collaborators, lab work, and data analysis. Additionally, there are likely to be opportunities for the student to assist with field collections. The student will gain extensive experience with lab techniques (using reduced representation sequencing technologies), bioinformatic analysis of sequencing data, pedigree analysis using hundreds to thousands of SNP markers, and effective population size estimation using a variety of approaches. While the source of support dictates several deliverables associated with this project,

the successful candidate is strongly encouraged to develop independent research questions that can be addressed with the large dataset generated for this research. Opportunities for training and professional development include internal workshops on cluster computing and bioinformatics, research ethics training, presenting at scientific conferences, and opportunities to gain teaching experience in the classroom.

Desired Qualifications: Applicants should have a B.S. in Biology, Ecology, Genetics, or a similar field. An M.S. is not required, but is strongly preferred. The successful candidate will display strong interests in population genomics, demographic inference, fish biology, and/or invasive species control. Experience with genetic lab techniques (DNA extraction, PCR, etc.), computer programming (one or more: R, Python, C++), and high performance computing are strongly desired. The ideal applicant would have high GPA / GRE scores, a record of peer-reviewed publications, strong networking and social skills, and interest / experience in applied research in population genetics.

To Apply: Submit a CV (including GPA and GRE scores), contact information for three individuals willing to provide letters of recommendation, and a letter of interest detailing background, accomplishments, skills, career aspirations, and fit of the applicant to the position to Dr. John Robinson (jdrob@msu.edu).

Closing Date: Open until filled, review of applicants will begin February 1, 2020.

jdrob@msu.edu

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### MississippiStateU EvolutionaryGenomicsReproduction

The Dapper Lab ([www.amy-dapper.com](http://www.amy-dapper.com)) at Mississippi State University is recruiting graduate students (M.S. or PhD) for positions starting Fall 2020.

The Dapper Lab is broadly interested in using evolutionary genetic approaches to understand the origin and maintenance of genetic diversity 'V primarily through studying the evolution of reproduction. Students will have the opportunity to develop independent research projects that combine population genetic, quantitative genetic, bioinformatic, mathematical models, and/or molecular genetic approaches. Current topics of interest in the lab include the evolution of meiotic genes in mammals, experimental evolution of recombination

in nematodes, and the rapid evolution of reproductive genes.

Interested students should contact Dr. Amy Dapper (dapper@biology.msstate.edu), providing a description of your research interests and experiences and a CV or resume.

For full consideration for the fall semester, applications should be submitted to the department by February 28th, 2018. Information on Graduate Studies in the Department of Biological Sciences (<https://www.biology.msstate.edu>) is available at <http://biology.msstate.edu/degrees/graduate/> Amy L. Dapper

Department of Biological Sciences

Mississippi State University

“Dapper, Amy” <dapper@biology.msstate.edu>

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## Museum Geneva OrthopteraBarcodes

A 4-years PhD position is available at the Geneva Natural History Museum, Switzerland.

Starting date: 1 April 2020

### BACKGROUND AND OBJECTIVES

The research project aims to improve knowledge on species and genetic diversity of Orthoptera in Switzerland. The project is organized around two axes. First, the development and the application of a multilocus barcoding method (whole mitochondrion, ribosomal DNA and UCEs) for the monitoring of orthopteran species all over Switzerland. Second, the museomics-based inference of demographic dynamics across the last century in four selected orthopteran species (population genomics using HyRAD-based hybridization-capture).

The PhD candidate will be involved in field collection, wet lab experiment (in particular DNA extraction, custom library preparation and NGS sequencing), analysis of NGS data using custom bioinformatic tools, as well as manuscript writing.

### APPLICATION PROCEDURE

The applicant should hold a Master degree or equivalent in biology.

Experience in molecular biology, analysis of next generation sequencing data and scientific writing are highly desirable. Skills in at least one usual analysis and script-

ing language (R CRAN, Perl or Python) would be an asset. The ideal candidate should be enthusiastic, team-player, self-motivated, and with a strong interest in insect diversity.

The applicant will have full time to conduct his PhD research.

Applicants should submit the following documents:

- Cover letter emphasizing on the intrinsic motivation for applying to this position, on the fit of the position with the applicant’s profile and on his/her professional goals (2 pages max)

- Curriculum Vitae (2 pages max)

- Summary of previous research experience (1 page max)

- Copies of degree certificates and list of coursework, including grades

- Names, addresses and e-mails of two professional references

- An electronic copy of previous works (master degree thesis or other scientific publications).

Short-listed candidates will be invited in Geneva for an interview.

The application should be sent by email as a single pdf file to Nadir ALVAREZ, e-mail : nadir.alvarez@ville-ge.ch

For any additional information, please contact Nadir ALVAREZ (nadir.alvarez@ville-ge.ch) or Jeremy GAUTHIER (jeremy.gauthier@ville-ge.ch).

Application deadline : 31 January 2020

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## NottinghamTrentU Palaeogenomics

PhD opportunity in palaeogenomics/population genomics

Nottingham Trent University is currently offering 50 fully funded PhD studentships: deadline Feb 15th, anticipated start date Oct 2020 or Jan 2021.

[https://www.ntu.ac.uk/c/phd-studentships?gclid=CjwKCAiA3uDwBRBFEiwA1VsajGN3uutyEXoQJSnTT4hVg6jW3e9a5l-1e1uTbvyNOa6METEIXTjghoCC5oQAvD\\_BwE](https://www.ntu.ac.uk/c/phd-studentships?gclid=CjwKCAiA3uDwBRBFEiwA1VsajGN3uutyEXoQJSnTT4hVg6jW3e9a5l-1e1uTbvyNOa6METEIXTjghoCC5oQAvD_BwE)

Masters-level students and graduates interested in the general topics of palaeogenomics and population genomics are invited to contact Dr. Axel Barlow to

discuss applying for this scheme. Our lab investigates the population genomics of various extinct and living mammals, such as cave bears, mammoths, brown bears, big cats, etc. We are also developing new research themes in vertebrate conservation genomics. Applicants are expected to develop their own research projects within these general areas.

Check out our website for further info: <https://pleistocenegenomics.com/> Example projects would include (but are not limited to):

- Population genomics of Pleistocene mammals (for e.g. see Barlow et al. 2018. *Nature Ecol & Evol*, and Sheng et al. 2019. *Current Biology*)
- Development of statistical methods and bioinformatics tools for palaeogenomic data analysis (for e.g. see Barlow et al. 2020. *Genes*)
- Development of laboratory methods for palaeogenomics (for e.g. see Alberti et al. 2018. *Mol Ecol Res*)

Please note this is a competitive NTU-wide scheme, and any applicants would be in competition with other students and supervisors at NTU. Interested students should contact me before the end of January to give sufficient time to discuss project ideas and preparation of the application.

I look forward to hearing from you,

Axel Barlow

Lecturer in Molecular Bioscience (Bioinformatics)  
School of Science and Technology Nottingham Trent University

website: [pleistocenegenomics.com](https://pleistocenegenomics.com)  
email: [axel.barlow@ntu.ac.uk](mailto:axel.barlow@ntu.ac.uk)

Axel Barlow <[axel.barlow.ab@gmail.com](mailto:axel.barlow.ab@gmail.com)>

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## PotsdamU PlantStressGenomics

\*PhD position Evolutionary genomics of heat stress responses in Brassicaceae at Potsdam University\*

The Bäurle lab studies the long-term adaptation of plants to abiotic stress (see <https://baurlelab.org>). The successful candidate will be investigating the plasticity of heat stress responses in the genus *Capsella*. The aim of the project is the genetic analysis and molecular characterization of genes that cause differential heat stress acclimation in *Capsella* spec., and will provide insights into the adaptation to elevated temperatures,

as well as into the evolution of heat stress response and its plasticity. The project is part of a newly established focus area on “Evolutionary Systems Biology” at the University of Potsdam.

The PhD position is funded for three years. Salary is according to TV-L 13 (50%). A Masters degree in molecular Life Sciences and previous experience in molecular biology and genetics are required, ideally matched with an evolutionary understanding. A strong interest in the research question, flexibility, and the ability to work both independently and in a team are essential. The working language of the laboratory is English.

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.

The Potsdam/ Berlin area provides a vibrant scientific environment for molecular plant research. The area is renowned for its high quality of life. Potsdam University takes an effort to assist its members in family-related issues and has repeatedly been awarded the total e-quality award.

To apply please send your application including a complete CV, a copy of your degree certificate, a letter detailing your motivation to apply, and contact information of two referees to Isabel Bäurle ([isabel.baeurle@uni-potsdam.de](mailto:isabel.baeurle@uni-potsdam.de)). Applications will be considered until the position is filled.

[tiedeman@uni-potsdam.de](mailto:tiedeman@uni-potsdam.de)

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## Poznan Poland ParasiteEvolution

Reminder: PhD position in Evolutionary Biology; application deadline: 17.01.2020.

–Original message–

PhD-position in Evolutionary Biology: “Parasite evolution in response to climate warming”

The position is available from 1st June 2020 and limited to 3 years.

The proposed research is collaboration between Polish and German scientific teams: PD Dr. Slawek Cerbin from Adam Mickiewicz University (Poland) and Prof. Justyna Wolinska from IGB and Free University Berlin, jointly financed by Polish National Science Centre and German Research Foundation. The position is mainly

based in Poland; however, a six-month research stay at the IGB-Berlin is planned. Funding for attending national/international conferences is available.

Project description:

It is commonly believed that global warming will result in a “sicker world”, with infectious diseases increasing in prevalence and virulence. However, these predictions are based on short-term experiments that have not recognized evolution that could lead to thermal adaptation. This project aims at answering the question whether parasites’ prevalence and virulence is altered under elevated temperatures and if long-term exposure to warming amplifies this effect. The successful candidate will use a combination of experimental evolution and field approaches to generate new predictions regarding the evolution of parasites in a warmer world. He/she will use a model system consisting of the crustacean *Daphnia* and their microparasites. The project offers opportunities to learn state-of-the-art methods and a range of transferable skills.

Duties and responsibilities

\* laboratory experiments \* field work (including artificially heated lakes which serve as a globally unique model of “warmer world”) \* advance statistical analyses of experimental (life history and genomic) and field (environmental and genetic) data \* writing scientific publications

Requirements

\* MSc degree in biology \* strong background in evolutionary biology, population genetics or ecology \* hands-on experience with experimental work \* experience in molecular or genomic research would be an advantage \* excellent analytical skills and very good knowledge in statistics (R programming) \* previous experience with *Daphnia* culturing and field work are considered advantageous \* excellent communication and writing skills in English \* good work ethic \* creative thinking

How to apply:

Please send complete application documents as a single pdf-file by email to dr. S. Cerbin (cerbins[at]amu.edu.pl; In the subject field include “Paradapt PhD”): no later than 17th January 2020.

The application should include:

1) CV

Please include the following statement in your CV: “Pursuant to Article 6 (1) of the General Regulation on the Protection of Personal Data of 27 April 2016 (Journal of Laws EU L 119/1 of 4 May 2016) I agree on the processing of personal data such as: name, (names) and

surname, parents’ names, date of birth, place of residence (correspondence address), education, course of previous employment, included in my job offer for the needs of current recruitment.”

2) A letter of motivation

3) A scan of MSc diploma

4) Contact details to two/three potential referees, including MSc supervisor

The beneficiary of the National Science Centre stipend will be chosen by a selection committee based on regulations about scientific scholarships for young researchers in research projects financed by the Polish National Science Centre. The recruited person will be required to enroll as a regular PhD-student in PhD School of the Adam Mickiewicz University.

Prof. Justyna Wolinska

Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) Mueggelseedamm 301 12587 Berlin, Germany Group Leader at the IGB & Professor for Aquatic Evolutionary Ecology at the Free University of Berlin Phone: +49 (0)30 64181 686; Fax: +49 (0)30 64181 682; email:wolinska@igb-berlin.de <http://www.igb-berlin.de/en/profile/justyna-wolinska-0> <http://www.igb-berlin.de/en/wolinska> Justyna Wolinska <wolinska@igb-berlin.de>

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## QueenMaryU London AnnelidEvoDevo

The development of an entire animal from a single totipotent cell 'V the zygote 'V is arguably one of the most fascinating processes in Nature. Strikingly, how this process is regulated at the lower levels of biological complexity, such as at the level of the genome and its regulation during the early phases of development, is still poorly understood. Moreover, our understanding relies on what is known for only a handful of species, such as mammals and flies. To solve this major knowledge gap, the Martin-Duran lab is establishing annelid embryos as experimental systems to understand the genomic regulation of early animal development. Annelid embryos are unique in that they exhibit interspecific variation in the way the zygote gives rises to the major progenitor cells during early cleavage. What are the epigenetic mechanisms controlling annelid development? How do these mechanisms generate variability among species? How can annelid development inform us of the

fundamental principles of animal embryogenesis?

- In this project you will rigorously answer these questions combining state-of-the-art experimental and computation approaches. - You will have access to large genomic databases, and in-house live organisms to fuel your investigation. - You will gain experience of developmental biology and molecular techniques (gene expression analyses, epigenomics), bioinformatics (pipelines to analyse ATAC-seq, ChIP-seq and HiC), and statistics. - You will be encouraged to develop your own ideas and hypotheses.

This is an ERC-Starting Grant PhD funded position. The student will become part of Queen Mary's Doctoral College, which provides training and development opportunities and financial support for research. The student will also have access to a Researcher Development Programme designed to help recognise and develop key skills and attributes needed to effectively manage research, and to prepare and plan for the next stages of their career.

Skills preferred In a multidisciplinary project like this, candidates are unlikely to have a background in all disciplines involved. The most important qualification is motivation, enthusiasm and that the project appeals to you. However, previous computational experience would be a plus. We can envisage strong candidates coming through a variety of routes including:

- practical molecular biology - developmental and cell biology - computational biology

To apply, students should have a 1st class degree or have received a MSc in a relevant field (i.e. molecular biology, genetics, developmental and cell biology, bioinformatics) or are about to finish their MSc.

For informal requests, do not hesitate to contact Dr Chema Martin at [chema.martin@qmul.ac.uk](mailto:chema.martin@qmul.ac.uk)

Apply via: <https://www.qmul.ac.uk/sbcs/postgraduate/phd-programmes/projects/-display-title-760193-en.html> Chema Martin  
<[chema.martin@qmul.ac.uk](mailto:chema.martin@qmul.ac.uk)>

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## QueenMaryU London HorizontalGeneTransfer

Horizontal gene transfer in the evolution of insects: a genomic approach

\*Background\* Horizontal gene transfer has played a

major role in the evolution of bacteria, however, its importance in animals is less clear. Recent evidence suggests that insects have repeatedly acquired genes from symbiotic bacteria that have provided them with key adaptation that has led to their incredible success. Examples of this include, the horizontal acquisition of genes for lignocellulose digestion that has led to herbivory in beetles, and toxin encoding genes that may underlie protection from natural enemies in aphids and vinegar flies. However, it is currently unclear how common the horizontal transfer of symbiont genes is across insect species, and in most cases whether the newly acquired genes actually provide insects with adaptive functions. It is crucial to understand the dynamics of horizontal gene transfer in insects as the acquisition of novel traits from microbes is transforming our view of how arthropods evolve. This is of particular importance for insect pests as it may underlie their capacity to colonise new environments and resist efforts to control them.

The successful applicant will use several insect families as models to rigorously test hypotheses on horizontal gene transfer in the evolution of insects. This may include: using whole genome sequence data to explore horizontally acquired genes involved in nutrition and defence across phylogenetically diverse insect species; investigating gene expression profiles to determine gene activity; and performing functional assays to reveal whether horizontally acquired genes provide insects with novel adaptive functions.

- You will have access to large genetic databases, insect collections, in-house live organisms and cutting-edge research facilities to fuel your investigation. - You will gain experience in bioinformatics, comparative/metagenomics, molecular/experimental biology, and statistics (e.g. comparative phylogenetics). - You will be encouraged to develop your own ideas and hypotheses. Eligibility Applications are open to international students, as well as those in the EU and UK who have been awarded, or expecting to be awarded, at an upper-class bachelors degree, or equivalent qualification, in biological or computational sciences (or similar). A masters degree is desirable, but not essential.

Students with a background in bioinformatics are particularly encouraged to apply.

For informal questions, contact Lee Henry [l.henry@qmul.ac.uk](mailto:l.henry@qmul.ac.uk) The Henry Lab <https://www.qmul.ac.uk/sbcs/staff/leehenry.html> Applications have to be submitted to: <https://www.qmul.ac.uk/sbcs/postgraduate/phd-programmes/projects/-display-title-762150-en.html> \*\*\*\*Application deadline is Friday, January 31, 2020\*\*\*\*



< <https://www.qmul.ac.uk/sbcs/postgraduate/phd-programmes/projects/display-title-762150-en.html>  
>

Lee Henry Senior Lecturer Queen Mary University of London School of Biological and Chemical sciences Mile End Rd London E1 4NS

lee henry <leehenrym@gmail.com>

## QueensU Belfast 2 EvoBiol

We are recruiting 2 PhD students at Queen's University Belfast. The ideal candidate has experience and strong interests in evolutionary biology/evolutionary ecology and in phylogenetic comparative methods.

The studentship funds UK/EU nationals and provides funding for tuition fees, stipend and a research training and support grant subject to eligibility.

For more information please contact Dr Isabella Capellini at I.Capellini@qub.ac.uk.

(1) NERC QUADRAT DTP CASE: UNDERSTANDING AND PREDICTING THE SUCCESS OF ALIEN FRESHWATER FISH

DEADLINE: 29/1/2020

Overview:

Alien species, those introduced outside their native range, are a major driver of environmental change that may lead to the extinction of local biodiversity, alter ecosystem services and cause huge economic damage. With increasing global trade, the number of new alien species is growing rapidly. Thus, identifying which species may establish and become invasive is an urgent global challenge. However, with no history of past invasion, it is hard to predict which new alien species will establish, and which ones will go naturally extinct. Freshwater fish are among the most frequently introduced vertebrates and many have major detrimental effects on the most vulnerable ecosystems on Earth: freshwater habitats. Surprisingly, we know remarkably little of why some fish species are more likely to establish and spread in novel regions, and which species are likely to be the future successful aliens.

Aim:

To identify which species traits facilitate the introduction, establishment and spread of alien freshwater fish and predict the probability of success of potential future

invaders, at global and local scale.

Objectives:

- 1) To build a global scale database on freshwater fish introductions, introduction pathways, and species traits;
- 2) To test which species characteristics determine the probability of introduction, establishment and spread of alien freshwater fish using the database, phylogenetic comparative methods and theoretical modelling;
- 3) To produce a Horizon scanning output that informs policy, by quantifying how different pathways to introduction (e.g. angling, fisheries, pet trade) influence the probability of release in novel regions, and deriving their probability invasion at global and local scale for species likely to be introduced globally and in the UK and Ireland in particular.

There is also the possibility to carry out case studies in the field in Ireland, Argentina or Indonesia.

For further details see: <http://www.qub.ac.uk/courses/-postgraduate-research/phd-opportunities/quadrat-dtp-case-understanding-and-predicting-the-success-of-alien-freshwater-fish.html>

(2) BBSRC DTP CASE: UNDERSTANDING THE ECOLOGY AND COEVOLUTION OF APHIDS AND PARASITOIDS

DEADLINE: 06/03/2020

Parasitoids are insects that play a fundamental ecological role in both natural and agricultural ecosystems by regulating the population of herbivore pests, such as aphids. Despite much work on the ecology and evolution of parasitoids, we still ignore to what extent the demography of the enemy (the parasitoid) is adapted to that of the host (the crop pest) and viceversa; how the degree of specialisation of parasitoids to the host(s) facilitates or undermines their population persistence in the environment; whether more patchy and diverse environments offer refugia points for parasitoids, and how populations of pest hosts and their parasitoids will respond to predicted climate change. The student will address these fundamental questions using a powerful combination of approaches. Specifically, the student will:

Derive general principles using phylogenetic comparative methods by investigating questions at the global scale across hundreds of parasitoid species and their hosts, on (i) how different reproductive strategies evolved in hosts and in parasitoids, and coevolved between them; (ii) how the degree of host specialisation affects the population dynamics in both hosts and parasitoids.

Run experiments with plants, pests and parasitoids to investigate their response to predicted future climate and extreme climatic events.

Run field trials to investigate whether habitat patchiness supports parasitoid populations using the agri-environments and a cereal-aphid-parasitoid complex as models in both natural and agri-environments. The project is designed to offer the student the opportunity to expand or reduce the experimental and field components as best suited to their interests or as needed. For further details see <https://research.reading.ac.uk/foodbiosystems/wp-content/uploads/sites/145/advert-files/FBS2020-14-CAPELLINI-QR-ADVERT-final.pdf>

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

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## QueensU SeabirdEvolutionaryGenomics

I have an opening for a graduate student (preferably PhD) to study evolutionary genomics of birds. A variety of projects are possible, spanning genomics of adaptation, speciation, and conservation genomics. Most projects involve Arctic seabirds, but some involve temperate land birds or tropical seabirds. Several have direct conservation or management applications. A solid theoretical foundation in evolutionary genetics is essential - do not apply if you do not have this. Preference will be given to candidates with prior experience with genomics/bioinformatics. Projects involve field work on remote islands, and so prior field experience is an asset, preferably with birds or marine animals. The successful applicant will join a dynamic group of faculty and students studying ecology and evolution at Queen's University (see <http://post.queensu.ca/~birdpop/index.html> and <https://biology.queensu.ca/>). Please send a resume or curriculum vitae, informal transcript, and contact information for two academic references to Dr. Vicki Friesen ([vlf@queensu.ca](mailto:vlf@queensu.ca)). Deadline for non-Canadian applicants: Jan. 20 2020. Deadline for Canadian applicants: Jan. 31 2020.

Dr. Vicki Friesen, Professor Department of Biology, 4443 Biosciences, 116 Barrie Street, Queen's University, Kingston, ON K7L 3N6, Canada Tel: 613-533-6156 Fax: 613-533-6617 Email: [vlf@queensu.ca](mailto:vlf@queensu.ca)

Vicki Friesen <[vlf@queensu.ca](mailto:vlf@queensu.ca)>

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## SGN Frankfurt Biodiversity

Job announcement!

For over 200 years the Senckenberg Gesellschaft für Naturforschung (SGN) represents one of the most relevant institutions investigating nature and its diversity. Currently, scientists from more than 40 countries across 11 locations in Germany conduct research in the fields of biodiversity, earth system analysis and climate change. The head office of Senckenberg is Frankfurt am Main together with the Senckenberg Research Institute and Natural History Museum Frankfurt.

The Department of River Ecology and Conservation at Senckenberg in cooperation with the Faculty of Biology at the University of Duisburg-Essen jointly invite application for a

PhD Position / Research Associate (m/f/d) - Research field: Ecology

Within a large EU-funded research project (eLTER PLUS; 33 partner institutions from 20 countries; 10 Mill. euro), unique long-term biodiversity and environmental data across Europe will be analyzed to unravel pattern of biodiversity change and the drivers of such changes. The data comprise various terrestrial, marine and freshwater taxa groups as well as in situ environmental data and belong to the most comprehensive long-term datasets in the world.

Your tasks

Identifying temporal pattern of various species communities  
Identifying drivers of temporal changes in populations and communities  
Statistical analyses using R,  
preparation of manuscripts  
Working together with other PhD students and Postdocs within the department as well as within the eLTER PLUS project

Your profile

Master degree/Diploma in Ecology or a related field  
Solid background in ecology (preferably zoology)  
Advanced skills in the statistical analysis of (large) ecological datasets  
Very good written and oral communication skills

What awaits you?

Salary and benefits are according to a public service position in Germany (TV-H E 13, 50%), starting around April 1st, 2020. The position is limited for 3 years.

The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment will be Gelnhausen (Hesse), Germany. The university for the finalization of the PhD will be Duisburg-Essen. The employer is the Senckenberg Gesellschaft für Naturforschung.

You would like to apply?

Please send your complete application documents (in a single PDF file) mentioning the reference number of this job announcement (ref. #04-19009) until January 23, 2020 and include - a cover letter outlining your motivation and suitability for the position - a detailed CV copies of your educational certificates and transcripts - a list of publications and solicited funding (if available) contact details of 2 referees

Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt

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

For scientific enquiries please get in contact with Prof. Dr. Peter Haase, [peter.haase@senckenberg.de](mailto:peter.haase@senckenberg.de) .

Mit freundlichen Grüßen / Sincerely yours

Isabel Gajcevic, M.A.

Personalsachbearbeiterin

SENCKENBERG

Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß § 22 BGB) Senckenberganlage 25 60325 Frankfurt am Main

“[recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)”

<[recruiting@senckenberg.de](mailto:recruiting@senckenberg.de)>

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## SGN Frankfurt Evolutionary Genomics

Job announcement ref. #12-20002

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 - Evolutionary genomics of invertebrates (part time, 50 %)

Your tasks:

Comparative genomic analysis of mobile DNA in non-model organisms, with a focus on ribbon worms

Evolutionary inference of mobile DNA to study dynamics, phylogeny, and/or mode of transmission

Phylogenomic analysis of whole genome data using state of the art methodology

Taxonomic description of new species from the Northern and Southern Hemisphere

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. Access 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 E 13, 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 (m/f/d) will be given preference.

Please send your application, mentioning the reference

of this job offer (ref. #12-20002) before February 2nd, 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](mailto:recruiting@senckenberg.de)

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

Mit freundlichen Grüßen / Sincerely yours

Isabel Gajcevic, M.A.

Personalsachbearbeiterin

SENCKENBERG

Gesellschaft für Naturforschung

(Rechtsfähiger Verein gemäß § 22 BGB)

Senckenberganlage 25

60325 Frankfurt am Main

Besucheradresse: Mertonstraße 17-19, 60325 Frankfurt am Main (1. OG)

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

Leiterin Personal & Soziales

- 1458 Loke, Uta

Stellv. Leiterin Gruppe Personal & Soziales

- 1319 Elsen, Carina

Mitarbeiter/in Personalbeschaffung (Recruiting)

- 1564 di Biase, Maria

- 1478 Gajcevic, Isabel

- 1313 Helm, Jessica

Fax: 0049 (0)69 / 7542-1445

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

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

Präsidentin: Dr. h. c. Beate Heraeus

Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Senckenberg forscht für Ihr Leben gern!  
[www.200jahresenckenberg.de](http://www.200jahresenckenberg.de)

Job announcement ref. #12-20001

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

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

## StockholmU Microbiome Parasitoid Interaction

We are currently opening a PhD-position at Stockholm University working with ' Gut microbiomes and plant-host-parasitoid interactions'.

Description:

The general aim of the project is to study how the gut microbiome affects the ecology and evolution of the host, both host plant use and the ability to defend against parasitic wasps, in a phylogenetic context. The PhD-project aims to (i) sequence the gut microbiome to find differences in microbiome community composition between host species, (ii) identify mechanisms whereby the gut microbiome is transferred between generations (mainly between adult and larvae), (iii) study how the gene expression within the host depends on the microbiome community composition in relation to host plant use and to defense mechanisms against parasitic wasp attack. The project will involve a set of leaf beetle species, their host plants and the parasitic wasps attack beetle larvae. Within the project group, there is more than 20 years' experience in working with the system, including a thorough understanding of the ecological and physiological processes affecting species interactions as well

as a comprehensive genomic background information (involving both DNA- and RNA-sequencing).

For further information see: <https://www.su.se/english/about/working-at-su/phd?rmpage=-job&rmjob=11290&rmlang=UK> Peter Hambäck <peter.hamback@su.se>

<https://tinyurl.com/yxyp5cu5> Please feel free to contact Prof. Rhonda Snook for questions about the position: rhonda.snook@zoologi.su.se

Reference number for the application: SU FV-4595-19

Closing Date: February 28, 2020

Rhonda Snook <rhonda.snook@zoologi.su.se>

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## StockholmU SexualSelection

### PhD in Sexual Selection

A four year full time PhD position focused on sexual selection is available in Professor Rhonda Snook's group in the Department of Zoology, Stockholm University.

Snook's lab is generally interested in how sexual selection influences the rapid (co)evolution of male and female reproductive traits, typically using *Drosophila* fruit flies. The PhD project aims to improve understanding in this area, and will involve laboratory based phenotyping of male and female reproductive traits and quantitative genetic analyses, with opportunities for experimental and genomic work. While several research questions are already available to pursue in the Snook lab in this general area, the student will also have the opportunity to contribute to development of the project. The ideal candidate will have a strong background in evolution, but training for both general and specific skills required for the project will obviously be part of training in a vibrant lab environment, with potential for interaction with international collaborators. Working language in the lab is English.

It is strongly recommended that you read relevant literature and tailor your cover letter and application accordingly. Applications without this will not be considered. Start date is flexible but ideally before October 2020. 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 Department of Zoology is a vibrant international community, consisting of five interactive and collaborative divisions: Ecology, Ethology, Functional Morphology, Population Genetics, and Systematics and Evolution. The advertised PhD will be part of the Division of Ecology.

For more details in English, including how to apply, see: <https://tinyurl.com/ver5gju> For Swedish, see:

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## TrentU AvianPhysiologicalEvolution

MSc and/or PhD positions in avian physiological ecology (Canadians only)

Position background: We are seeking 1-2 highly motivated MSc/PhD students interested in avian thermal physiology. Areas of ongoing research in the lab include understanding impact of developmental temperature on adult physiology and metabolism, climatic warming as a constraint on activity in wild birds, and the use of non-invasive techniques to evaluate stress. Planned research includes identifying physiological factors underlying fine-scale movement of aerial insectivores using automated radio-telemetry. Specific thesis topics are flexible, and you are encouraged to contribute your own ideas and explore your own interests.

Requirements: You should have an interest in animal physiology/physiological ecology. Experience and/or interest in handling large data sets in R would be an asset (although not required). To apply for an M.Sc., you will require a B.Sc. (Hons) in Biology or a related field. PhD applicants will require a completed MSc (or equivalent) by the start date. Currently, we can only consider Canadian applicants. However, we seek a diversity of ideas and perspectives in the lab, so we especially welcome applicants who are from underrepresented groups.

How to apply: Interested? Please send me a cover letter outlining your research interests, a curriculum vitae (CV), and an unofficial transcript. The minimum stipend for an MSc student is \$19,274 for each of 2 years, and for a PhD student is \$21,274 for each of 4 years. Students holding external funding (e.g., NSERC) are particularly encouraged to apply.

Start date: Sept 2020. Applications will be considered as positions are filled.

Contact and enquiries: Dr. Gary Burness, Department of Biology, Trent University, Peterborough, Ontario (garyburness@trentu.ca)

Gary Burness <garyburness@trentu.ca>

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## TUMadrid MutationDrivenEvolution

Description of the offer: The Technical University of Madrid is currently offering a fully funded PhD opportunity via La Caixa Foundation to investigate the role of mutation bias as a force directing evolution. The successful candidate will join an emerging team led by Dr Couce at the Centre for Plant Biotechnology and Genomics (CBGP), a mixed research centre supported by the Technical University of Madrid (UPM) and the National Institute for Agricultural and Food Research and Technology (INIA). The everyday working language in the laboratory is English, and administrative tasks, training and seminars arranged by the institute are conducted in English. Being the third-largest metropolitan area in the EU, Madrid is a vibrant, multicultural hub with a high quality of life and a thriving cultural scene. The position offers a highly competitive salary with all the benefits of the Spanish National Social Security System, comprising generous sick/maternity/paternity leaves and health, unemployment and retirement insurances.

Background: The evolution of mutation rates has fascinated evolutionary biologists for decades (Sniegowski 2000, Bioessays), and continues to be a major topic due to the importance of elevated mutation rates in bacterial infections (Bartell et al., Nat Comm 2019) and in cancer (Campbell et al., Cell 2017). In addition, work led by the host lab has shown that even short pulses of hypermutability can leave deep and long-lasting signatures in bacterial genomes, challenging previous views on the evolution of bacterial genome size and composition (Couce et al., PNAS 2017). Even more recently, work by the host lab has shown that different codon usage patterns can alter the probability that a particular mutational spectrum generates strong-effect amino acid changes, which implies that hypermutators might display different evolutionary properties in species with contrasting GC content (Couce et al., Nat Comm 2019).

Description of activities: In this project, you will follow up on this work and provide a first empirical account on the role of mutation spectrum in the emergence and subsequent evolution of hypermutability and stress-induced mutagenesis in different species. Briefly, you will conduct Mutation Accumulation Experiments (Halligan

& Keightley, Annu Rev Ecol Evol 2009) to measure the mutational load of different mutators in species with contrasting GC content. These lineages will be later subjected to experimental evolution for hundreds of generations to quantify the costs of mutation erosion in novel environments, and how readily these costs can be overcome by de novo adaptation. In parallel, you will characterise the mutational spectrum of stress-induced polymerases from different species, for which some differences have been reported but not conclusively established (Nohmi, Annu Rev Microbiol 2006). Finally, you will conduct a survey among wild isolates of plant and animal opportunistic pathogens to study the natural, within-species polymorphisms in mutation rate and spectra.

How to apply: Interested candidates please send a single PDF file with a cover letter and a short CV to Dr Alejandro Couce (a.couce@upm.es). Please include the word "MutDrivenEvolution" in the subject line. The deadline for applications is Feb 1th and the anticipated start date is Sep 2020 to Jan 2021.

More info at: <https://euraxess.ec.europa.eu/jobs/-/467348> – Dr Alejandro Couce Group Leader - Severo Ochoa Fellow Centre for Plant Biotechnology and Genomics Technical University of Madrid, Spain & Visiting Fellow Department of Life Sciences Imperial College London, UK

A Couce <a.couce@upm.es>

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## UAntwerp InfectionsSmallMammals

The Evolutionary Ecology Group at the University of Antwerp, Belgium ([www.uantwerpen.be/eveco](http://www.uantwerpen.be/eveco)) is starting three new projects on the ecology of infections carried by small mammals (use the links to see the project summaries)

\*BIODIV-AFREID: Biodiversity changes in African forests and Emerging Infectious Diseases: should we worry? (<https://www.uantwerpen.be/en/research-groups/eveco/research/main-ongoing-project/new-biodiv-afreid-/>)

\*BioRodDis: Managing biodiversity in forests and urban green spaces. Dilution and amplification effects of rodent microbiome and rodent-borne diseases (<https://www.uantwerpen.be/en/research-groups/eveco/research/main-ongoing-project/new-bioroddis-mana/>)

\*Co-infections, heterogeneity and behaviour: models and real rodents. ([https://www.uantwerpen.be/en/research-groups/eveco/-](https://www.uantwerpen.be/en/research-groups/eveco/)

[research/main-ongoing-project/new-co-infections-/\)](#)

We are looking for smart and enthusiastic PhD-students to work in these projects. We offer a starting grant of one year; extension may be possible, but we require each PhD-student to also apply for a competitive PhD-grant from the Flemish Research Foundation FWO ([www.fwo.be](http://www.fwo.be)). We are on the outlook for candidates with excellent study results, an interest in population ecology, epidemiology and modelling and who are not afraid to combine field work with diagnostic work in the lab. Positions can start from March 2020 or soonest thereafter.

To apply, please send a cv and a brief motivation letter to [herwig.leirs@uantwerpen.be](mailto:herwig.leirs@uantwerpen.be) before 31 January.

“[herwig.leirs@uantwerpen.be](mailto:herwig.leirs@uantwerpen.be)”  
<[herwig.leirs@uantwerpen.be](mailto:herwig.leirs@uantwerpen.be)>

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## UBasel CichlidComparativeDevelopment

Graduate position: [UBasel.CichlidComparativeDevelopment](#)

A 4-year PhD position is available in the lab of Patrick Tschopp at the University of Basel, Switzerland, to study the ontogenetic basis and developmental plasticity of dietary adaptations in vertebrates, with a focus on African cichlid fishes. This project is part of a Sinergia grant by the Swiss National Science Foundation (SNF) to H. Kaessmann (UHeidelberg), M. Clauss (UZurich), P. Tschopp (UBasel) & W. Salzburger (UBasel).

We are looking for a highly motivated candidate with strong interests in developmental biology, single-cell functional genomics and bioinformatic analyses, as well as experimental work with fish. We offer a highly interactive, stimulating and interdisciplinary research environment, state-of-the-art research infrastructure, and a competitive salary.

The University of Basel ([www.unibas.ch](http://www.unibas.ch)) is the oldest university in Switzerland, located in one of Europe’s most important life science hubs at the border between Switzerland, France and Germany. The Tschopp lab ([www.evolution.unibas.ch/tschopp/research/](http://www.evolution.unibas.ch/tschopp/research/)) studies the gene regulatory mechanisms of cell type specification and evolution in vertebrates.

Applications should include a motivation letter, a CV, a list of publications, a statement about research interests, as well as the names and contact details of at least two referees. Applications (in the form of

a single .pdf file) should be sent to Patrick Tschopp ([patrick.tschopp@unibas.ch](mailto:patrick.tschopp@unibas.ch)); the deadline is February 7th, 2020.

[patrick.tschopp@unibas.ch](mailto:patrick.tschopp@unibas.ch)

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## UBasel CichlidDietaryAdaptations

A 4-year PhD position is available in the lab of Walter Salzburger at the University of Basel, Switzerland, to study the molecular basis of dietary adaptations in vertebrates, with a particular focus on African cichlid fishes. This project is part of a Sinergia grant by the Swiss National Science Foundation (SNF) to H. Kaessmann (UHeidelberg), M. Clauss (UZurich), P. Tschopp (UBasel) & W. Salzburger (UBasel).

We are looking for a highly motivated candidate with strong interests in organismal and evolutionary biology, genomic and bioinformatic analyses, as well as experimental work with fish. We offer a highly interactive, stimulating and interdisciplinary research environment, state-of-the-art research infrastructure, and a competitive salary.

The University of Basel ([www.unibas.ch](http://www.unibas.ch)) is the oldest university in Switzerland, located in one of Europe’s most important life science hubs at the border between Switzerland, France and Germany. The lab of Walter Salzburger ([www.salzburgerlab.org](http://www.salzburgerlab.org)) studies the dynamics of adaptation and organismal diversification in cichlids from African Lake Tanganyika and other exceptional groups of fishes.

Applications should include a motivation letter, a CV, a list of publications, a statement about research interests, as well as the names and contact details of at least two referees. Applications (in the form of a single .pdf file) should be sent to Walter Salzburger ([walter.salzburger@unibas.ch](mailto:walter.salzburger@unibas.ch)); the deadline is February 7th, 2020.

Prof. Dr. Walter Salzburger

Zoologisches Institut, Universität Basel Vesalgasse 1,  
4051 Basel, Switzerland

phone: +41 (0) 61.207.0303; fax: .0301  
eMail: [walter.salzburger@unibas.ch](mailto:walter.salzburger@unibas.ch) web:  
<http://www.salzburgerlab.org> fb: [http://-](http://www.facebook.com/waltersalzburgerlab)  
[www.facebook.com/waltersalzburgerlab](http://www.facebook.com/waltersalzburgerlab) Walter  
Salzburger <[walter.salzburger@unibas.ch](mailto:walter.salzburger@unibas.ch)>

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## UBern Switzerland PopGenomicsPlantEvolution

A PhD position is available in evolutionary biology to work in the Institute of Plant Sciences at the University of Bern, Switzerland. The position is funded for 4 years, to begin Autumn 2020. The ideal candidate will be self-motivated with a strong interest in integrating computational and empirical approaches. Experience working in R or python coding languages is highly desirable.

**BACKGROUND AND OBJECTIVES** The research projects are in population genetics/genomics, with the main scientific goal being to understand how populations successfully expand their species ranges, adapting to novel environments as well as surviving detrimental mutation load incurred during this demographic process of expansion. These questions will be addressed with an integrative approach that combines theoretical simulation studies with empirical analysis of wild-sampled *Arabis alpina*. Field sampling in Italy and the Swiss Alps is an aspect of this project, but prior experience working with plants is not required

In general, I seek a student who is strongly motivated to learn, ask questions, and think critically about topics in evolutionary biology. Prior experience in bioinformatics is a plus; top candidates will be those interested and committed to working both on the computer and in the wet lab. A Master's degree in biology or a related field is a prerequisite for this position. Any significant changes in research field should be described and explained in the applicant's motivation letter.

The Institute for Plant Sciences is a vibrant community of evolutionary biologists, ecologists, and plant physiologists, located within the beautiful Botanical Gardens of Bern, the capital city of Switzerland. The projects are funded by a Swiss National Science Foundation (SNF) Ambizione grant to Dr. Kimberly Gilbert, who will be the main supervisor, within the lab of Prof. Dr. Christian Parisod. More information on previous research can be found here: <http://kjpgilbert.github.io/> and [https://www.ips.unibe.ch/research/ecogen/index\\_eng.html](https://www.ips.unibe.ch/research/ecogen/index_eng.html). The working language is English, but knowledge of German can be useful for everyday life. Quality of life in Switzerland is high, and Bern is ideally located to both nature and several major cities.

**APPLICATION PROCEDURE AND DEADLINE** The deadline to apply is 29 February, 2020 Please submit by via email to Dr. Kimberly Gilbert at [kjpgilbert.evolution@gmail.com](mailto:kjpgilbert.evolution@gmail.com) using the subject line "PhD Application" the following items: 1) letter describing motivation for joining this project, fit, and professional goals (1 page) 2) CV/Resumé that includes publications and previous research experience 3) summary of the master's thesis (1/2 page) 4) contact information for two professional references Informal inquiries may also be directed to the same email address above. After a first round of consideration, candidates will be interviewed either in person or by video conference. A copy of the master's degree and transcript, along with evidence of writing experience may be requested at a later stage.

Kimberly Gilbert <[kimberly.gilbert@unil.ch](mailto:kimberly.gilbert@unil.ch)>

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## UBristol AntDiseaseEvolution

PhD position in collective behaviour and social immunity at the University of Bristol (UK)

A fully funded PhD position is available in the Ant Lab headed by Dr Nathalie Stroeymeyt at the School of Biological Sciences, University of Bristol, UK, to investigate the strategies used by ants to decrease epidemic risk in environments with high pathogen pressure.

**Background** Group living offers favourable conditions for the spread of infectious diseases, because high population densities and frequent social contacts facilitate pathogen transmission. To mitigate that risk, social animals have evolved a variety of defence mechanisms to prevent the entry and propagation of pathogens within the group, ranging from raised investment in personal immunity to highly coordinated collective sanitary actions conferring social immunity. Recent studies have shown that social groups can also adopt organisational features, such as the subdivision into well-separated subgroups, which reduce epidemic risk through transmission bottleneck effects. However, the importance of such organisational immunity features in disease risk management by real animal groups is still poorly understood. Research in our group adopts an empirical approach based on the experimental manipulations of garden ant colonies (*Lasius niger*) to (i) quantify the effect of social organisation on disease transmission and test key predictions from network epidemiology, and (ii) evaluate the relative of importance of personal im-



munity, collective sanitary actions and organisational features under different environmental conditions and at different stages of development (for more detail see <https://stroeymeyt-lab.ch/research>).

The project The goal of this PhD project will be to understand how ant colonies adjust different components of their disease defences (personal immunity, collective sanitary actions and transmission-inhibiting social organisation) in response to repeated disease challenges. The project will involve a combination of controlled pathogen inoculations, behavioural experiments (automated tracking of individually marked ants), molecular work (physiological assays and immune gene expression analysis), and computational analyses of tracking data (social network analyses and simulations). The project will aim to elucidate whether ants use changes in spatial and social organisation as an active strategy to decrease epidemic risk.

Desired profile We are looking for candidates with experience in quantitative behavioural analysis and programming and/or molecular biology techniques, and a willingness to apply a variety of approaches (behavioural tracking, writing own code to analyse the data, and lab work). A good working knowledge in statistics and experimental design is also desirable. Experience with social insects and insect immunity would be a plus. Candidates must be creative, motivated and passionate about science, have excellent oral and written communication skills, and be at ease working both independently and as part of a team.

The position The position will be part of an overall project team consisting of two PhD students and two post-doctoral researchers and will be fully funded for 3.5 years by an ERC Starting Grant. The candidate will receive a maintenance stipend at the minimum UKRI rate and home (UK/EU) tuition fees will be covered by the grant.

Location The School of Biological Sciences at the University of Bristol is a highly dynamic, international and interdisciplinary environment, spanning a wide range of research in Evolutionary Biology, Animal Behaviour and Sensory Ecology, Plant and Agricultural Sciences, and Ecology and Environmental Changes (<http://www.bristol.ac.uk/biology/research/>).

Expected starting date May 1st 2020 (flexible)

How to apply Please send your application by email to [nathalie.stroeymeyt@bristol.ac.uk](mailto:nathalie.stroeymeyt@bristol.ac.uk). Your application should consist of a single merged pdf file including: (i) a full CV and publication list; (ii) a 1-2 page research statement describing your past research experience, current research interests, and why you are a suitable candidate

for this project; (iii) a short proposal (0.5-1 page) on how you would address the project's goal; (iv) the names and contact details of at least two referees; (v) copies of (or links to) your publications and/or your Master's thesis (if available). Evaluation of candidates will begin on February 15th, 2020 and continue until the position is filled.

References Stroeymeyt et al. (2014). Organisational immunity in social insects. *Current Opinion in Insect Science* 5, 1.

Stroeymeyt et al. (2018). Social network plasticity decreases disease transmission in a eusocial insect. *Science* 362, 941.

Nathalie Stroeymeyt <[nathalie.stroeymeyt@bristol.ac.uk](mailto:nathalie.stroeymeyt@bristol.ac.uk)>

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## UCentralFlorida AntParasites

PhD position in Integrative and Conservation biology at the University of Central Florida (Orlando, FL, USA)

As part of our NSF CAREER project (Award Number 1941546), we have a fully funded PhD position available in the Parasitic Behavioral Manipulation Lab headed by Dr Charissa de Bekker in the Department of Biology at the University of Central Florida, to investigate the molecular mechanisms that fungal parasites use to manipulate ant behavior.

Background Information Infected animals generally behave differently from healthy animals. These changes can go beyond mere sickness behaviors to reflect precise manipulations induced by parasites to increase that parasite's chances to spread. How manipulative parasites can alter host behavior is currently unknown. The behaviorally tractable "zombie ant system" has the potential to expose the mechanisms underlying parasitic behavioral manipulation and fundamentally transform perceptions of parasite-host interactions and their behavioral ecology effects. Our lab uses these fungus-infected "zombie ants" as a model to systematically quantify disease progression and accompanying behavioral phenotypes, to determine where sickness behavior ends, where manipulation begins, and which intricate molecular mechanisms are involved.

What would you be working on? The goal of this PhD project will be to better understand 1) how ant behavior changes throughout infection; 2) how ant and fungal tissues interact throughout this progression; 3) reveal which genes and pathways from both parasite

and host give rise to behavioral phenotypes; and 4) elucidate the functions of these genes and pathways. The work that the PhD researcher will perform will span the integration of multiple technological approaches to understand how zombie-making fungi of the genus *Ophiocordyceps* interact with ants; from the molecular level to the behavioral output displayed by the whole organism. The integrative research activities of this project will prepare them for an increasingly cross-disciplinary STEM job market. Moreover, the project will leverage the public's interest in zombie-making parasites to create immersive pedagogies for teaching biology to a diverse student population. As such, the PhD investigator will also be involved in the development of a research-based, educational virtual reality experience about microbial infections and insects that we plan to take to K-12 schools, museums and fairs. For more detailed information about the project, please visit the NSF website at: [https://www.nsf.gov/awardsearch/showAward?AWD\\_ID=41546&HistoricalAwards&olse](https://www.nsf.gov/awardsearch/showAward?AWD_ID=41546&HistoricalAwards&olse)

Who are we looking for? We are looking for motivated candidates who would be eager to perform integrative research that spans multiple disciplines within the broad field of biology. To be considered for this PhD position, candidates should have a strong interest in either (or al) of the following: the molecular workings of parasite-host interactions and parasitic manipulations, ant behavior, and/or fungal biology. Having experience in live insect husbandry, quantitative behavioral analyses and programming (i.e., behavioral tracking and coding to analyze data) or molecular microbiology (e.g., CRISPR-Cas technology, cloning techniques, fungal culturing and transformation) will be considered a big plus. Already having a master's degree is also perceived as favorable, together with a good working knowledge in statistics and experimental design. It is desirable that candidates are passionate about science, creative, motivated to participate in scientific outreach and have excellent oral and written communication skills. Candidates will also need to be able to work both independently and as part of a team.

The PhD position The position will be part of an NSF CAREER project team consisting of two PhD students and several undergraduate students. Because of the collaborative nature of our lab, the candidate will also be working with a post-doctoral scholar and a PhD student who work on closely related projects. The position will be fully funded for 4 years such that the candidate will receive a maintenance stipend, tuition fees will be covered and travel to two conferences per year will be covered.

Preferred starting date August 1st, 2020 or later (flexible)

The Location The University of Central Florida is an emerging preeminent research university located in metropolitan Orlando. According to U.S. News & World Report's Best Colleges of 2019 guide, UCF ranks among the nation's 10 most innovative universities. UCF is also ranked as a best-value university by Kiplinger, as well as one of the nation's most affordable colleges by Forbes. The university confers almost 17,000 degrees each year and benefits from a diverse faculty and staff who create a welcoming environment and opportunities for all students to

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## UConnecticut MarineEvolutionaryBiol

An NSF funded PhD position is available in the Dam lab at the University of Connecticut to work on eco-evolutionary dynamics between temperature, selective feeding, and thermal adaptation in copepods. The overall goal of this project is to examine how thermal adaptation affects the ecological / trophic role of omnivorous copepods. This project will also examine the fitness effects of temperature-dependent selective feeding. By comparing effects between populations of copepods with differentiated thermal performance curves, we will examine how thermal adaptation might modify the effects of ocean warming on marine food webs.

Candidate Qualifications:— A bachelor's or M.S. degree in the natural sciences.

Starting date: August 2020

Interested candidates should contact: Hans Dam (hans.dam@uconn.edu).

Matthew Sasaki <matthew.sasaki@uconn.edu>

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## UHouston 2 ComputationalMolEvol

Two PhD positions are available in Dan Graur's Lab at the University of Houston.

The positions are available for candidates with some computational skills interested in researching topics in molecular and genome evolution by using computational methods.

Potential projects include methodological topics related to the detection of species introgression and positive selection

Previous experience with computational work, statistics, and bioinformatics will be highly regarded. Independent research is highly valued in Graur's lab.

If you are interested in joining the lab, please contact me directly at [dgraur@uh.edu](mailto:dgraur@uh.edu) with a CV and a brief description of your research interests and experience.

Additional information can be found here: <http://bchs.uh.edu/graduate/prospective-students/index.php>

If you have any questions about our Graduate Program you should contact our Graduate Ms. Rosezelia Jackson ([rejacks2@central.uh.edu](mailto:rejacks2@central.uh.edu)).

Soft deadline for applications is February 1st.

Dan Graur, Ph.D. Moores Professor of Evolutionary Biology Department of Biology & Biochemistry University of Houston

[dgraur@gmail.com](mailto:dgraur@gmail.com)

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## UKentucky Endosymbionts

Many arthropods are infected with bacterial endosymbionts that confer a variety of phenotypic effects on their hosts. We are seeking **two graduate assistants** to conduct research on symbiont interactions in a species of Linyphiid spider, *Mermessus fradeorum*. This spider is infected by up to 5 different strains of inherited symbiont, which result in different reproductive anomalies for the host depending on which combination of symbionts are present. The first graduate position will be based out of the Entomology Department

(<https://entomology.ca.uky.edu/>) under supervision of Dr. Jen White (<https://entomology.ca.uky.edu/person/-jennifer-white>) and will focus on empirically testing host reproductive phenotype and population dynamics. The second graduate position will be based out of the Biology Department (<https://bio.as.uky.edu/>) under supervision of Dr. Jeremy Van Cleve (<http://-vancleve.theoretical.bio/>), and will focus on modeling feedbacks between within-host and among-host dynamics.

## Selection Criteria ##

Required: - BS in Biology, Entomology, Mathematics or a related field - One or more years of lab experience - Strong organizational and computer skills

Preferred: - MS in Biology, Entomology, Mathematics or related field - Demonstrated communications skills - Experience with molecular techniques including (at a minimum) DNA extraction, PCR, and gel electrophoresis - Previous experience working with spiders or bacterial endosymbionts

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Previous experience/training in mathematical modeling or scientific computing

## Location ##

The University of Kentucky is located in Lexington, Kentucky, a mid-sized city of ~300,000 people, within a 1.5 hr drive from both Cincinnati, OH and Louisville, KY. Visit the [University of Kentucky Website](<http://www.uky.edu>) for more information about UK. We are less than an hour from great hiking, camping, and climbing in the [Red River Gorge]([https://en.wikipedia.org/wiki/Red\\_River\\_Gorge](https://en.wikipedia.org/wiki/Red_River_Gorge)) and [Daniel Boone Nat. Forest]([https://en.wikipedia.org/wiki/Daniel\\_Boone\\_National\\_Forest](https://en.wikipedia.org/wiki/Daniel_Boone_National_Forest)).

## Selection Process ##

For more information, please send an email to Dr. Jen White at ([jenwhite.uk@gmail.com](mailto:jenwhite.uk@gmail.com)), indicating which position(s) are of interest to you. For serious inquiries, please include a copy of your CV or resume, unofficial college transcripts, and contact information for at least three references. We will conduct phone or Skype interviews with short-list applicants before encouraging top candidates to submit an application to the University of Kentucky graduate school (<https://gradschool.uky.edu/>)

\*The University of Kentucky is an equal opportunity institution and encourages applications from minorities and women.\*

Jeremy Van Cleve

Assistant Professor Department of Biology University of Kentucky E-mail: [jvanclave@uky.edu](mailto:jvanclave@uky.edu) Webpage: <http://vanclave.theoretical.bio> Phone: (859) 218-3020

[jvanclave@uky.edu](mailto:jvanclave@uky.edu)

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## UKonstanz PaleoEnvironmentalDNA

PhD position on past anthropogenic impacts using sedimentary ancient DNA -

Analyses of past climate and anthropogenic impact on Lake Constance biota using sedimentary ancient DNA

Topic/Questions: The project will investigate sediment core DNA from Lake Constance, reaching back multiple millennia. Lake Constance has a rich archaeological and historical record of human occupation reaching back through times of variable climate. During the 20th century it furthermore experienced a documented period of anthropogenic eutrophication and subsequent re-oligotrophication. The lake therefore lends itself as a great model to study the relative effects of human impact and climatic changes on lake ecosystems throughout the last millennia. We will address the following questions: 1) How stable was the lacustrine ecosystem in preceding centuries compared to the 20th century, and have patterns of response, resilience and reversibility changed in the “Anthropocene”? 2) Were earlier periods of change in lacustrine community composition related to changes in terrestrial ecosystems and human presence? 3) Were these changes driven by human land use or by climate? The PhD will be conducted within the Research Training Group R3 - Resilience of Lake Ecosystems. Within the Research Training Group R3, a diverse group of doctoral researchers is investigating the response of community structure, biological interactions and carbon and nutrient flows to changing conditions in Lake Constance. This is a great and collaborative environment to conduct a PhD! More information can be found at <https://www.rtg-resilience.uni-konstanz.de>

Work: The doctoral researcher will analyze DNA extracted from dated sediment cores of Lake Constance and retrieve detailed information on a variety of aquatic and terrestrial organisms, with a focus on indicators of human impact (cultivated plants, livestock, aquatic indicators of eutrophication). The work will comprise DNA extraction, metabarcoding techniques as well as non-PCR based approaches to obtain NGS sequencing data. Biotic records will be compared to archaeological

and historical records, as well as existing paleoclimate records of the area.

PIs: Laura Epp, Mark van Kleunen & David Schleheck

Requirements: Master in a relevant subject (Biology, Ecology, .), a keen interest in the research questions addressed as well as interest in interdisciplinary, collaborative science. An ideal candidate would have experience with next generation sequencing data acquisition and analysis, and/or statistical data analyses, and/or paleoecological work. Experience with environmental DNA and/or ancient DNA are an asset, but not a prerequisite to apply.

All applications and supporting materials (motivation letter including research interests and motivation to become part of the RTG R3, curriculum vitae including degree certificates, abstract of master thesis, two letters of recommendation) have to be submitted in English as one pdf via the Online Application Portal including reference number 2019/263. Questions can be directed to Prof. Dr. Laura Epp via E-Mail: [laura.epp@uni-konstanz.de](mailto:laura.epp@uni-konstanz.de), or to Dr. Tina Romer via E-Mail: [applicationRTGR3@uni-konstanz.de](mailto:applicationRTGR3@uni-konstanz.de) or by phone: (+ 49 (0)7531 / 88 - 3124).

We welcome applications until February 29 2020.

Prof. Dr. Laura Epp Junior Professor for Environmental Genomics in Aquatic Systems Limnological Institute University of Konstanz Mainaustraße 252 78464 Konstanz / Egg Germany [https://www.researchgate.net/profile/Laura\\_Epp](https://www.researchgate.net/profile/Laura_Epp) <https://www.limnologie.uni-konstanz.de/umweltgenomik/>  
Laura Epp <[laura.saskia.epp@gmail.com](mailto:laura.saskia.epp@gmail.com)>

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## UMaine AnimalBehaviorConservation

PhD Position in Animal Behavior and Conservation, University of Maine

An NSF funded PhD position is available to work in Alessio Mortelliti's lab ([alessiomortelliti.weebly.com](http://alessiomortelliti.weebly.com)) focusing on how individual variation in behavior (personality) impacts population, community, and ecosystem dynamics. The PhD student will design and implement a series of field experiments focusing on the ecological consequences of personality, using small mammals and seed dispersal as a model systems. The study will be conducted in the context of an ongoing large scale field experiment focused on land-use change and will include

a citizen science component. The ideal candidate would have a strong passion for field work as well as strong quantitative and writing skills. Previous experience working with small mammals is not mandatory. The position is at the University of Maine flagship institution in Orono, with an active and diverse wildlife graduate department. The position includes a stipend (through RA and TA, for up to 5 years), full tuition waiver and 50% of the health insurance. Expected start of the position: June 2020. More information available here:

<https://alessiomortelliti.weebly.com/prospective-students.html> Informal inquiries are welcome. Applicants with an MS degree are strongly preferred. To apply please send (as one unique PDF file): 1) A cover letter addressing why you want this position and what skills you would bring to the project, 2) curriculum vitae, 3) unofficial transcripts (undergraduate and MS), 4) GRE scores (if available) to: Dr. Alessio Mortelliti (alessio.mortelliti@maine.edu) Application review will begin on January 27, 2020 and continue until the position is filled.

Dr. Alessio Mortelliti Assistant Professor of Wildlife Habitat Conservation Department of Wildlife, Fisheries, and Conservation Biology University of Maine 5755 Nutting Hall, Room 228 Orono, ME 04469 Office: 207-581-2915

<http://alessiomortelliti.weebly.com> Alessio Mortelliti <alessio.mortelliti@maine.edu>

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## UMaine MooseDiseaseEcoEvolution

Title: PhD Assistantship: One Health Moose disease ecology and evolution

Location: University of Maine, Orono

Description: A PhD position is available in the Kamath and De Urioste-Stone Labs at the University of Maine, through a new interdisciplinary NSF Research Traineeship (NRT) program in One Health, starting in the Fall 2020 semester. The student will examine the drivers and impacts of parasite infections in Maine moose (*Alces alces*). Integrating biological, social, and environmental data, the student will identify risk factors for parasite infections in moose, use genomic approaches to examine the genetic basis for infection phenotypes, and use social science tools to evaluate perceptions of risk, disease management strategies and communication tools. This study will provide key information to evaluate poten-

tial management approaches that will be supported by diverse stakeholders in order to ensure the long-term viability of moose in Maine.

The student will be co-advised by Drs. Pauline Kamath (<https://kamathlab.weebly.com/>) and Sandra De Urioste-Stone (<https://forest.umaine.edu/faculty-staff/sandra-de-urioste-stone/>), through the Ecology and Environmental Sciences program (<https://umaine.edu/ecologyandenvironmentalsciences/>). The student will also participate in an NSF-NRT One Health program that involves training in the integration of ecological, molecular, and social science approaches, professional development, and a management/policy internship. Traineeships include an annual stipend, free tuition and fees, and subsidized health insurance.

Qualifications: Competitive applicants will have a MS degree; previous research experience in ecology, evolution, or related field; experience in genomics and bioinformatics; a strong background in statistical modeling; and a demonstrated ability to work in diverse teams. U.S. citizenship or permanent residency is required to receive NRT funding.

To apply: Please send (1) a cover letter describing your qualifications, including relevant research experience, coursework, experience working in interdisciplinary teams, as well as a description of how your interests relate to One Health; (2) a CV; (3) GRE scores; (4) unofficial transcripts; and (5) contact information for three references. Combine materials into one (PDF) application file, and email it with the subject line, "One Health NRT PhD Position," to Pauline Kamath at pauline.kamath@maine.edu. All applications received before February 15, 2020 will receive full consideration, but will be accepted on a rolling basis until the position is filled.

UMaine One Health NRT Program: A new One-Health and Environment (<https://nsfa.umaine.edu/one-health/>) initiative at the University of Maine was awarded \$3 million from the National Science Foundation. The five-year project will train 71 graduate students, including 21 funded trainees, from a variety of STEM fields. It complements an NSF-funded program which recruits undergrads for a 10-week summer research experience in One Health. The project encourages interdisciplinary research in a range of systems, provides management and policy internships to encourage solutions-oriented practice and training to empower students to communicate with diverse audiences. We encourage women, first-generation students, veterans, students with disabilities and other under-represented groups to apply.

– Pauline L. Kamath, Ph.D. Assistant Professor of

Animal Health Animal and Veterinary Sciences School of Food & Agriculture 5735 Hitchner Hall, Rm 342 University of Maine Orono, ME 04469-5735 Phone: +1 207-581-2935 Email: pauline.kamath@maine.edu Website: <https://umaine.edu/foodandagriculture/-kamath2/> “pauline.kamath@maine.edu” <pauline.kamath@maine.edu>

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## UMainz 2 GenomicsOfCoevolution

2 PhD positions in Genomics of Coevolution

between a slavemaking ant and its host Susanne Foitzik and Barbara Feldmeyer

IomE JGU Mainz and Senckenberg Bik-F Senckenberg Frankfurt

We invite you to apply for one of two open 3-year PhD positions (65% TV-L E13) on a project investigating the genomic basis of coevolution between the slavemaking ant *Temnothorax americanus*, an obligate social parasite, and its related host *T. longispinosus*, two species that coevolve in an evolutionary arms race and for which we recently obtained the genomes. We will use populations of a “natural experiment”, in which host and parasite evolve in sympatry (=coevolve) or allopatry. The aim of this study is to identify genomic signatures of this coevolutionary arms race and to functionally validate candidate genes playing a role in the reciprocal host-parasite co-adaptation. For these goals, we will use a suit of different techniques such as behavioral assays, cuticular hydrocarbon profiling (GCMS), transcriptome analyses (RNA-seq), population genomics (Pool-seq, individual genome resequencing) and gene knockdown (dsRNAi).

We are looking for two highly motivated candidates with an MSc degree (or equivalent) in Biology, Bioinformatics or related fields. The successful applicant should have a strong background in evolutionary biology, population genetics, behavioral ecology and / or bioinformatics. Experience with social insects are advantageous, but not a must. The working language of our laboratories is English. The University of Mainz / the Senckenberg Bik-F Institute aim to increase the number of women in science, and applications by women are strongly encouraged. Similarly, qualified candidates with disabilities will be preferred.

Successful applicants will join an international and dynamic scientific environment. Associa-

tions with the GenEvo Graduate School might be possible <https://www.imb.de/about-imb/joint-research-initiatives/genevo>. Both PhD students will start at the JGU Mainz with one of the two students conducting the population genomics project parts in Frankfurt after 1 year (both labs are only 30 min apart by car). Mainz and Frankfurt are beautiful, lively cities located at the Rivers Rhine and Main with high students numbers and rich social and cultural life. The positions are funded by the German Research Foundation (DFG) for a period of 3 years. Salary is at the scale 13 TV-L (65%). Starting date should be April 1st 2020 or soon thereafter. If you wish to apply, please send your application as a single pdf file containing your CV, a 1- page motivation letter, your research experience and interest, BSc and MSc grades, publications (if any), and the names of two potential references. Applications should be sent to Prof. Dr. Susanne Foitzik (foitzik@uni-mainz.de) or Dr. Barbara Feldmeyer (barbara.feldmeyer@senckenberg.de) until February 4th, 2020. Skype interviews with selected candidates will likely take place on February 6th and onsite interviews on February 13th 2020. Do not hesitate to contact us if you have further questions.

Prof. Dr. Susanne Foitzik Dr. Barbara Feldmeyer Institute of Organismic and Molecular Evolution Molecular Ecology Group Johannes Gutenberg University of Mainz Biodiversity and Climate Research Centre (BiK-F) Hanns-Dieter-Hüsch-Weg 15 Georg-Voigt-Str. 14-16 55128 Mainz, Germany 60325 Frankfurt am Main, Germany foitzik@uni-mainz.de barbara.feldmeyer@senckenberg.de

Prof. Dr. Susanne Foitzik Institute of Organismic and Molecular Evolution Johannes Gutenberg University Mainz Biozentrum Hanns Dieter Hüsch Weg 15 D-55128 Mainz Germany Tel: 49 (0) 6131 39 27840 Fax: 49 (0)6131 39 27 850 Email: foitzik@uni-mainz.de

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

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## UNeuchatel EvolutionaryBotany

A four-year PhD position combining ecology and evolutionary botany is available in the Laboratory of evolutionary genetics, Institute of Biology, University of Neuchâtel, Switzerland. The thesis is financed by the Swiss National Science Foundation (SNF) within the framework of a Sinergia project. It is directed by Prof. Jason Grant (UniNe) and co-supervised by Dr. Pierre-Emmanuel Du Pasquier (UniNe) and Dr. Beryl Laitung

(Université de Bourgogne, UMR Agroécologie, Dijon, France).

**BACKGROUND AND OBJECTIVES** Anthropogenic pressure may lead to the rapid and sometimes irreversible decline of botanical diversity, or on the contrary, favors the expansion of certain non-native species. In Europe, since the mid-20th century, the intensification and modernization of agricultural practices (mechanization with deep ploughing, use of herbicides, seed sorting, densification of monocultures and systematic use of certified seeds) has had an unprecedented impact on archaeophyte messicole species (crop-related species that were introduced mainly from the Middle East before the year 1500). As messicole species are generally therophytes (annual plants that spend the difficult season in the form of seeds), modernization quickly destroys seed stocks in the soil and contributes to the decline of these populations that were common until the mid-20th century. Although messicolous species are part of the floristic richness of the different countries where they are now native, they seem to have been introduced in the past by man in the form of seed since the domestication of crops from the Neolithic period (11000 to 9000 years ago). Some species introduced secondarily and recently into new regions may be locally abundant and may pass from archaeophyte to neophyte status: this is the case, for example, of the cornflower (*Centaurea cyanus* or *Cyanus segetum*), introduced into North America from Europe. The main goal of this PhD is to study the population dynamics of different archaeophyte messicole taxa with varied population dynamics using functional ecology (life history trait analysis) and evolutionary botany (genetic analysis of evolutionary history) approaches. From herbarium collections, we plan to recreate populations from the 18th century to the present from which genetic analysis and mapping will be carried out. Experiments will be done in the field (experimental station in Dijon) in order to analyze current populations. Fieldwork is necessary to sample populations and establish the current status and future of the taxa.

**REQUIREMENTS** The successful candidate holds a master's degree in ecology, evolutionary biology or an equivalent field with an excellent academic record. A strong interest in ecology, evolutionary genetics and a good knowledge of botany is desirable. Periods of work in experimental fields, in the laboratory, in herbaria and in the field are an integral part of this thesis.

**APPLICATION PROCEDURE AND DEADLINE** The candidate should send a single PDF file by e-mail containing 1) a letter of motivation describing research interests, willingness to do a PhD, and suitability for this subject, 2) a curriculum vitae, 3) a copy of master's degree and transcript, 4) a summary of the master's the-

sis, and 5) the names and contacts of two referees. The application file should be sent to both Prof. Jason Grant ([jason.grant@unine.ch](mailto:jason.grant@unine.ch)) and Dr. Pierre-Emmanuel Du Pasquier ([pierre-emmanuel.dupasquier@unine.ch](mailto:pierre-emmanuel.dupasquier@unine.ch)). The deadline is Monday, January 20, 2020.

GRANT Jason <[jason.grant@unine.ch](mailto:jason.grant@unine.ch)>

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## UNewOrleans HawaiianDrosophila

Graduate positions (M.Sc. and Ph.D.) are available in the Atallah Lab (<https://sites.google.com/view/-atallahlab>) in the Biological Sciences Department at the University of New Orleans (UNO). We are currently looking for students interested in working on the genomics, transcriptomics and genetic modification of Hawaiian *Drosophila* species. Students with a molecular background who are excited about the potential of CRISPR-Cas9, and students interested in the collection and husbandry of non-model *Drosophila* species, are particularly encouraged to apply.

Applicants should send an email to [jatallah@uno.edu](mailto:jatallah@uno.edu). Please include a brief description of your background (or a CV or resume), mentioning why you're excited about this project.

The University of New Orleans is a public research university and part of the University of Louisiana system. New Orleans is a diverse and historic city with a vibrant culture.

Joel Atallah, Ph.D. Assistant professor 202 Biology Building Department of Biological Sciences University of New Orleans New Orleans, LA 70148 (504) 280-7057 <https://sites.google.com/view/atallahlab> Joel Atallah <[jatallah@uno.edu](mailto:jatallah@uno.edu)>

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## UNorthDakota WildlifeGenomicsPaleoecology

U. North Dakota. WildlifeGenomicsPaleoecology.

The Laboratory of Evolutionary and Forensic Genetics at the University of North Dakota ([www.und.edu](http://www.und.edu)) is inviting applications from highly motivated students who pursue a PhD degree. MS candidates will be also

considered.

Students will be engaged in a project on the historic, current and future status of bison herds from biological, archaeological, and cultural perspectives. This cross-disciplinary project represents an opportunity to get intensive training in the methods of ancient and modern DNA analyses including high-throughput genome sequencing, stable isotope studies, computational analysis and statistical modelling. The examples of our recent publications: Ovchinnikov et al. Diversity and Origin of the Feral Horses in Theodore Roosevelt National Park. PLoS One, 2018, 13(8); Davies et al. Isotopic Paleoecology of Northern Great Plains Bison during the Holocene. Scientific Reports, 2019, 9(1): 16637. Although the wildlife project is focused on bison genetics and paleoecology, we have opportunities to develop new projects on computational analysis of big oral and environmental microbiome data as well as on genomics and microbiome study of human migrations and evolution.

Candidates should demonstrate motivation for hard laboratory work and strong interest in genomics and computational biology. Preference will be given to candidates with a proven record of computational analysis and bioinformatics skills. Additional experience in sequencing technologies is a plus.

If you are interested, you need to apply to the University of North Dakota Biology Graduate Program using the regular procedure. Requirements and How to Apply procedure can be found in the UND Biology Graduate School websites:

<https://und.edu/programs/biology-phd/requirements.html> <https://und.edu/programs/biology-phd/how-to-apply.html> The additional information can be also found in the Biology Department website:

<https://arts-sciences.und.edu/academics/biology/> The position starts in August 2020. To receive full consideration, the Biology Graduate Program needs to receive your applications and required materials by February 15, 2020.

Potential graduate students are also encouraged to make contact with Dr. Igor Ovchinnikov.

Contact information:

Dr. Igor Ovchinnikov Associate Professor Lab. of Evolutionary and Forensic Genetics Department of Biology Forensic Science Program University of North Dakota

Email: [igor.ovtchinnikov@und.edu](mailto:igor.ovtchinnikov@und.edu)

“Ovtchinnikov, Igor” [<igor.ovtchinnikov@und.edu>](mailto:igor.ovtchinnikov@und.edu)

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## uOttawa 4 QuantGenWildPop

1 PhD and 3 Msc positions on quantitative genetic and reproductive strategies in natural systems at uOttawa

Multiple graduate student positions (Msc and PhD) available in Julien Martin lab's at the University of Ottawa (<https://juliengamartin.github.io> < <https://juliengamartin.github.io/> >). Enthusiastic graduate students will carry out research on reproductive strategies and life-history trade-offs using a quantitative genetic approach based on several long-term studies including the yellow-bellied marmots project in Colorado (>55 years of data) and the alpine swifts project in Switzerland (>25 years of data). For more details about the projects go to <https://juliengamartin.github.io/opportunities/>. Financial support is available for 4 and 2 years for PhD and Msc respectively.

The ideal candidate should have: - BSc or Msc. in biology. - A strong interest for statistical analyses and R programming. - The ability to work alone and in teams. - The motivation for long field seasons.

Students that are interested should send a writing sample (thesis, paper or scientific article), a CV, a motivation letter, and the contact of two references to Dr. Martin ([julien.martin@uottawa.ca](mailto:julien.martin@uottawa.ca) <<mailto:julien.martin@uottawa.ca>>). We will continue to consider applications until the position is filled.

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Plusieurs positions aux études graduées sont disponible dans le laboratoire de Julien Martin à l'université d'Ottawa (<https://juliengamartin.github.io> < <https://juliengamartin.github.io/> >). Les projets seront orientés sur l'étude des stratégies de reproduction et des compromis biodémographiques en utilisant une approche de génétique quantitative basée sur des systèmes d'études à long-terme incluant les marmottes à ventre jaune au Colorado (>55 années de données) et les martinets alpins (>25 années). Pour plus de détails sur ces opportunités, visitez le site <https://juliengamartin.github.io/opportunities/>. Idéal posséder: - B.Sc. en Biologie - Un fort intérêt pour l'analyse statistique de données avec le logiciel R - La capacité de travailler de manière autonome et en équipe - La volonté de travailler en français et en anglais

Les personnes intéressées par ce projet devraient envoyer un exemple d'écriture scientifique (travail de



session, mémoire, ou article scientifique), leur CV, une lettre de motivation, et les coordonnées de deux personnes références par courriel au Pr. Martin (julien.martin@uottawa.ca). Nous continuerons à considérer les dossiers jusqu'à ce que le poste soit comblé.

Julien Martin <Julien.Martin@uottawa.ca>

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## UOulu StatisticalGenomics

[https://rekry.saima.fi/certiahome/-open\\_job\\_view.html?did=5600&jc=1&id=-00008534&lang=en](https://rekry.saima.fi/certiahome/-open_job_view.html?did=5600&jc=1&id=-00008534&lang=en) Doctoral student in Statistical Genomics, Mathematical Sciences

The University of Oulu (<http://www.oulu.fi/english/>) is one of the largest universities in Finland, with approximately 15 000 students and 3 000 employees. The University of Oulu Graduate School (UniOGS) (<http://www.oulu.fi/uniogs/>) provides the framework and conditions for high-quality, research-driven doctoral education at the University of Oulu, and field-specific doctoral training is provided by its multidisciplinary doctoral programmes.

Doctoral student (PhD student) position in Statistical Genomics, 4-year position 2020-2023 in Faculty of Science, Research Unit for Mathematical Sciences, University of Oulu.

Applications are invited for a full-time doctoral student position for a maximum of four years, starting at the earliest on 1.3.2020 in an Academy of Finland research project "Forest Tree Evolution Via Regulation". The principal investigators of the project are Dr. Tanja Pyhäjärvi (Research Unit of Ecology and Genetics, Faculty of Science), Professor Katri Kärkkäinen (LUKE), Dr. Jarkko Salojärvi (University of Helsinki) and Professor Mikko Sillanpää (Research Unit for Mathematical Sciences, Faculty of Science).

The project concentrates on studying the role of regulatory genomic regions in the evolution and environmental adaptation of forest trees. Statistical, genomic, population genetic and molecular methods will be applied. The PhD position focuses on statistical method development for time-series analysis of gene expression and other dynamic data, genome wide association studies and understanding polygenic adaptation. The thesis will be supervised by Prof. Mikko Sillanpää and Tanja Pyhäjärvi

See: <http://cc.oulu.fi/~misillan/oulu.fi/pyhajarvilab>

Requirements for a doctoral student

To successfully occupy the position of a doctoral student, the candidate must possess a Master's degree or an equivalent degree (e.g. licentiate) preferably in statistics and data science or genetics. Degree must have been completed with good grades by 30.1.2020 (or latest before the job contract starts). Motivation to pursue independent research and English writing and communication skills are expected. The doctoral student position is intended for an Early Stage Researcher (ESR) who, according to the "European Charter for Researchers and the Code of Conduct for the Recruitment of Researchers", is defined as a researcher in the first four years (full-time equivalent) of his/her research activity, including the period of research training. Applicants will be either starting their doctoral training, or will have completed no more than two full years of training (adjusted for possible previous part-time status) at the time the position is filled. The selected candidate will carry out his/her doctoral studies in the University of Oulu Graduate School (UniOGS) and must meet the minimal requirements to receive doctoral study rights as defined in [http://www.oulu.fi/uniogs/-requirements\\_for\\_admission](http://www.oulu.fi/uniogs/-requirements_for_admission) . Salary

The salary of the selected doctoral student will be set on levels 2 - 4 of the national salary scale for the teaching and research staff of Finnish universities. In addition, a supplementary remuneration will be given for personal achievement and performance (max. 50%). The total salary for these levels (before tax) currently ranges from about 1985 to 3621 Euros/month for full-time employment.

### Application

Applications must be submitted using the electronic application form by February 14, 2020, 24:00 (Finnish local time), with the following attachments as three separate pdf files:

- Complete CV containing contact information of at least two referees (Max. size limit of the attachment: 5 Mbytes)
- Motivation letter (maximum 1 page) describing prior knowledge and research interests and career plans (1-2 pages; max. size limit of the attachment: 2 Mbytes).
- Certificates/Diplomas: Scanned electronic copies of diplomas and transcripts of the records of relevant previous degrees. If the original documents are not in English, Finnish or Swedish, each document must be accompanied by an official certified translation into English or Finnish. (Max. size limit of the attachment: 5 Mbytes)

[https://rekry.saima.fi/certiahome/-open\\_job\\_view.html?did=5600&jc=1&id=-](https://rekry.saima.fi/certiahome/-open_job_view.html?did=5600&jc=1&id=-)

00008534&lang=en Other relevant information

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## UOxford HumanAnthropology

DPhil position in bio-anthropology to investigate the genetic history of human populations, under the supervision of Laura Fortunato (School of Anthropology) and Cristian Capelli (Department of Zoology), to begin in Autumn 2020 at the University of Oxford.

The project will focus on modern-day human populations from Italy, to investigate the impact of cultural dynamics in shaping the genetic variation of human groups. The work will include the collection and processing of samples, genotyping and data analysis.

Criteria:

- a) the project requires extensive interaction with local communities in Italy, so a good knowledge of written and spoken Italian is highly desirable
- b) some background in genetics and/or bio-anthropology
- c) some experience in programming in R and/or Python
- d) confidence with statistical analyses in R
- e) previous experience in DNA collection, extraction and genotyping (Y chromosome and mtDNA in particular) would be advantageous
- f) excellent communication and writing skills
- g) the ability to work as part of an interdisciplinary team, and independently when needed
- h) a solid record of excellent academic achievements

Applications are due on \*24 January 2020\*. A scholarship is available to support this project. The scholarship is open to applicants of any nationality, but who have been ordinarily resident in the UK for at least five years before the start of the course. Further details on eligibility and on the application procedure are available at:

<http://www.ox.ac.uk/admissions/graduate/courses/-dphil-anthropology> <https://www.ox.ac.uk/admissions/-graduate/fees-and-funding/fees-funding-and-scholarship-search/standard-scholarship-selection-terms>

Potential applicants who meet the eligibility criteria are invited to send their CV to Laura Fortunato (School of Anthropology, [www.santafe.edu/~fortunato/-contact/](http://www.santafe.edu/~fortunato/-contact/)) and Cristian Capelli (Department of Zoology, <https://www.zoo.ox.ac.uk/people/dr-cristian-capelli>) ahead of the deadline for consideration.

Cristian Capelli <cristian.capelli@zoo.ox.ac.uk>

## UppsalaU EvolutionaryGenomics SexDetermination

PhD position in Evolutionary Genomics, Uppsala University.

A PhD position is available in the research group of Sophie Karrenberg at the Evolutionary Biology Centre in Uppsala, Sweden. We investigate the ecological genomics of speciation and adaptation in plants.

The environment. The Evolutionary Biology Centre (<http://www.ebc.uu.se/>) is one of the world's leading research institutions in evolutionary biology. It is part of Uppsala University considered one of Europe's leading universities in the subject of biology with a broad variety of disciplines. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. Our lab is part of the Department of Ecology and Genetics and of the program in Plant Ecology and Evolution (<http://www.ieg.uu.se/>), an active environment addressing fundamental evolutionary and ecological questions with a wide range of different approaches. We are situated in the student town of Uppsala that offers rich opportunities in cultural and outdoor activities. Sweden's capital, Stockholm, is less than an hour's train ride away.

Project description: The evolution of separate sexes is of fundamental importance in biology. Sex-determining mechanisms are highly variable and labile and sex chromosomes often degenerate; however, the underlying evolutionary mechanisms are unclear. Theoretical studies predict that sex chromosome evolution is driven by sex ratio selection and/or by different forms of genetic conflict, for example, between males and females or between cytoplasm and nucleus. Empirical evidence for these predictions is scarce, in part because the best-studied systems are animals with ancient and degenerate sex chromosomes. The overarching aim of this project is to contribute to the understanding of sex determination and sex chromosome evolution by closing this gap be-

tween theory and empirical studies. In this project, we use a plant genus, *Salix*, with a high turnover of nascent sex chromosomes. Strong sex ratio bias in crosses and in natural populations and in crosses is common in *Salix* suggesting that sexual antagonism or some other form of genetic conflict operates in this system. The project has three main aims: (1) to identify the mechanisms determining sex and sex ratio bias in *Salix herbacea*, (2) to analyze the extent of degeneration and signs of selection in sex-associated region(s) and (3) to study possible turnover events of genomic regions associated with sex and/or sex ratio. We will combine whole-genome assembly and individual re-sequencing with allele transmission analysis of at loci with sex-associated polymorphisms in controlled crosses and with population genomic analyses and theoretical modeling. This comprehensive approach will allow us to gain novel insights into sex chromosome evolution and evolutionary processes at large.

The project will be conducted under the supervision of Sophie Karrenberg, Uppsala University (main supervisor) and Pär Ingvarsson (SLU Uppsala, second supervisor).

Application. You are welcome to apply until February 17, 2020, with the reference number UFV-PA 2020/120. For further information on requirements, application instructions and a link for submission of your application go to:

<https://www.uu.se/en/about-uu/join-us/details/?positionId=311040> For more information, please contact: prof. Sophie Karrenberg (sophie.karrenberg@ebc.uu.se)

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> Sophie Karrenberg <sophie.karrenberg@ebc.uu.se>

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## UppsalaU PrimateSpeciationPopGen

A PhD student position in Primate Speciation and Population Genomics is available in the group of Katerina Guschanski at the Department of Ecology and Genetics, Uppsala University, Sweden. For more information about the department see [www.ieg.uu.se](http://www.ieg.uu.se). Project description: Our group is broadly interested in understanding how long-term evolutionary and short-term human-mediated processes shape biological diversity. The advertised project has the goal to study primate evolution from multiple angles and on different evolutionary time scales. You will have the chance to study population and species level processes in a number of primate taxa using newly generated and publically available genomic data. Research topics include, but are not limited to:

- i) Speciation genomics and the role of ancient hybridization in driving species diversity. You will focus on a group of highly diverse African monkeys (guenons) that are renown for their ecological, morphological and karyotypic diversity and readily hybridize in captivity and the wild. Although the main focus will be on speciation genomics, there are possibilities to extend this project to include cytogenomics, morphological and ecological analyses, depending on the candidate's interests.
- ii) Population and conservation genomics. Using target DNA capture from fecal samples you will study genetic diversity, population structure, demography and local adaptation in wild primate populations. The generated insights will have direct relevance for conservation decision-making.

The exact project will be developed with the successful candidate and tailored towards their interests and skills.

Duties: The selected candidate will mainly engage in large-scale phylogenomic and population genomic analyses that require solid bioinformatics skills, but will also conduct work in the wet lab to produce genomic sequencing data from non-invasively collected low-quality samples. Duties include active participation in the research group activities, training of junior group members in relevant techniques and engagement in collaborative projects.

Qualifications required: To be eligible for a PhD-student position the applicant must hold a master degree (or

equivalent) in evolutionary biology, bioinformatics, or a related field. The technical skills of the candidates will be evaluated based on the experience with large-scale sequence analysis, bioinformatics proficiency and experience with phylogenomic and population genomic studies. The ideal candidate will have a strong interest and documented knowledge in evolutionary biology, with a drive to understand processes shaping species diversity. Perseverance and high intrinsic motivation are required to work on non-model organisms using difficult samples and data. You will be highly reliable, driven and well-organized, curious and willing to think outside the box, with the ability to quickly acquire new skills. Proficiency in spoken and written English is required.

Qualifications desired: Previous experience with wet lab molecular techniques, ideally with low-quality samples, is highly desired.

Starting date: As early as possible, ideally by 2020-04-01 or as otherwise agreed.

Position: The graduate program covers four years of full-time study. The position can be combined with teaching or other duties at the department (maximum 20%), which prolongs the employment with the corresponding time.

How to apply: The application should include 1) a cover letter describing your research interests, your proficiency with molecular laboratory techniques and programming, experience in handling genomic data, other technical skills relevant for the project, as well as other qualifications that make you a suitable candidate, 2) your CV, including any produced publications, 3) a copy of your master degree, your course grades and a copy of your master thesis, if available, 4) the names and contact information of 2-3 reference persons (e-mail address and phone no; you are welcome to include this information at the end of your cover letter or as attachment under point 6 of the online application form). As the application form requires you to upload Description of your education under point 2, you are welcome to upload your CV here, as long as it provides the relevant information. You are also not required to fill out other tabs, as long as your CV covers the relevant points. The application should be written in English.

To apply, please follow this link (UFV-PA 2020/247): <https://uu.varbi.com/center/tool/position/312817/> <https://www.uu.se/en/about-uu/join-us/details/?positionId=312817> You are welcome to submit your application no later than 2020-02-24.

For further information about the position please contact:

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## USussex FlowerEvolution reminder

\* PhD position available to study plant plasticity and local adaptation to new pollinators after range expansion at the University of Sussex, UK \* (reminder)

Supervisor: Maria Clara Castellanos (<http://www.sussex.ac.uk/lifesci/plant-evolutionary-ecology-lab>)

I am looking for an enthusiastic student interested in plant-pollinator interactions and evolutionary biology. The PhD project will focus on how plants can rapidly adapt to new pollinator environments. Our work with a developing study system in recently colonised environments (*Digitalis purpurea*, the common foxglove) shows that floral morphology can change in a few generations under new pollinators (including different bees and hummingbirds in tropical mountains) but we still know relatively little about how this occurs. The project will use this exciting model system to examine how adaptation to new pollination environments takes place, and in particular, the potential role of phenotypic plasticity in the process. We will use a combination of approaches that include: 1) experimentally testing for local adaptation using translocation experiments in the field, 2) measuring plastic variation in floral traits in the greenhouse using quantitative genetics, 3) measuring pollinator-mediated selection on floral traits, including male components of fitness using novel techniques to track pollen grains. There will be scope for developing further new ideas within this system.

This 3.5-years fully funded studentship is open to UK and EU citizens. The project will have a significant field component in the UK and abroad (e.g. South and Central America), so it is essential that applicants are committed and available to spend time in the field. For fieldwork in the UK and abroad, a driving licence and driving experience are essential. Experience with plant growing and some knowledge of Spanish are a plus.

For further details on the project and the application process, please visit <https://www.sussex.ac.uk/study-fees-funding/phd-funding/view/1133-PhD-Studentship-for-School-of-Life-Sciences>. The student will be part of the vibrant Evolution, Behaviour and Environment

subject group within the University of Sussex (<http://www.sussex.ac.uk/lifesci/ebe/>). Our campus is located within a national park, 10 minutes from the lively seashore city of Brighton.

The closing date for applications is January 31st 2020. Applications should be submitted through Sussex University's graduate application system: <http://www.sussex.ac.uk/study/phd/apply>. Please include a CV, statement of interest and the names and email addresses of two academic referees. On the application system use Programme of Study - PhD Biology. For enquiries about the application process contact Emma Chorley (mailto:lifesciphd@sussex.ac.uk). The expected starting date is May 2020.

Feel free to email me for informal inquiries: Maria Clara Castellanos - [m.c.castellanos@sussex.ac.uk](mailto:m.c.castellanos@sussex.ac.uk)

"[m.c.castellanos@sussex.ac.uk](mailto:m.c.castellanos@sussex.ac.uk)"  
<[m.c.castellanos@sussex.ac.uk](mailto:m.c.castellanos@sussex.ac.uk)>

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## UTartu PhylogeneticComparativeInsects

PhD position: comparative phylogenetic studies on insect body size

We are looking for a PhD student to perform part of a larger, lab wide project entitled: "Comparative studies on insects: a focus on body size" financed by Estonian Research Council (2020-2024) and carried out at Estonia's leading research centre: the University of Tartu (<https://www.ut.ee/en>). The lab wide project focuses on reconstructing moth phylogenies on the basis of DNA sequences and performing various analyses of trait evolution on the basis of these novel phylogenies. The PhD thesis work advertised here will concentrate on body size specifically, and we propose that the student will address questions such as associations between body size and environment, macroevolutionary trends in body size, and inferring constraints on body size. Body size is perhaps the most obvious trait of any organism but the drivers of the evolution of size are far from being understood, especially in insects in which case the universal positive relationship between body size and fecundity would lead to the prediction of a permanent evolutionary increase in size. Most recently, data and methods have started to become available to find out if such increase has actually occurred in the course of evolution, and which factors have set limits

to it. The PhD student will primarily be running comparative analyses on pre-existing phylogenetic trees (e.g. using R packages such as OUwie and BAMMtools) and will also participate in data collection (incl. examining museum specimens). The work will be supervised by Prof. Toomas Tammaru (<http://kodu.ut.ee/~tammarut>) and Dr. John Clarke (<http://bit.ly/2qimTCy>). The group has a solid background in evolutionary ecology of insects, phylogenetic analyses and taxonomy of Lepidoptera, as well as collaboration ties with various universities in Europe (e.g. potential to collaborate with Niklas Wahlberg at Lund University, and Sebastian Höhna at LMU Munich) and North America. PhD studies in Estonia last for 4 years and publishing research papers is a requirement; PhD students receive competitive scholarships allowing them to work on their thesis full time (alongside taking some relevant classes). A successful candidate will have an excellent academic record, experience with statistical analyses and interest in evolutionary biology. Some experience and/or genuine interest in the ecology/evolution/taxonomy of insects as well as previous experience with phylogenetic comparative methods is an advantage. The candidate should have their master's degree by August 01, 2020 (if you are due to complete in September 2020, still contact us, we may be able to find a solution); the enrolment as a PhD student will be from September 01, 2020. If you are considering applying, please e-mail Toomas Tammaru ([toomas.tammaru@ut.ee](mailto:toomas.tammaru@ut.ee)) before the end of February 10 (any time zone). Open to applicants from all nations.

Toomas Tammaru <[toomas.tammaru@ut.ee](mailto:toomas.tammaru@ut.ee)>

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## UTasmania SexDeterminationTransitions

PhD position:transitions in sex determination systems

\*\*\* In the first instance (prior to January 19, 2020), this position is only available to citizens of the People's Republic of China

\*\*\* Chinese applicants will apply to the University of Tasmania, and if accepted, the Chinese applicant will then apply for Scholarship support from the Chinese Scholarship Council (CSC)

Applicants from other countries may be considered subsequent to January 19.

Project theme:

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

A PhD position is available to contribute to this research. This student will conduct advanced cytogenetic research on species of Australian lizards to help understand the genomic changes accompanyingtransitions between genetic and temperature sex determination.

The project is administered by the University of Tasmania (Assoc Profs Chris Burridge and Erik Wapstra), but will involve significant amounts of time at the cytogenetics laboratory of Prof Tariq Ezaz (University of Canberra).Cytogenetic techniques to be employed includeC-Banding, Comparative Genomic Hybridisation (CGH), chromosome microdissection, fluorescent in situ hybridisation (FISH), BAC library screening, and Next-Generation Sequencing (NGS). Bioinformatics such as comparative mapping will be also be conducted.

Chinese applicants should familiarise themselves with:

The China Scholarships Council eligibility requirements:

<https://www.csc.edu.cn/> The University of Tasmania English Language requirements for entry into a PhD

<https://www.utas.edu.au/research/degrees/what-is-a-research-degree#746043> Interested applicants should submit a CV, a copy of their academic transcript and a cover letter outlining their research interests tochris.burridge@utas.edu.au

The Discipline of Biological Sciences provides a diverse research environment within which to study, and has a large PhD cohort (80 students) with representatives from throughout the world.

Details of our individual research groups are here:

<https://beergrouputas.wordpress.com/> <https://evogentas.org/> Chris Burridge | Associate Professor, Molecular Ecology & Evolution School of Natural Sciences | University of Tasmania | Private Bag 55 | Hobart | Tasmania 7001 | Australia Room 320a Life Sciences Building | Ph &#43;61 3 6226 7653 | Fax &#43;61 3 6226 2698 | <https://rmdb.research.utas.edu.au/->

[public/rmdb/q/indiv\\_detail\\_warp\\_trans/3975#research-tab-5](public/rmdb/q/indiv_detail_warp_trans/3975#research-tab-5) <http://scholar.google.com.au/citations?user=4cYH8ZYAAAAJ&hl=en> evogentas.org

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

## UWashington PublicHealthGenetics

The Institute for Public Health Genetics (IPHG) at the University of Washington offers an MS in Genetic Epidemiology, an MPH in Public Health Genetics and a PhD in Public Health Genetics. All three degrees address advances in genetics and the societal implications of these advances. Program graduates find employment in academia, government and the private sector. Program details are at [iphg.biostat.washington.edu](http://iphg.biostat.washington.edu) or from me or from [phginfo@uw.edu](mailto:phginfo@uw.edu)

The goal of IPHG is to strengthen the preparation for careers in the science and implications of genetics of students from all backgrounds, especially those from groups historically underrepresented in STEM such as racial and ethnic minority groups, low income, first generation college students, veterans, and differently abled and 2SLGBTQ groups.

Bruce Weir IPHG Director [bsweir@uw.edu](mailto:bsweir@uw.edu)

Bruce S Weir <[bsweir@uw.edu](mailto:bsweir@uw.edu)>

## Vienna ThermalAdaptation

PhD position Dissecting the genetic basis of co-selected traits during thermal adaptation Principal advisors: Neda Barghi and Christian Schlotterer Institute of Population Genetics, Vetmeduni, Vienna, Austria

Background Both temperature mean and temperature fluctuations have important roles in thermal adaptation. Recent studies suggest that adaptation to mean temperature and fluctuation in temperature are distinct traits but their genetic basis and distinct effects of these selective pressures, i.e. constant and fluctuating temperature, on thermal adaptation are still largely unknown.

Aim This project aims to characterize genomic regions involved in thermal adaptation and to dissect the genes responsible for adaptation to either higher mean tem-

perature or fluctuating temperature. This work will take advantage of 30 replicates of *Drosophila simulans* evolved for over 100 generations in two temperature regimes (constant 23 Å°C and fluctuating between 18 and 28 Å°C).

**Task** You will have the opportunity to investigate two traits, i.e. adaptation to mean temperature and fluctuation in temperature, by combining time series Pool-Seq data, gene expression profiling and phenotypic assays.

**Preferred skills** - Background in experimental or computational fields such as bioinformatics, evolutionary genetics, or experimental population genetics - Experience in programming (Python/R) - Good oral and written communication skills

**Why do your PhD with us?** We offer - 1 month intensive course in population genetics - Weekly seminar series with internationally renowned experts in the field - International and interdisciplinary environment - Vienna is among the most liveable cities in the world

**Apply** Send CV, names and contact information for 2 professional references, and a motivation letter with a statement of research interests to [neda.barghi@vetmeduni.ac.at](mailto:neda.barghi@vetmeduni.ac.at) and [Christian.Schloetterer@vetmeduni.ac.at](mailto:Christian.Schloetterer@vetmeduni.ac.at) until March 31, 2020

For more information about the institute: [www.vetmeduni.ac.at/en/population-genetics/](http://www.vetmeduni.ac.at/en/population-genetics/) Salary: EUR 2,162.40 before tax, based on Austrian Science Fund (FWF)

Related literature

Barghi, N. et al. Genetic redundancy fuels polygenic adaptation in *Drosophila*. *PLoS biology* 17, e3000128, doi:10.1371/journal.pbio.3000128 (2019)

Mallard, F., Nolte, V., Tobler, R., Kapun, M. & Schlotterer, C. A simple genetic basis of adaptation to a novel thermal environment results in complex metabolic rewiring in *Drosophila*. *Genome Biology* 19, 119, doi:10.1186/s13059-018-1503-4 (2018)

Schlotterer C. et al. Combining experimental evolution with next-generation sequencing: a powerful tool to study adaptation from standing genetic variation. *Heredity* 114, 431-440 (2015)

Orozco-terWengel, P. et al. Adaptation of *Drosophila* to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles. *Molecular ecology* 21, 4931-4941, doi:10.1111/j.1365-294X.2012.05673.x (2012)

## WageningenU FungicideResistance

PhD position in unravelling the causes and consequences of fungicide resistance in the human fungal pathogen *Aspergillus fumigatus* (<https://www.wur.nl/en/vacancy/PhD-position-in-unravelling-the-causes-and-consequences-of-fungicide-resistance-in-the-human-fungal-pathogen-Aspergillus-fumigatus.htm>)

WE ARE:

The mission of Wageningen University & Research is "To explore the potential of nature to improve the quality of life". Within Wageningen University & Research, nine specialised research institutes from the Wageningen Research Foundation and Wageningen University have joined forces to help answer the most important questions in the domain of healthy food and living environment.

With approximately 30 locations, 5,000 employees, and 10,000 students, Wageningen University & Research is one of the leading organisations in its domain worldwide. An integrated approach to problems and the cooperation between various disciplines are at the heart of the unique approach of Wageningen.

For further information about working at Wageningen University & Research, take a look at the special career site.

Wageningen Plant Sciences Group, Laboratory of Genetics: The Laboratory of Genetics investigates causes and consequences of natural genetic variation within species. Because genetic variation plays an essential role in ecological and evolutionary processes, we ask ecologically and evolutionary motivated research questions. We use a wide array of model organisms, ranging from bacteria, fungi, plants and insects (<https://www.wur.nl/en/Research-Results/Chair-groups/Plant-Sciences/Laboratory-of-Genetics.htm>).

Radboud University Medical Centre The Radboud University Medical Centre is an academic hospital and centre of expertise in medical mycology, providing care and consultation for patients with complex fungal diseases. Antifungal drug resistance is an important research topic which is approached from a One-Health perspective.

WE LOOK FOR:

We are looking for an enthusiastic and motivated PhD candidate with a keen interest in evolutionary biology

and genetics and/or medical microbiology/mycology.

You will work in a project that addresses the One-Health consequences of circularity through the resistance development to environmental and medical azoles in the fungus *Aspergillus fumigatus* in accumulated organic residues. The objectives are to (i) use the diversity of organic waste disposal in the bulb growing sector to discern the key factors driving resistance development, (ii) use these factors to draw up an intervention plan that will be tested in the laboratory and on-site, and (iii) extend the obtained knowledge to general organic waste disposal to assess resistance, transmission routes and health risk across the system. Throughout, patient-risk will be monitored via local, regional, and national spore-trapping as well as patient isolates through hospital surveillance. The project is expected to deliver a quantitative and qualitative One-Health risk-assessment for the pressing problem of rapidly spreading azole-resistance world-wide.

The project has been recently awarded to the Laboratory of Genetics (Wageningen) and the Radboud University Medical Center (Nijmegen) by the Dutch funding organization NWO (see <https://www.nwo.nl/en/news-and-events/news/2019/12/three-awards-for-groundbreaking-research-in-agriculture-and-horticulture.html>, and full application available on request). The project contains a Postdoc and technician position, and this PhD position. Thus, you will be working in this team

with clear own responsibility and ample intellectual freedom to pursue the various biological aspects of azole resistance. Moreover, the consortium contains a variety of relevant stakeholders (e.g. from the bulb sector, waste disposal and composting companies, the chemical sector, and several governmental organizations) with which you will interact during for instance progress meetings.

WE ASK:

Our ideal candidate,

- is highly motivated and enjoys working in a team with the Postdoc, technician, and the supervisors;
- has a strong background in evolutionary biology and genetics. Some experience with handling large (genomic) datasets and bioinformatics will be a bonus;
- likes the combination of field and on-site sampling in combination with state-of-the-art laboratory experiments and analyses;
- is proficient in the English language, is good in communication, and enjoys working in a team.

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## ArizonaStateU SeniorResSpecialist PrimateEvolution

A full time Research Scientist position is available in the Snyder-Mackler lab in the Center for Evolution and Medicine at Arizona State University starting February 1, 2020 (start date is flexible). The Snyder-Mackler lab studies between behavior, the social environment, and the genome, with a focus on nonhuman primates and dogs. We combine detailed behavioral and demographic information with modern genomic data sets, focusing on gene regulation. Current projects focus on: i. The gene regulatory mechanisms linking the social environment to aging and resilience in rhesus macaques ii. The genomic signature of early life social adversity in gelada monkeys iii. Characterizing the rhesus macaque brain at single-cell resolution iv. Molecular aging in domestic dogs as part of the Dog Aging Project v. Genomic and phenotypic signatures of high-altitude adaptation in gelada monkeys.

The Research Specialist's duties will include the following:

- Next-generation library preparation for high throughput sequencing.
- Cell culture and experimental treatment.
- Sample collection and DNA/RNA extraction.
- Experimental design of genomics experiments including assisting in the development and optimization of novel protocols relevant to the SMack Lab's objectives.
- Manage day-to-day logistics of the lab including purchasing lab equipment/supplies for experiments, coordinating visitors and their lab use, and training lab assistants.

For more information about the lab and our work, see: <https://smack-lab.com/> Compensation commensurate with experience.

Requirements: Bachelor's degree in Biology, Genetics, or a related field and at least 4 years of experience in a research laboratory OR Master's degree in Biology, Genetics, or a related field and at least 2 years of experience in a research laboratory Familiarity with fundamentals of molecular biology

Required skills/traits include: Aseptic technique Molecular techniques Attention to detail Ability to work independently Meticulous record keeping

If interested, please send a CV and the names of at least 2 references to Dr. Snyder-Mackler: [nsnyderm@asu.edu](mailto:nsnyderm@asu.edu)

Noah Snyder-Mackler

Assistant Professor School of Life Sciences Center for Evolution and Medicine Arizona State University 214 Life Sciences C <http://smack-lab.com/> Co-director, Simien Mountains Gelada Research Project <https://geladaresearch.org/> Please join me and my family in our fight against ALS write to me or log on to: The ALS Association of Philadelphia

Noah Snyder-Mackler <[nsnyderm@asu.edu](mailto:nsnyderm@asu.edu)>

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## ColoradoStateU QuantitativeGenetics

Dear Colleagues,

We have an open faculty position in Quantitative Genetics of Crops at the Assistant / Associate level in the Dept of Soil and Crop Sci at Colorado State University.

The short advert and url are below. Please share with anyone you think is relevant.

Also, please note the due date is 10 February 2020, so just a month away.

thanks, John

The Department of Soil and Crop Sciences at Colorado State University invites applications for a tenure-track faculty position in Crop Quantitative Genomics. We seek dynamic and motivated scientists who have expertise and demonstrated capacity to facilitate integration of genomics, quantitative genetics, phenomics, bioinformatics, and statistics to develop novel approaches to help meet food system challenges. Commitment to teaching, mentoring excellence, and diversity are important parts of this position. Min. reqs: PhD in a

related field by application date; strong record of scholarly achievement; exp. in quantitative genetics and related computational methodologies; effective communication skills; commitment to diversity and inclusion. Complete applications due by 02/10/20 for full consideration. Full job description and application procedures at <https://jobs.colostate.edu/postings/73801>. CSU is an EO/EA/AA employer and conducts background checks on all final candidates.

“John.McKay@ColoState.EDU”  
<John.McKay@ColoState.EDU>

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### CornellU FieldAssist PlantPopulation

The Geber lab at Cornell University seeks a highly motivated, detail-oriented assistant for summer 2020 field research in the Southern Sierra Nevada (May-July) and lab work in Ithaca, NY (July-August). We are studying the population biology of the annual plant species *Clarkia* throughout its range and have yearly population censuses to conduct. We also have a large reciprocal transplant experiment in place that needs to be monitored.

Our research sites are located in the Kern River Canyon in Kern County, California. The lab rents a house on a property where other labs working in this system are also based in the summer. This field assistant would have a private bedroom, access to a shared bathroom and a communal kitchen, and wireless Internet access. Frequent trips are made into town (Lake Isabella and Kernville) for groceries and other supplies.

Successful applicants are expected to assist in data collection and data entry, and flower in the field; work in Ithaca will consist of sample processing (lots of seed counting!). The assistant will work a 39-hour workweek. Weather conditions in the Sierras can be very hot and dry (100+ degrees F) in the summer, so the assistant should be prepared to work in hot conditions. Applicants must be able to hike up and down steep hills for up to 1 mile at a time, stoop or kneel for extended periods of time, and work in proximity to bees and snakes. The work can be physically demanding and tiring, and the research team typically collects data 7 days a week. A good sense of humor and a positive attitude are essential.

Qualifications: 1) Citizenship and availability: appli-

cants must be US citizens and must be available to begin working in California as of May 1, 2020. The exact end date of the position in August is flexible. 2) Education: some undergraduate education in biology, ecology, or related field, or equivalent experience. 3) Experience: experience with and enthusiasm about working outdoors, and/or previous field research experience. Previous experience working with plants is preferable but not required. 4) Tasks: perform repetitive tasks with attention to detail, daily hiking. 5) Personality: interpersonal skills and willingness to live and work in close quarters with other researchers.

Compensation: transportation to and from California, a private room with Internet access in the field house, and pay (\$13-\$15 an hour depending on experience) will be provided. Applicants will be responsible for securing their own housing in Ithaca for July and August.

The deadline for applications is Feb 10, 2020. Applicants should submit: 1) a short (1 page maximum) cover letter describing their qualifications as well as future academic and professional goals; 2) a resume or CV outlining previous work experience and relevant courses (completed or in progress), extracurricular activities; and 3) name and contact information for two referees. Please send application to [mag9@cornell.edu](mailto:mag9@cornell.edu).

Applications will be reviewed as they are submitted.

Cornell University is an affirmative action/equal opportunity employer. Cornell University and we in the Geber lab have a commitment to support equality of education and employment opportunity by affirming the value of diversity. We welcome and encourage scientists of all backgrounds to apply to work with us! <http://blogs.cornell.edu/geberlab/> Email to: Monica Geber, Professor of Ecology and Evolutionary Biology [mag9@cornell.edu](mailto:mag9@cornell.edu)

“mag9@cornell.edu” <mag9@cornell.edu>

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### CWooster EvolutionaryPhysiology

#### 1-Year Visiting Position

The Biology Department at The College of Wooster invites applications for a visiting position in Animal Behavior/Physiology at the level of Assistant Professor, beginning in August 2020.

We are especially interested in hiring faculty who can contribute to the intellectual vibrancy and diversity of

the academic community through their teaching, research, and service. The College of Wooster enrolls a diverse student body (21% domestic students of color and 15% international students); all applicants are expected to discuss their experience working with diverse student populations.

The successful candidate will teach the equivalent of 6 courses, which may include introductory and advanced courses in general biology, organismal and evolutionary biology and animal behavior/physiology. In addition, they will advise independent thesis projects in animal behavior/physiology as part of the College's Independent Study program, and may participate in teaching courses for non-majors.

Applicants should submit a letter of application; curriculum vitae; unofficial graduate transcripts; a teaching philosophy statement; a statement of research interests; a statement detailing how the applicant has engaged and/or expects to engage with issues of diversity and inclusion in the classroom and the curriculum, as well as on campus and in the broader community; and three reference letters through Interfolio. Applications received by Friday, January 31st 2020, will receive full consideration. If you have questions regarding Interfolio, please contact Beth Lingenfelter, Administrative Coordinator, Biology Department, at bsnyder@wooster.edu Questions about the position should be directed to Stephanie Strand, Chair of Search Committee, sstrand@wooster.edu

Application link: <http://apply.interfolio.com/72959>  
Posted Date: 01/08/2020

Drug Free Workplace Affirmative Action < <https://wooster.edu/offices/hr/aa/> >

Rick Lehtinen <RLEHTINEN@wooster.edu>

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## DrexelU 2

### AssocDirectoryScholarsProgram

Drexel University seeks an ambitious, resourceful, highly skilled, and adaptable professional to serve as Associate Director of the GENTE Scholars Program. The GENTE Scholars Program is an educational program for university graduates from Equatorial Guinea (EG) that provides US-based training in English as a second language and experience in US university programs, including graduate degree opportunities at GENTE Consortium universities, leadership mentoring, teaching fellowships and grants; establishing an online degree program for

Equatoguinean students; and providing scholarships to train skilled craftsman in EG. The Associate Director will manage the GENTE Scholars Program, report to the GENTE Consortium Executive Director, and will have overall operational responsibility for the Scholars Program.

The Guinea Ecuatorial - Naturaleza, Turismo y Educacion (GENTE) Consortium is led by Drexel University. Its mission is to provide interconnected educational and biodiversity conservation solutions to benefit the people of Equatorial Guinea by increasing national human capacity and protecting national biodiversity. The project builds on long term efforts in EG by the Bioko Biodiversity Protection Program ([www.Bioko.org](http://www.Bioko.org)).

The Associate Director will be responsible for the management of the educational programs; development of budgets and financial tracking; communications with team members, consortium members, boards and councils; and preparation of outcome evaluations.

The Associate Director will participate with the Director in strategic planning, program innovation and growth management. The successful candidate should have outstanding organizational and management skills with experience working at the national and international level, either in the public or private sectors.

Apply at:

<https://careers.drexel.edu/en-us/job/494322/associate-director-gente-scholars-program> Questions:

Katy Gonder, mkg62@drexel.edu Professor of Biology  
Drexel University Director Bioko Biodiversity Protection Program [www.Bioko.org](http://www.Bioko.org) Essential Functions:

Manage GENTE Scholars Program in US and EG

Work with Executive Director to ensure ongoing excellence in programming, finance and administration, communications, and systems management.

Conduct strategic planning to ensure that the organization achieves its mission and is making consistent and timely progress.

Ensure effective systems to track scaling progress, and regularly evaluate program components to ensure they remain within the contractual guidelines of the GENTE program.

Support work of GENTE External Advisory Board and Councils, including coordinating programmatic efforts, succession planning, resource provisioning, and communications. Manage GENTE Consortium partners and members and recruit new members.

Required Qualifications:

Master's Degree, international education, international development, project management, law, business, hospitality, or related field.

At least 5 years experience.

Other Requirements:

MA/MS, MBA, JD or PhD, or an equivalent combination of education and professional experience.

At least 5 years of progressively responsible management experience international education, international development, project management, law, business, hospitality, or related field.

Advanced project management skills and abilities; understanding project goals and objectives and ability to develop team, tools, practices, tracking and communication systems to successfully execute same; ability to recognize and overcome program challenges

Strong ability to set priorities and manage workflow to fulfill objectives and goals according to deadlines in a fast-paced work environment with diverse and dispersed groups of people.

Ability to implement an entrepreneurial approach to strategy and tasks - equally adept at working alone, in small working groups, and effectively across a distributed, virtual team by establishing and maintaining cooperative relationships.

Understanding of monitoring and evaluation approaches for education and development programs.

Experience working with international scholars.

Excellent verbal, written, and interpersonal skills to accurately and effectively communicate to a wide spectrum of professionals and experts such as staff, University administrators, potential donors, and educators in a diverse working environment.

Public speaking, including ability to represent program in front of large audiences.

Advanced skills with Microsoft Office Suite - Word, Excel, PowerPoint, and Outlook. Advanced skills and experience working with complex budgets and financial projections.

Ability to write and speak Spanish.

Willingness to travel for extended periods in Equatorial Guinea and other countries as needed to fulfill GENTE Consortium objectives.

Preferred Qualifications:

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

## DrexelU Biology DepartmentHead

Position Title: Department Head, Biology

Drexel University, a top-ranked Carnegie R1-classified research institution located in Philadelphia, seeks an innovative leader and research scientist for the position of Head, Department of Biology < <https://drexel.edu/coas/academics/departments-centers/biology/> >, in the College of Arts and Sciences starting in September 2020.

About Drexel Biology:

The Department is made up of 16 tenured or tenure track faculty and 8 teaching faculty, whose research and teaching activities take place alongside a vibrant population of over 800 Biology undergraduate majors, and over 40 PhD/MS students and postdoctoral trainees. Faculty with active research programs and a strong record of extramural funding pursue research in the areas of molecular, cellular and organismal biology, and STEM education. Several Biology faculty hold appointments and pursue collaborations with colleagues in the College of Medicine; the School of Biomedical Engineering, Science and Health Systems; and the Department of Biodiversity, Earth, and Environmental Science, which is tightly integrated with the Academy of Natural Sciences.

The Department of Biology is housed in the Papadakis Integrated Sciences Building (PISB), a state-of-the-art five-story building with naturally-lit open-design laboratories, modern classrooms and conference rooms, and a comprehensive light microscopy core facility with advanced imaging capabilities, including confocal, super resolution, and 2 photon excitation microscopy. Located in University City, which includes the University of Pennsylvania, the Children's Hospital of Philadelphia, and the Wistar Institute, PISB is in the heart of a vibrant neighborhood with numerous collaborative opportunities and resources. Additional resources are available to Biology faculty as consortium members of the Sidney Kimmel Cancer Center at Thomas Jefferson University, an NCI-designated Cancer Center.

Biology faculty and graduate students undertake innovative, evidence-based teaching practices that emphasize experiential and student-centered learning. Educational

practices and innovation have been fostered through collaboration and interaction with the Center for the Advancement of STEM Teaching and Learning Excellence (CASTLE) and funding from the Howard Hughes Medical Institute (HHMI) for improving undergraduate retention in STEM disciplines. The Department is also engaged in the nationally renowned, HHMI-supported SEA-PHAGES program.

#### Required Qualifications:

Department Head responsibilities are described elsewhere in full (i.e. see section VI of this website < [https://drexel.edu/provost/policies/-department\\_heads\\_selection/](https://drexel.edu/provost/policies/-department_heads_selection/) > from the Office of the Provost). For this particular position, candidates should exhibit:

- \* A doctoral degree in the broader discipline of biological sciences
- \* A proven record of teaching and service activities
- \* Research achievements consistent with qualification for the rank of full professor at an R-1 institution
- \* Academic administrative experience
- \* Exceptional oral, written, and interpersonal communication skills
- \* A strategic vision and ability to guide and nurture the research, teaching, and service missions undertaken by a diverse faculty
- \* Commitment to building a culture of transparency and shared governance
- \* Experience in mentoring students and faculty
- \* An ability to bolster the Department's extramurally funded research programs and strengthen undergraduate and graduate student training
- \* Understanding of the enrollment and retention challenges of an undergraduate-serving Department
- \* An ability to advocate for the Department's personnel and priorities

Applications, including a cover letter, curriculum vitae, two-page statement of leadership philosophy and the names of five references, should be submitted via <https://careers.drexel.edu/en-us/job/494272/-professor-and-department-head-biology>. Preferences will be given to those received before January 31. Inquiries should be addressed to the Chair of the Search Committee, Dr. Jacob Russell (jar337@drexel.edu). The Committee aims to select candidates for a first round of interviews to take place in February and March, 2020.

Drexel University is an Equal Opportunity/Affirmative Action Employer. The College of Arts and Sciences is especially interested in qualified candidates who can contribute to the diversity and excellence of our academic community. The University offers an attractive benefits package including tuition remission and a generous retirement package.

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## IllinoisStateMuseum AnthropologyCurator

The Illinois State Museum is hiring a Curator 1 in Anthropology at our Dickson Mounds Museum site in Lewiston, IL.

See link for details: <https://-agency.governmentjobs.com/illinois/-default.cfm?action=viewJob&jobID=2679122> Job posting closes February 28, 2020.

Meredith J. Mahoney, Ph.D. Curator of Zoology Acting Curator of Geology

[meredith.mahoney@illinois.gov](mailto:meredith.mahoney@illinois.gov)

Illinois State Museum [www.illinoisstatemuseum.org](http://www.illinoisstatemuseum.org)  
 Zoology Section on Facebook [www.facebook.com/-ISMZoology](http://www.facebook.com/-ISMZoology)  
 Research and Collections Center 1011 E. Ash St Springfield, IL 62703 ph. 217-785-4843 fax 217-785-2857

“Mahoney, Meredith” <[Meredith.Mahoney@illinois.gov](mailto:Meredith.Mahoney@illinois.gov)>

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## KewGardens UK Bioinformatics 18Months

Job:, Bioinformatics Developer, Plant and Fungal Trees of Life Project (PAFTOL), Royal Botanic Gardens Kew, London, UK

Hours of work: Full time

Contract Type: Fixed Term (FTA)

Contract duration: 18 Months

Salary: 34,933 - 37,865 per annum depending on skills and experience

Location: Royal Botanic Gardens Kew, London, United Kingdom

Closing Date: Monday 3rd February

Job advert:

Bioinformatics Developer, Plant and Fungal Trees of Life Project (PAFTOL).

Kew is the world's leading botanic gardens, at the forefront of plant and fungal science, a UNESCO World Heritage Site and a major visitor attraction. We want a world where plants and fungi are understood, valued and conserved - because our lives depend on them. We use the power of our science and the rich diversity of our gardens and collections to provide knowledge, inspiration and understanding of why plants and fungi matter to everyone.

The successful candidate will be an active member of PAFTOL's multi-disciplinary team. The post holder, together with PAFTOL's other bioinformatics staff, will be responsible for completion of the design and build of software systems and data analysis necessary to ensure the long-term operation of the PAFTOL project.

You will be an excellent bioinformatician or software engineer with appropriate professional experience and a proven background in genomic data manipulation, ideally in a research environment. You will have a track record of helping to design and build robust bioinformatics pipelines, with good knowledge of distributed compute environments and workflow management systems. Experience of phylogenomics is desirable but not essential. You will be a proven team player, with the ability and appetite to help deliver project outputs, outreach, and to train and support researchers and students as required.

The salary will be 34,933 - 37,865 per annum, depending on skills and experience

We offer a fantastic range of benefits including a broad range of Learning and Development opportunities, with access to the Civil Service training curriculum, generous annual leave entitlement for new starters, family friendly policies, a choice of competitive pensions and flexible benefits scheme as well as free entry into a wide range of national museums and galleries.

We are committed to equality of opportunity and welcome applications from all sections of the community. We guarantee to interview all disabled applicants who meet the essential criteria for the post.

To apply and for further information visit: <https://careers.kew.org/vacancy/bioinformatics-developer-plant-fungal-trees-of-life-project-409534.html> The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, United Kingdom.

Vanessa Barber <V.Barber@kew.org>

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## MiddleEastTechU EvolutionaryBiol

Assistant Professorships in EVOLUTIONARY BIOLOGY and in ECOLOGY

The Department of Biological Sciences at the Middle East Technical University (METU) in Ankara is inviting applications for Assistant Professor positions in EVOLUTIONARY BIOLOGY and in ECOLOGY.

We seek researchers with a PhD and postdoctoral training and a significant publication record. The successful applicants will: - Run an independent research group, including mentoring graduate students and obtaining extramural funds, - Teach undergraduate and graduate courses in their fields (the METU language of instruction is in English).

They will be provided with office and lab space, and will have access to the Department's research infrastructure, such as wet labs and servers.

METU Biological Sciences hosts a vibrant research environment with 20 research groups working on diverse topics, including conservation biology, aquatic ecology, comparative genomics and transcriptomics, bioinformatics, cancer biology, microbiology, plant biology, and archaeogenomics.

Unique opportunities for research include METU's Ecosystems Research Center, which investigates diverse ecosystems from lakes to steppes and forest in the region. The METU campus, a 3,000 hectare area including forest and steppe habitats and a 100 hectare lake, is among the Center's prime study sites.

The Department's unique facilities further include an experimental apiary hosting 40 hives, aquatic mesocosms on lake and on land with warming facilities, a fully functional aquatic ecology laboratory with a climate room as well as walk-in cold room, an ancient DNA clean room, plant growth chambers, and a greenhouse (for more information check <http://bio.metu.edu.tr/en>).

METU is among Turkey's top public research universities, with the largest share of national science funding. METU researchers have traditionally achieved 30% success rates in TUBITAK (Turkey's national science agency) grant applications, such as the regular TUBITAK 1001 scheme (providing ~100,000 euros for 3 years). METU is again Turkey's best scoring university with the highest success rates in EU-H2020 grants.

The successful candidates will have access to on-campus housing and child care. The METU campus, with its forest, steppe area and lake, provides a wide selection of outdoor as well as indoor recreational sport opportunities. Foreign applicants will find it easy to integrate into the METU community, with between 5-10% of faculty and students being international.

METU provides a small-scale start-up grant, while the chosen applicants will be encouraged to apply to a wide range of national and European extramural funding sources. These include TUBITAK Start-Up Grants (2232 and 3501), Turkey's Science Academies' Young Scientist Awards (BAGEP and GEBIP), the EMBO Installation Grant, as well as ERC Starting and Consolidator Grants. The chosen applicants may also make use of fellowships such as Marie Curie, MSCA Widening and the MSCA Co-Fund.

The call will be open until the positions are filled. Chosen applicants will be invited for online or on-site seminars.

Applicants are expected to send a cover letter that include: (i) Cover letter, (ii) CV, (iii) Publication record, (iv) Research statement, (vi) Teaching statement (courses taught and/or proposed), (v) Full contact information for three references.

For inquiries, please contact: Mehmet Somel (somelmehmet@gmail.com) and Meryem Beklioglu (meryem@metu.edu.tr)

Mehmet Somel <somel.mehmet@googlemail.com>

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## Museum Geneva OrthopteraMultilocusBarcodes

A 4-years PhD position is available at the Geneva Natural History Museum, Switzerland.

Starting date: 1 April 2020

### BACKGROUND AND OBJECTIVES

The research project aims to improve knowledge on species and genetic diversity of Orthoptera in Switzerland. The project is organized around two axes. First, the development and the application of a multilocus barcoding method (whole mitochondrion, ribosomal DNA and UCEs) for the monitoring of orthopteran species all over Switzerland. Second, the museomics-based inference of demographic dynamics across the last century in four selected orthopteran species (population genomics

using HyRAD-based hybridization-capture).

The PhD candidate will be involved in field collection, wet lab experiment (in particular DNA extraction, custom library preparation and NGS sequencing), analysis of NGS data using custom bioinformatic tools, as well as manuscript writing.

### APPLICATION PROCEDURE

The applicant should hold a Master degree or equivalent in biology.

Experience in molecular biology, analysis of next generation sequencing data and scientific writing are highly desirable. Skills in at least one usual analysis and scripting language (R CRAN, Perl or Python) would be an asset. The ideal candidate should be enthusiastic, team-player, self-motivated, and with a strong interest in insect diversity.

The applicant will have full time to conduct his PhD research.

Applicants should submit the following documents:

- Cover letter emphasizing on the intrinsic motivation for applying to this position, on the fit of the position with the applicant's profile and on his/her professional goals (2 pages max)

- Curriculum Vitae (2 pages max)

- Summary of previous research experience (1 page max)

- Copies of degree certificates and list of coursework, including grades

- Names, addresses and e-mails of two professional references

- An electronic copy of previous works (master degree thesis or other scientific publications).

Short-listed candidates will be invited in Geneva for an interview.

The application should be sent by email as a single pdf file to Nadir ALVAREZ, e-mail : nadir.alvarez@ville-ge.ch

For any additional information, please contact Nadir ALVAREZ (nadir.alvarez@ville-ge.ch) or Jeremy GAUTHIER (jeremy.gauthier@ville-ge.ch).

Application deadline : 31 January 2020

Nadir Alvarez <alvarez.museum@gmail.com>

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## OregonStateU FishGenomics

Research Assistant in Fisheries Genomics

The State Fisheries Genomics Lab at Oregon State University (OSU) is seeking applications for a Faculty Research Assistant. The individual will work with a team of researchers to address the science and management needs of OSU's Coastal Oregon Marine Experiment Station (COMES) and the Oregon Department of Fish and Wildlife (ODFW).

Primary responsibilities include providing leadership in research, maintaining an efficient laboratory, archiving tissue samples and associated phenotypic data, training graduate students in genetic and genomic techniques and working collaboratively with Oregon State University's Center for Genome Research and Biocomputing (CGRB).

This position is located at the Hatfield Marine Science Center (HMSC) in Newport, Oregon.

For additional details and how to apply: <https://jobs.oregonstate.edu/postings/87250> For questions, please contact Dr. Kathleen O'Malley (Kathleen.omalley@oregonstate.edu)

Kathleen O'Malley Associate Professor, State Fisheries Geneticist Oregon State University Coastal Oregon Marine Experiment Station 2030 SE Marine Science Drive Newport, Oregon 97365

ph: (541) 961-3311 email: kathleen.omalley@oregonstate.edu  
website: marinegenomics.oregonstate.edu

"O Malley, Kathleen G"  
<Kathleen.OMalley@oregonstate.edu>

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## ReedCollege EvolutionaryBiology 2YrVisitingProf

Dear fellow evolutionary biologists—

Please see the job posting below for a 2 year visiting professor position at Reed College. Although it does not explicitly list 'evolutionary biology' as a focus in

the ad, I am on the search committee and evolutionary questions/foci are most welcome (e.g., climate change biologists, folks studying specific ecological adaptations, folks looking at urban ecology/invasive species evolution and ecology, etc. come to mind as some examples of research programs that would be highly competitive in this search). Many of us in the department are tackling evolutionary questions, whether related to animal behavior shifts, evolution of pathogenicity, or flower color evolution. Note—Reed is a special place. While it is a 4 year primarily undergraduate institution, it has a very strong emphasis (and a lot of support for) research. Most of the faculty in our department have one or more multi-year NSF or NIH grants supporting our research, to give you an idea of the intellectual/scholarly environment. Plus, it's in Portland!

If you have further questions, please check out the link and email me, or the search chair. All best, Sarah Schaack

\*Two-Year Visiting Position in Ecology/Environmental Biology at Reed College \* The Biology Department at Reed College invites applications for a two-year visiting faculty position in ecology and/or environmental biology. Specifically, we seek applicants whose approach(es) to research include field-based methods and whose study system is focused on plants, algae, fungi, and/or single-celled eukaryotes to teach courses in their area of expertise and conduct collaborative research that involves students. Teaching responsibilities will include a combination of courses (a 3/2 load), as well as senior thesis research mentorship in areas that support the Biology curriculum and Environmental Studies program. Specific courses are to be determined, but will include some combination of the following over the two years: participating in the team-taught introductory biology course, teaching an upper level lecture/lab courses in the candidate's area of expertise, leading an advanced topic seminar course based on the primary literature, and/or team-teaching in interdisciplinary classes offered as part of the Environmental Studies program.

Reed College, a highly selective liberal arts institution with a distinguished record of educational accomplishment and a strong commitment to scholarship (<http://web.reed.edu>), is also a community that values cultural and intellectual pluralism as essential to the excellence of our academic program (<http://www.reed.edu/diversity/>). In your application materials, please convey how your teaching, scholarship, mentorship and/or community service might support these values.

For full consideration, application materials (cover letter, curriculum vitae, statements of research and teaching interests, and contact information for three refer-



ences) should be submitted through interfolio at <http://apply.interfolio.com/72829> by February 14th, 2020.

Specific inquiries should be directed to Keith Karoly, Chair, Visiting Biologist Search Committee, [kkaroly@reed.edu](mailto:kkaroly@reed.edu).

Sarah Schaack, PhD Associate Professor Department of Biology Reed College [schaackmobile@reed.edu](mailto:schaackmobile@reed.edu)  
<https://sites.google.com/site/schaackwork/> [schaackmobile@gmail.com](mailto:schaackmobile@gmail.com)

## SouthAfrica 2 Managers StripedMouseProject

1 position as station manager (starting as soon as possible)

1 position as research manager (starting May 2020 or later)

at the striped mouse project in South Africa

(NOTE: We also advertise one postdoc position for two years and unpaid volunteer positions for 2-12 months. See other advertisements or ask via email [carsten.schradin@iphc.cnrs.fr](mailto:carsten.schradin@iphc.cnrs.fr))

We are looking for an extremely motivated and independent biology student with a master's degree to join the striped mouse project as soon as possible as station manager and a second student to start in July 2020 as research manager. Both managers are expected to stay until at last end of October 2021 while an extension for up to 3 years is possible. This position is suitable for somebody who would like to gain experience in field work and scientific management. Managers get free accommodation at the station and a compensation to cover their daily costs starting at R4000 for the first three months, rising to R5000 per month and more afterwards, which is sufficient to pay all costs of living (approx. 3500/month). Travel costs can be refunded by up to an additional R 16 000 / year. As such, the position compensates for all arising costs but does not represent a legal employment.

The station manager and the research manager work closely together and both managers share many responsibilities. However, each will have specific main duties, but should also be able to deal with all other duties (for example when the other manager is on leave, or when a new manager has to be trained). The new manager will be instructed by the present managers, with which they

will overlap for several months.

You must be hard-working, highly motivated, able to work independently, good in communicating with people, able to supervise others, and not afraid of snakes. You must have a drivers licence and you must love to live at a remote place in nature, without regular internet and cell-phone reception. Most importantly, you are fascinated by nature and science!

Skills needed: Good experience in field work and good knowledge of behavioural ecology or a similar field of research. Experiences in working with small mammals, radio-tracking, blood sampling, and living at a remote location are of advantage. Handyman skills are of advantage and needed for the station manager position.

Great opportunity: This is a great opportunity to spend 1.5-3 years in Africa, acquiring important skills in field biology and project management, while improving your CV. These skills will become valuable whether you later continue with a PhD or other jobs. It will be very hard and demanding, but also a once in a life time experience!

Job description: Five working days a week (Mo, Tue, Thu, Fr, Sat), with Wednesday being used for a shopping trip to town (not counted as working day) and Sundays being free. Included are four weeks of holiday for 12 months, which has to be taken outside the main breeding season (so not during August to November) and during periods when the other manager is present at the research station (the two managers cannot be on leave at the same time).

Shared duties of managers at SKRS

Striped mice:

- . Trapping
- . Observing
- . Radio-tracking, putting on radio-collars
- . Blood sampling

Collect data for specific research projects (to be determined).

Primary duties station manager / secondary duties research manager

- . Technical support research station:
  - o Water system incl. sewage system
  - o Solar system
  - o Gas bottles replacement
  - o House and furniture
  - o Running of the respirometry laboratory
  - o Management of the captive colony

- o Management of the research station car
- o Management of bank account and cash box
- o Management of research station supplies

Primary duties research manager / secondary duties station manager

. Data:

- o Weekly data entry
- o Weekly data check
- o Monthly data backup
- o Monthly data report
- o Training and supervision of field assistants
- o Training of students and postdocs
- o Support for students and postdocs
- o Management of transmitters
- o Management of field and laboratory supplies

Compensation:

. Free accommodation.

. A monthly compensation of R 4000 for the first three months, raising to R5000 per month afterwards, which is sufficient to pay all costs of living (approx. 3500/month). The compensation can gradually rise up to R5900/month.

. For travel and other costs, R16 000 per year can be refunded, but proof (receipts) must be presented for this. This refund is only payable after October 2021 and will not be paid if the person leaves earlier than agreed.

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

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## UAntwerp EvolutionMammalPathogens

Tenure track lecturer position: Evolution of mammals and their pathogens

The Evolutionary Ecology Group at the University of Antwerp, Belgium ([www.uantwerpen.be/eveco](http://www.uantwerpen.be/eveco)) and the Royal Belgian Institute of Natural Sciences (RBINS,

Brussels) are jointly presenting a combined vacancy for a part-time (50%) tenure track lecturer at UAntwerp / part-time (50%) scientific researcher at RBINS in the domain of the evolution of mammals and their pathogens.

For more information, see: <https://www.uantwerpen.be/en/jobs/vacancies/ap/-2020zapfwetex040/> Deadline for applications: 15 March 2020

Herwig Leirs <[herwig.leirs@uantwerpen.be](mailto:herwig.leirs@uantwerpen.be)>

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## UExeter EvolutionaryPsychology

The jobs below are open to all areas of psychology, including evolutionary approaches to behaviour and cognition. Evolutionary researchers are advised to contact Tim Fawcett ([t.w.fawcett@exeter.ac.uk](mailto:t.w.fawcett@exeter.ac.uk)) before applying.

UP TO SEVEN LECTURESHIPS IN PSYCHOLOGY, UNIVERSITY OF EXETER We seek to employ seven new colleagues at the Department of Psychology, University of Exeter, across the Education and Scholarship (E&S) and Education and Research (E&R) job families. The successful candidates will be enthusiastic educators (for both E&S and E&R) and excellent researchers (E&R), who possess a competitive record for their career level. Successful candidates will possess a PhD, or be nearing completion, and able to teach and supervise undergraduate and masters research projects in core areas of Psychology—such as clinical psychology, cognitive psychology, neuroscience, developmental, health, organisational, personality, and social psychology. For an informal and confidential discussion about the post you can contact Prof Manuela Barreto (tel: 01392-722674, email: [m.barreto@exeter.ac.uk](mailto:m.barreto@exeter.ac.uk)) or Prof Celia Morgan (tel: 01392-714649, email: [Celia.Morgan@exeter.ac.uk](mailto:Celia.Morgan@exeter.ac.uk)). The closing date for applications is 30 January. Alongside the online application please submit a cover letter and your CV. The University of Exeter is an equal opportunity employer. More information about the posts can be gained here: E&S: [https://jobs.exeter.ac.uk/hrpr\\_webrecruitment/-wrd/run/ETREC107GF.open?VACANCY\\_ID=-216618RFlo&WVID=3817591jNg&LANG=USA](https://jobs.exeter.ac.uk/hrpr_webrecruitment/-wrd/run/ETREC107GF.open?VACANCY_ID=-216618RFlo&WVID=3817591jNg&LANG=USA) E&R: [https://jobs.exeter.ac.uk/hrpr\\_webrecruitment/-wrd/run/ETREC107GF.open?VACANCY\\_ID=-681438RFlo&WVID=3817591jNg&LANG=USA](https://jobs.exeter.ac.uk/hrpr_webrecruitment/-wrd/run/ETREC107GF.open?VACANCY_ID=-681438RFlo&WVID=3817591jNg&LANG=USA) “Fawcett, Tim” <[T.W.Fawcett@exeter.ac.uk](mailto:T.W.Fawcett@exeter.ac.uk)>

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## UMainz EvolutionaryPlantSciences

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](http://www.imb-mainz.de)), the Institute of Biotechnology and Drug Research (IBWF; [www.ibwf.de](http://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](http://www.bio.uni-mainz.de/-1517.ENG.HTML.php) should be submitted in electronic form not later than March 26, 2020 to the

Dean, Faculty of Biology ([biologie@uni-mainz.de](mailto:biologie@uni-mainz.de))

The symposium for invited candidates will take place on May 5 and May 8, 2020 in Mainz. Informal requests can be directed to Prof. Dr. Susanne Foitzik ([foitzik@uni-mainz.de](mailto:foitzik@uni-mainz.de)) or Prof. Dr. Andreas Wachter ([wachter@uni-mainz.de](mailto: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](http://www.verwaltung.uni-mainz.de) ”Foitzik, Susanne“ <[foitzik@uni-mainz.de](mailto:foitzik@uni-mainz.de)>

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## UMichigan HumanVariation

### Job Summary

The University of Michigan’s School of Public Health is searching for a full-time Research Area Specialist Intermediate or Senior to support the highly interactive Genes for Good research group. Genes for Good is involved in cutting edge genetics research, studying genetic variation in humans, with a focus on understanding how genetic variation contributes to the risk of complex behaviors and traits. This is an opportunity to work in a challenging and rewarding research area that is at the cutting edge of using new online resources for participant engagement.

You will contribute to the design and analysis of a new generation of genetic and health studies that use online instruments and social media to engage large numbers of participants. You will contribute to the design of survey instruments, data collection protocols, user interfaces and communication and participant engagement strategies. In addition to many opportunities to participate in research project coordination and design, interested candidates will also be able to develop data analysis

skills and independent decision-making skills.

#### Responsibilities

- Lead the design and evaluation of instruments for data collection to ensure participants are engaged in the study and useful health information is collected in a streamlined fashion. This will include the design of surveys and other instruments, modification of procedures and integration of new findings to improve data gathering and analysis.
- Engage with faculty and other team members to monitor the integrity of data collection and the accurate use of protocols and procedures. Develop process improvements to improve quality of study data and participant experiences.
- Participate in the reporting of study results by completing data analysis activities, writing technical reports for funders, and articles for publication.
- Collaborate and contribute to the development of engaging, informative interfaces and answer participant questions about the study.
- Independently draft Institutional Review Board and other documents required for regulatory compliance.
- Coordinate community events to enhance participant interest.
- For candidates with quantitative experience and interest in data analysis, there will be the opportunity to contribute analysis, visualization and interpretation of research data.

#### Required Qualifications

##### Research Area Specialist Intermediate

- Have a Master's degree in a health care or research related field. Candidates with degrees in Epidemiology, Biostatistics, Bioinformatics, Health Behavior and Health Education, or Human Genetics are expected to be highly qualified.
- Experience in genetic studies and a solid understanding of human genetic concepts.
- 4 to 5 years of prior research program coordination experience, particularly where it involves planning of interactions with research subjects and exceptional attention to detail are necessary.

##### Research Area Specialist Senior

- Have a Doctoral degree in a health care or research related field. Candidates with degrees in Epidemiology, Biostatistics, Bioinformatics, Health Behavior and Health Education, or Human Genetics are expected to be highly qualified.

- Experience in genetic studies and a solid understanding of human genetic concepts.

- 4 to 6 years of prior research program coordination experience, particularly where it involves planning of interactions with research subjects and exceptional attention to detail are necessary.

#### Desired Qualifications

- Experience performing statistical analyses using R and/or Python, particularly with genetic data and/or large disease registry or health related databases is not required, but highly desirable.
- Familiarity with Linux command-line tools is not required, but highly desirable.
- Excellent written, visual and verbal communication skills.
- Must be highly sensitive to confidential data and associated regulations and have an understanding of compliance issues with regards to human subject research.
- The candidate should have the ability to assess competing priorities and manage workflow.
- Candidate must be able to establish and maintain good working relationships with study personnel and coordinate efforts with a diverse group of people.

#### How to Apply

Please go to [https://careers.umich.edu/job\\_detail/-181512/research\\_area\\_specialist\\_sr](https://careers.umich.edu/job_detail/-181512/research_area_specialist_sr) to apply. A cover letter that addresses your specific interest in the position and outlines skills and experience that directly relate to this position is required for consideration.

Christine Dobski <cdobski@umich.edu>

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## UMichigan ResearchLabSpecialistInt Biodiversity

We are looking for a candidate to fill a full-time Research Laboratory Specialist Intermediate position in the Department of Ecology and Evolutionary Biology at the University of Michigan. You will be responsible for day-to-day operations of two specialized laboratories, the Genomic Diversity Laboratory in the Research Museums Center and the Biodiversity labs in the Biological Sciences Building, providing support to more than 11 faculty members and approximately 72 users.

Specific duties and responsibilities, required qualifications, and additional information can be found at the following website:

[https://careers.umich.edu/job\\_detail/180527/-research\\_laboratory\\_specialist\\_intermediate](https://careers.umich.edu/job_detail/180527/-research_laboratory_specialist_intermediate) University of Michigan job posting #180527

“tfduda@umich.edu” <tfduda@umich.edu>

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## UppsalaU JagiellonianU FieldAssistant BirdEvol

Expenses paid field assistant positions to study the breeding ecology of blue tits and collared flycatchers on the wonderful island of Gotland.

For the upcoming field season (20 April-20/30 June 2020) we are looking for an expenses-paid field assistant to join the team working on the Swedish island of Gotland. It is a famous bird study site, with over 40 years of bird ecology monitoring, and additionally an amazingly beautiful and unique location for all bird lovers, a major birding and bird migration hotspot, and a culturally rich location for all Scandinavia lovers.

Our current project concerns two species: the blue tit and the collared flycatcher. Apart from general monitoring of both species' breeding we conduct specific research, which now concentrates on colour biology and expression in the blue tit. The work is demanding, requiring long hours spent in the forest in variable weather conditions (although the weather has been very gentle

the past few seasons on Gotland), precision in handling the birds and recording the data, and the ability to work in a team. The team will consist of 7-11 assistants, plus an additional collaborating team of similar size from France, staying in another location close by. Basic procedures used during fieldwork involve catching adult birds with mist-nets, ringing of adults and nestlings, morphological measurements of young and adult birds, blood-sampling of some birds for genetic analyses. We provide training on the most crucial procedures, but a basic knowledge of bird morphology and bird handling experience is more than welcome.

Qualifications: (1) BSc/MSc in Biology, Ecology, Evolution or similar qualification (2) Previous field experience will be a big plus (3) Ability to work in small teams and sociable personality (4) Bird ringing and mist-netting experience is desired but can also be learned on site (5) EU-valid driving licence (6) Fluent in English

We will cover for the accommodation (lodging in rooms shared with other field assistants - usually 2 persons per room - in a beautiful & comfortable, large house in the middle of the fieldwork area), travel expenses from and to the—study site (within reasonable limits and up to 450 EUR; if more is expected - let's discuss possibilities on a case by case basis), as well as the living expenses.

Applications - including a CV, a letter of motivation (1/2 A4 page) and the name of two referees - should be sent to Szymon Drobniak [szymek.drobniak@gmail.com](mailto:szymek.drobniak@gmail.com), ideally as a single PDF file.

Full consideration will be given to applications received until the 15th of February. After that date applications will be monitored if any additional assistants would be required. Applications sent after the 20 of March will not be considered.

Please do not hesitate to write to me if you have more and specific questions.

Dr Szymon Drobniak Jagiellonian University (PL) & University of New South Wales (AU)

[geralttee@gmail.com](mailto:geralttee@gmail.com)

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## UTexas Austin FieldTech PlantEvolGenomics

We seek an energetic, motivated research technician to participate in experiments on the ecology, physiology, and genomics of switchgrass. This is an opportunity to participate in integrative research studying the genetic basis of ecological processes in an important native grass species. The position will be administered through the University of Texas at Austin and stationed with Philip Fay's group at the USDA Grassland, Soil, and Water Lab in Temple, TX (<https://www.ars.usda.gov/plains-area/temple-tx/grassland-soil-and-water-research-laboratory/people/philip-fay/>). This position is expected to continue until 14 August 2020 with possible extensions based on job performance, progress towards research goals, and new funding acquisition.

To apply, please submit a cover letter, CV, and contact information for three references to [https://utaustin.wd1.myworkdayjobs.com/UTstaff/job/-Texas/Research-Engineering-Scientist-Assistant-Temple-Texas-Juenger-Lab-R\\_00007566](https://utaustin.wd1.myworkdayjobs.com/UTstaff/job/-Texas/Research-Engineering-Scientist-Assistant-Temple-Texas-Juenger-Lab-R_00007566). Direct any questions about the position to Robert Heckman (robert.heckman@utexas.edu). Review of applications will begin immediately and the position will remain open until filled. Start date is negotiable, but preference will be given to applicants who are available earlier.

Robert Heckman <robert.heckman@utexas.edu>

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## UWashington ConservationDataAnalyst

Data Analyst: Research Consultant

The Center for Conservation Biology in the Biology Department at the University of Washington is seeking a highly qualified, innovative data analyst who will examine genetic and related data to address complex forensic and research problems. We are particularly interested in someone who has a keen interest in applying mathematics and algorithms to solve real world problems, and also has strong statistical, data analysis, bioinformatics, and coding skills (including R and C++). A major

part of this position involves use and optimization of our custom software for genetically assigning geographic origin to forensic samples. An ability to communicate and collaborate well with others is also important.

The Center uses innovative field and laboratory techniques to non-invasively study and monitor a wide variety of wildlife populations around the world. Our primary forensic projects use microsatellite DNA fragment and sequence analyses to identify the locations of major elephant and pangolin poaching hotspots across Africa over time. We also use these data to link transnational criminal organizations to multiple large ivory shipments based on direct and familial sample matching. Our main wildlife monitoring programs examine: (a) impacts of wolf recovery on the distributions, diets, microbiome and physiological health of sympatric predators and prey in Washington state and (b) impacts of prey loss, toxin and vessel traffic exposure on orca and baleen whales in the Salish Sea. The Center works closely with state, federal and international governments, law enforcement, and non-government organizations. More information about our program can be found at: <http://conservationbiology.uw.edu/>. Responsibilities: Analytics: (100%)

- \* Investigate how to integrate and interpret diverse data sets collected over large spatial scales with highly varied error components and develop data collection, storage, and analysis instruments for integrating and interpreting these diverse data sets.

- \* Develop and apply tools for processing and analyzing a wide variety of studies, including DNA methods for forensic investigation of transnational wildlife crimes, and ecological methods that are not adequately addressed by existing models.

- \* Investigate limitations in current datasets to determine what additional data are needed to resolve existing problems, and design appropriate analyses to test these fixes. Examples include:
  - o Using large reference data sets for genetic assignment of elephant tusks and/or pangolin scales seized in illegal transnational shipments made worldwide. Resource selection models and spatially-explicit mark-recapture models applied to genotyped, geo-referenced scat samples collected by detection dogs over large remote areas.

- \* Optimization of our DNA assignment and sample matching software, written in C++ and R

- \* Conduct statistical analyses using standard and advanced statistical techniques on a wide variety of genetic, ecologic and physiologic data

- \* Prepare results for reports, publications and/or presentations.

\* Lead continued development of the infrastructure for the assemblage of data and computer models. Here, the candidate will work with graduate students, post-doctoral students and staff.

\* Contribute to research study design including methodology and analysis for grant proposals. \* Other duties may be assigned.

Minimum Requirements:

\* BS or MS in biostatistics, bioinformatics, genetics, computer sciences, mathematics, or related field.

\* Solid understanding of mathematics, computer programming and biostatistics.

\* Ability to utilize computational tools in common scripting languages (e.g R, C++)

\* Experience working with high performance computing.

\* Ability to manage projects and solve problems independently.

\* Excellent collaboration skills with interdisciplinary teams.

\* Strong written and oral communication skills.

Working Conditions: On occasion, it will be necessary to respond immediately to urgent questions from the P.I. and other managers if problems arise that impact the work flow or deadlines for the Center - these may require that extra hours be worked on a given day.

\* Application Process

The application process for UW positions may include completion of a variety of online assessments to obtain additional information that will be used in the evaluation process. These assessments may include Work Authorization, Cover Letter and/or others. Any assessments that you need to complete will appear on your screen as soon as you select ??Apply to this position??. Once you begin an assessment, it must be completed at that time; if you do not complete the assessment you will be prompted to do so the next time you access your ??My Jobs?? page. If you select to take it later, it will appear on your "My Jobs" page to take when you

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## UWindsor Canada FishIdentification

Fully-Funded M.Sc., M.A., Ph.D. and Post-Doctoral Positions: Genomic Network for Fish Identification, Stress and Health

Join a revolution in freshwater fish conservation!

Our Canada-wide, multi-million-dollar program will be a game-changer for freshwater fish management and conservation. We are looking for science and social science graduate students to: \* Get in on the ground floor in the rapidly growing area of environmental DNA research; \* Be part of the largest aquatic eDNA experiment ever undertaken; \* Develop the first universal transcriptional array for freshwater fish; \* Be among the first to explore the potential ethical and legal challenges in aquatic genomics-based research.

Develop a professional network working side-by-side with our partners from academia, industry and government while you work in a state-of-the-art lab or do fieldwork in the most remote areas of Canada...or both!

Opportunities are available for positions in British Columbia, Manitoba, Ontario, Quebec and New Brunswick starting in 2020 to 2024. Canadian citizens and landed immigrants will be given first consideration.

GEN-FISH is a collaborative research project established by the University of Windsor and partners and funded by Genome Canada and Agriculture and Agri-Food Canada.

To find out what GEN-FISH can do for you, visit our website at [www.gen-fish.ca](http://www.gen-fish.ca) or contact the GEN-FISH Research Coordinator at Sara.Jamieson@gen-fish.ca.

Sara Jamieson <saraj@uwindsor.ca>

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## VirginiaCommonwealthU Bioinformatics

Virginia Commonwealth University Center for the Study of Biological Complexity Faculty Position in Bioinformatics/Data Science

The Center for the Study of Biological Complexity (CSBC) at Virginia Commonwealth University invites applications for a full-time renewable term (non-tenure track) faculty position in Bioinformatics/Data Science with an anticipated start date of August 2020. As part of VCU Life Sciences (lifesciences.vcu.edu), the Center is committed to interdisciplinary training and research that connects investigators across the University. The Center administers bachelor's and master's degrees in Bioinformatics and participates in the interdisciplinary Integrative Life Sciences doctoral program, also housed within VCU Life Sciences. General information about the Center for the Study of Biological Complexity may be found at <https://cbds.vcu.edu>. Additional resources and facilities within VCU Life Sciences include the Center for Environmental Studies, Center for Life Sciences Education, the Rice Rivers Center, and the Center for High Performance Computing.

This faculty position is predominantly envisioned as a term (non-tenure track) teaching position at the rank of Assistant Professor. We seek a broadly trained computational scientist who will excel in teaching undergraduate and graduate courses in the Bioinformatics programs. Successful candidates will be expected to develop and teach innovative courses in programming with languages such as Python or R, biological informatics, data science, or computational biology; mentor undergraduate and graduate students; and have a commitment to outreach and service both within and beyond the University community. There may be opportunities to conduct research in parallel with the teaching commitment.

**Required Qualifications:** A master's degree (M.S.) in bioinformatics, data sciences, computer science, the biological sciences, biological education, or a related field; demonstrated experience in teaching and mentoring students. The successful candidate must also have demonstrated experience working in and fostering a diverse faculty, staff, and student environment or commitment to do so as a faculty member at VCU.

**Preferred Qualifications:** A doctoral degree (Ph.D.) in bioinformatics, data sciences, computer science, the biological sciences, biological education, or a related field; the ability to teach an introductory undergraduate Python course; demonstrated experience in development of teaching materials and assessment of student learning at the undergraduate and graduate levels; demonstrated interest and experience in biological or computational science pedagogy; demonstrated ability working with a diverse student population.

Interested applicants must apply online at <http://www.vcujobs.com/postings/96718> with cover letter; CV; a statement of teaching philosophy; a statement on con-

tributions to diversity, equity, and inclusion; and contact information for three references.

For additional information or questions, please contact the chair of the search committee Dr. Rodney Dyer at [rjdyer@vcu.edu](mailto:rjdyer@vcu.edu).

Virginia Commonwealth University is an equal opportunity, affirmative action university providing access to education and employment without regard to race, color, religion, national origin, age, sex, political affiliation, veteran status, genetic information, sexual orientation, gender identity, gender expression, or disability.

Michael S. Rosenberg <[msrosenberg@vcu.edu](mailto:msrosenberg@vcu.edu)>

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## WoodsHole RotiferGeneEditing

**Position Title:** Research Assistant or Research Associate

**Position Summary:** The Marine Biological Laboratory seeks a motivated, creative and innovative Research Assistant or Research Associate to join the laboratories of Kristin Gribble and David Mark Welch in the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution. Our research combines comparative genomics, biochemistry, and life history to study aging, maternal effects, and DNA damage prevention and repair using rotifers, a novel aquatic invertebrate model system for studies of aging, neurobiology, genome evolution, and ecology. The successful candidate will develop genome editing techniques in rotifers, including CRISPR/Cas9, as part of a broad initiative at the MBL to advance new aquatic and marine models for biological discovery. Research will take place in the Bay Paul Center, with extensive DNA sequencing and bioinformatic resources, and in the NSF-funded Genome Editing Facility in the Marine Resources Center, where MBL scientists are developing new genetic and genomic tools for a wide range of marine invertebrates. We invite individuals with experience in genome editing in other animals to join this expanding program.

**Basic Qualifications:** Research Assistant applicants should have a B.A., B.S., or Master's degree in biology, cell/molecular biology, biochemistry, or a related field. Research Associate applicants should hold a Ph.D. or have commensurate laboratory experience. This position requires proficiency and previous experience in molecular biology, microscopy, microinjection, and CRISPR/Cas9 methodology. We are seeking an independent, organized, enthusiastic, and productive individual



with robust problem solving skills. Excellent interpersonal skills, attention to detail, and a strong work ethic are essential. Position level and salary will depend upon education and experience.

**Preferred Qualifications:** The ideal candidate will have working familiarity with RNAi and transgenic protocols. Proficiency in bioinformatics is a plus. Previous experience in established animal model or in non-model systems is preferred.

**Physical Requirements:** Ability to work with biohazardous chemicals using proper personal protective equipment. Occasional lifting of heavy objects (30 lbs). Spe-

cial Instructions: Please apply of the MBL website and submit the following three items with your application: (1) Cover letter describing your experience, research goals, specific interest in joining our group, and what you would contribute to the project (2) CV/resume (3) Contact information for 3-4 references (Please do not send letters at this time; we will contact references directly).

Jennifer Larkum Bay Paul Center Administrator Marine Biological Lab 7 MBL St., Woods Hole, MA02543 (508) 289-7137; Fax: (508) 457-4727

Jennifer Larkum <jlarkum@mbledu>

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## Other

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## AmericanGeneticAssoc SpecialEventsAwards DeadlineJan31

The American Genetic Association grants awards each year to its members for support of special events that advance the mission of AGA, particularly to help students attend the event.

Eligible events include specialized workshops and short courses in topical areas of organismal genetics and genomics, but any event relevant to AGA's purpose will be considered, especially those that could lead to Journal of Heredity articles.

Awards are between \$1,000-\$15,000. Funding is competitive, and applications must follow the guidelines.

To apply, visit <https://www.theaga.org/> Anjanette Baker, AGA Manager

[theaga@theaga.org](mailto:theaga@theaga.org)

[theaga@theaga.org](mailto:theaga@theaga.org)

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## AMNH NewYorkCity WomenSTEMFellowship DeadlineExtended

Dear Colleagues,

The BridgeUP: STEM program at the AMNH is excited to announce that the application for the Helen Fellowship is open. This fellowship is a one-year residency for post-baccalaureate, self-identifying females, to devote time immersed in computational scientific research and educational outreach at the AMNH. This fellowship is an initiative at the AMNH dedicated to increasing the diversity of the talent pipeline by providing underrepresented students access to the skills and tools required for the 21st Century.

To learn more about the fellowship and the application process, visit <https://www.amnh.org/learn-teach/higher-education/helen-fellowship> . A colorful PDF flyer can be downloaded at this website.

Who is eligible to apply? The fellowship is intended for recent college graduates with a conferred bachelor's or master's degree in computer science, natural sciences, applied mathematics, computational science, or other

relevant majors prior to the fellowship start date in September.

What are the benefits? Fellows will receive an annual salary of \$70,000 plus generous benefits. Funding is also available for research, travel and equipment expenses.

How do I apply? The online application is now open and is due by midnight of February 2nd, 2020. To learn more about application requirements, visit <https://www.amnh.org/learn-teach/higher-education/helen-fellowship> . With Regards,

The BridgeUP: STEM Team

Email: [bridgeupstem@amnh.org](mailto:bridgeupstem@amnh.org)

[crowley@amnh.org](mailto:crowley@amnh.org)

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## ASN YoungInvestigatorAwards Jan15Deadline

The Jasper Loftus-Hill Young Investigator's Award of the American Society of Naturalists honors outstanding promise and accomplishments of young investigators who conduct integrative work in the fields of Ecology, Evolutionary Biology, Behavioral Ecology, and Genetics. Applicants working in any of these fields are encouraged to apply.

The award honors outstanding promise and accomplishments of young investigators (3 years post-Ph.D., or in the final year of their Ph.D) who conduct integrative work in ecology, evolution, behavioral ecology, and genetics. The award was established in 1984 to recognize exceptional work by investigators who received their doctorates in the three years preceding the application deadline, or who are in their final year of graduate school. The award commemorates Jasper Loftus-Hills (1946-1974), an Australian biologist of exceptional promise who died tragically during the course of fieldwork three years after receiving his degree.

Winners of this award will present a research paper in the Young Investigator's Symposium at the ASN annual meeting and receive a \$500 prize, a travel allowance of \$700, cost of registration for the meetings, and a supplement of \$500 in case of intercontinental travel. Four awards are made annually. Recipients need not be members of the Society.

Please see the ASN announcement for this award < <https://www.amnat.org/announcements/-NomYIAforms.html> > for more details on the

application process and how to apply. The award deadline is January 15th, 2020.

“Duckworth, Renee A - (rad3)”  
<rad3@email.arizona.edu>

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## ASSAB Student Research Grants

Applications for the Australasian Society for the Study of Animal Behaviour’s 2020 student research grants are now 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](http://www.assab.org/student-grants). Once completed, applications should be emailed in PDF format to [grants@assab.org](mailto: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](http://www.assab.org/student-grants)).

Dr. Thomas E. White Grants Officer Australasian Society for the Study of Animal Behaviour [www.assab.org](http://www.assab.org)  
ASSAB Grants Officer <[assabgrants@gmail.com](mailto:assabgrants@gmail.com)>

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## Best Graduate Student Paper Nominations

Best Graduate Student Paper of 2019

Dear SMBE Members,

SMBE is calling for nominations for Best Graduate Student Papers of 2019. These awards provide recognition

for outstanding papers in both our SMBE journals, Molecular Biology & Evolution (MBE) and Genome Biology & Evolution (GBE). There will be one Best Graduate Student Paper award for each journal.

All articles published in the calendar year 2019 are eligible for nomination. This corresponds to papers published in the printed volume 36 in MBE and volume 11 in GBE. Please see below for additional information on eligibility.

Winners will be given a certificate, a prize of \$2,000 and a travel award to either the 2020 or 2021 SMBE meeting.

Best Regards, Marta L. Wayne President, SMBE

Eligibility & Nomination

1. All articles published in the two SMBE journals, Molecular Biology & Evolution and Genome Biology & Evolution (one prize for each journal), in the calendar year 2019 are automatically eligible if the final publication date of the nominated paper is not more than two years later than the date of the nominee’s Ph.D.
2. The nominated graduate student must be the first author or joint first- author of the nominated paper.
3. An article and its first author can be nominated by anyone; self- nominations are acceptable.
4. A signed letter from the Ph.D. advisor, MSc advisor, or equivalent, confirming that the paper was part of the nominee’s thesis or graduate work is required.
5. The deadline for submitting nominations is March 11, 2020.

How to Enter

Please send the name of the nominee, a scan of the signed advisor letter, and the name of the paper for which the award is to be considered as a SINGLE PDF to [smbe@allenpress.com](mailto:smbe@allenpress.com). Please use the email subject line “MBE/GBE Best Student Paper Nomination”, deleting journal name as appropriate.

Society for Molecular Biology & Evolution  
[smbe@allenpress.com](mailto:smbe@allenpress.com)

Society for Molecular Biology & Evolution  
<[smbe@allenpress.com](mailto:smbe@allenpress.com)>

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## DelawareStateU SummerInternship EvolutionaryNeuroscience

The Delaware Center for Neuroscience Research is offering a summer research opportunity for undergraduate students who are interested in a career related to neuroscience research, and opportunities exist to study evolutionary neuroscience.

Students will spend 10 weeks over the summer carrying out neuroscience research with researchers at Delaware State University and the University of Delaware. The students, accompanied by their mentors, will also have the opportunity to travel to present their research at a regional or national conference.

Students accepted to the program will choose a faculty research mentor and will spend approximately 35 hours/week working in their mentor's laboratory. Students will also participate in career, academic and professional development activities. Participants in the program will receive a stipend of \$4,000 over the summer and will be eligible for additional travel support over the following academic year. Housing is available at Delaware State University for participants who need it. The program is open to undergraduate students who are US citizens or permanent residents or who have DACA status. Students must have completed at least 25 credits of college-level work, and will not receive a Bachelor's degree before December 2020. Students can be of any major as long as they have an interest and career plans related to neuroscience. Students in the program can work on projects on evolutionary neuroscience, as well as other topics in Neuroscience (e.g., the mechanisms of Alzheimer's disease, ALS, autism, fetal alcohol syndrome, spinal muscular atrophy, anxiety, epilepsy, Parkinson's disease, PTSD). If you are interested in opportunities in evolutionary neuroscience, contact Christine Charvet at [ccharvet@desu.edu](mailto:ccharvet@desu.edu) and/or specify Dr. Charvet as your mentor. The deadline is March 16, 2020; Apply here: <https://www.delawareneuroscience.org> [charvetcj@gmail.com](mailto:charvetcj@gmail.com)

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## EastCarolinaU Peru URA FrogColorEvolution

The Summers lab at East Carolina University is searching for an undergraduate student research participant to train and learn how to carry out research associated with a National Science Foundation (NSF REU) supported project focused on the genetic underpinnings of mimicry and color pattern evolution in a mimetic radiation of poison frogs in north central Peru (see description below), in the summer of 2020 (May 'V August). Desirable qualifications for this position include an interest in the ecology and evolutionary biology of tropical amphibians, coursework or experience in evolutionary biology and tropical ecology, and previous work with live animals (especially amphibians). The position will involve assisting graduate students on specific projects, and also learning how to gather data for a project they student take the lead on. This intensive field research training assistantship will be funded by a National Science Foundation Research Experience for Undergraduates award, and will provide funds for travel, living expenses, field supplies, and a stipend for three months. Fieldwork will involve long, hard days working under difficult conditions (heat, humidity, insects), and will require careful planning and perseverance. Knowledge of Spanish will be helpful for this work. The successful applicant will receive training in tropical biology and fieldwork in the rainforest, and will receive authorship on presentations and manuscripts to which she/he has made a substantial contribution. The trainee will submit a report and presentation after the research period that will describe how she/he has learned to approach these methods and concepts and how this has shaped his/her knowledge.

**Project Description:** The evolution of color pattern diversity in the context of mimicry has been a focus of theoretical and empirical attention, yet knowledge of the genetic basis of this diversity remains limited. This research project combines three research groups with complementary skills and realms of expertise to investigate the genetic basis and population genomic processes underlying color pattern divergence in the context of mimicry in the Peruvian mimic poison frog, *Ranitomeya imitator*: Dr. Kyle Summers (East Carolina University), Dr. Rasmus Nielsen (UC Berkeley) and Dr. Matthew MacManes (University of New Hampshire). The project focuses on four specific aims: 1. Identify key genetic factors involved in color pattern development in *R. imi-*

tator by investigating differential gene expression across developmental stages and color pattern morphs, in the field and in the laboratory. 2. Identify the causal gene(s) underlying differences in color pattern between morphs using genome-wide marker arrays (exome capture sequences) to screen transition zone samples and enable admixture mapping. 3. Test the association of specific candidate loci with color pattern using pedigree analyses of candidate genes identified from Aims 1 and 2, using a multigenerational pedigree. 4. Test specific hypotheses regarding selection and demographic processes in the transition zones and between mimics and models. Together these complementary, mutually reinforcing approaches will begin to reveal the genetic underpinnings and population genomics of color pattern diversity in this mimetic radiation of poison frogs.

The Department of Biology at ECU is large and multidisciplinary, with strong research groups in evolution, ecology, behavior and genomics: see [www.ecu.edu/biology](http://www.ecu.edu/biology) for more information. See <http://blog.ecu.edu/sites/-summersk/research-page/> for more information on previous research in the Summers lab. I encourage applications from minorities and under-represented groups of all kinds. Please send a letter detailing your research interests and experience, as well as a current CV (including coursework and grades), and the names and addresses of two references, to Kyle Summers ([summersk@ecu.edu](mailto:summersk@ecu.edu)). Please contact me with questions if you would like further information.

“Summers, Kyle” <[SUMMERSK@ecu.edu](mailto:SUMMERSK@ecu.edu)>

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## ESEB Conference Travel Awards Deadline Mar 15

### \*ESEB CONFERENCE TRAVEL AWARDS 2020\*

The European Society of Evolutionary Biology (ESEB) is pleased to announce the call for applications for conference travel awards 2020.

These stipends are for students and young scientists to attend the Evolution meeting (<https://www.evolutionmeetings.org/>) of ASN/SSB/SSE in Cleveland, OH, on 19-23 June 2020. The stipend will contribute to covering travel, living expenses, and early bird congress registration fees. Note that the registration fee will be waived by the congress organizers as part of the stipend. The remaining funds will be paid out as a reimbursement after the congress, based on specification of the expenses.

**\*\*DEADLINE: 15 March 2020\*\***

Eligibility:

- Applicants must be ESEB members before the deadline (for becoming an ESEB member, please visit <https://eseb.org/society/membership/>).
- Applications can be submitted by scientists at various stages of their professional career (e.g., Masters and PhD students, postdocs, and lecturers).
- Scientists working in a country with high GDP are not eligible (for the list of excluded countries see below).
- People who received an ESEB travel stipend in the last five years are not eligible.
- Applicants must submit to present either an oral communication or a poster to be eligible for the stipend. This will be verified before the reimbursement, but no proof that a poster or talk is accepted is necessary at the application stage.

PLEASE NOTE THAT THESE STIPENDS ARE GIVEN IN CONJUNCTION WITH ANALOGOUS STIPENDS OFFERED BY THE SSE (separate call), SO THERE IS NO NEED TO APPLY TO BOTH.

How to apply:

Send your application by email to the ESEB Travel Bursary Committee, c/o Dr. Martijn Egas ([egas@uva.nl](mailto:egas@uva.nl)).

The application should be no more than 2 pages long and include:

- Name of the applicant;
- ESEB membership number;
- Budget, including sources of additional support;
- An explanation of how attendance to the meeting will support the attendant's professional goals;
- and a short CV.

Please submit the application as a single PDF-file. A support letter from the applicant advisor/mentor/senior colleague is also required. Support letters should be sent to the same email address ([egas@uva.nl](mailto:egas@uva.nl)) by the applicant's mentor.

DEADLINE: 15 March 2020

Members professionally based in the following countries are not eligible for the travel stipend: Australia, Austria, Belgium, Canada, China,— Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Israel, Italy, Japan, Latvia, Lithuania, Luxembourg, Malta, Malaysia, Netherlands, New Zealand, Norway, Poland, Portugal, San Marino, Singapore, Slovakia, Slovenia, South Korea, Spain, Swe-

den, Switzerland, United Kingdom, United States of America.

Dr. Ute Moniatte | ESEB Office Manager | office@eseb.org European Society for Evolutionary Biology | [www.eseb.org](http://www.eseb.org) ESEB <office@eseb.org>

## Grants PlantFungalInvasions Brazil Jun20-23

Dear all,

We have a number of grants available for early career researchers (student and post-doctoral researchers with up to five years' experience since gaining/defending their PhD, excluding career breaks) wishing to attend the 45th NPS: Ecological and evolutionary consequences of plant-fungal invasions, which will take place in Campinas-SP, Brazil, on 20-23rd June 2020.

ECRs have until Thursday 19th March 2020 to apply ([www.newphytologist.org/grants/index/49](http://www.newphytologist.org/grants/index/49)).

Please share with anyone who may be interested in applying for a grant. Promotional tweet: [twitter.com/NewPhyt/status/1221742189878878208](https://twitter.com/NewPhyt/status/1221742189878878208) Facebook post: [facebook.com/NewPhytologist/photos/a.512921032100812/2812301975146528/](https://www.facebook.com/NewPhytologist/photos/a.512921032100812/2812301975146528/)

The poster abstract deadline is Thursday 16th April 2020 < <https://www.newphytologist.org/posters/index/49> >, and further information can be found on the symposium website: [www.newphytologist.org/symposia/45](http://www.newphytologist.org/symposia/45) . Please let me know if you have any questions.

Best wishes, Freja

Freja Kärman-Bailey (pronouns: she/her they/them)  
Events and Promotions Co-ordinator, New Phytologist Trust

New Phytologist Trust, Bailrigg House, Lancaster University, Lancaster, LA1 4YE, UK Tel: +44 1524 594691

The New Phytologist Trust, registered charity number 1154867

## MacquarieU VolFieldAssist AvianHybridZone

Volunteer (with expenses paid) field assistant position to study breeding ecology in the long-tailed finch hybrid zone in the Kimberley Region of Australia, March-June 2020

I am looking for an expenses-paid field assistant for the upcoming field season (March-June 2020) for my PhD project studying breeding behaviour of long-tailed finches in their genetic hybrid zone. The Kimberley is a striking and iconic but challenging area in the northern tropical savanna of Western Australia 'V it consistently reaches very high temperatures, but has amazing local wildlife, including rich and unique birdlife, and beautiful landscapes.

We are interested in the breeding behaviour and patterns where the two subspecies of long-tailed finch come into contact and will be monitoring breeding in nest-boxes set up around Kununurra township. We will collect an array of data, including banding adults and chicks, collecting blood and sperm samples, measuring body condition, and possibly performing some behavioural experiments. The work will be demanding, requiring long hours spent outside often in the heat while handling birds and recording data, and working well as part of the team. We can provide training for the techniques we use, but bird handling experience or previous field experience would be highly valuable. That said, enthusiasm and a positive attitude are the most important attributes someone could bring to the team. We will alternate between staying in a caravan park in town or in a national park close by. The costs for accommodation and travel around the field site will be paid for, as well as domestic travel to the field site 'V if you would be travelling from further afield, we can discuss possibilities on a case by case basis.

Applications should include a CV, a short letter outlining your interests and motivation and the name of two referees and can be sent to Callum McDiarmid at [callum.mcdiarmid@hdr.mq.edu.au](mailto:callum.mcdiarmid@hdr.mq.edu.au). They will reviewed as they are received, until the position is filled. If you have any further questions feel free to shoot me an email.

Callum McDiarmid ([callum.mcdiarmid@hdr.mq.edu.au](mailto:callum.mcdiarmid@hdr.mq.edu.au))

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## MolluscEvolution 2 Grants

\*Conchologists of America (COA) Academic Grants, 2020\* Deadline: February 28, 2020 Please see the website: <http://www.conchologistsofamerica.org/grants/>  
 \*Eligibility:\* - Degree-seeking students and anyone engaging in malacological research is eligible. - Persons of any nationality and country of residence may apply. - Applicants from previous years may re-apply. - Recipients of previous years may re-apply, but must include a submitted manuscript to or published article in the American Conchologist based on the previous award. - Degree-seeking students must have a letter of recommendation by their advisor emailed to \*jannvendetti@yahoo.com\* by the Feb. 28th deadline with the applicant's name in the subject line.

\* Rules & Guidelines:\* - All applications must be submitted via email in one file, preferably as a .pdf under 3 MB. Letters of recommendation may be sent separately. - The proposal must concern a malacological topic with any molluscan taxon or taxa as the focus, e.g., parasite studies should focus on the molluscan side of the interaction. All disciplines from autecology to zoogeography, including paleontology, are eligible. - The project must be self-contained. In other words, with the funding requested it must be possible to answer the question posed. However, the proposal may be a component of the applicant's overall research. - Major permanent equipment is not an allowable expense, but use of equipment at another institution is. For example, time using a piece of permanent equipment (for example, SEM beam time) is allowable. - Institutional overhead is not permitted. - The maximum award is US \$2500. Smaller requests, depending on costs and nature of research, may be more likely to receive funding. Partial funding is possible at the discretion of the Academic Grants Committee. - If a grant is awarded, please consider options to avoid having to pay personal income tax on it. Many educational and non-profit organizations manage such grants; please inquire with such entities. COA and/or its representatives are not liable for any tax consequences of the award. - All recipients are expected to submit a summary of their work to American Conchologist within 12 months of receiving the award. - All applications are evaluated by the Academic Grants Committee composed of three professional malacologists appointed by the Chair of the COA Academic Grants program. - Although any research topic within Mol-

lusca is eligible, there are several special categories for named awards focused on: 1) Ecology, Natural History, Systematics and taxonomy, 2) Museum-based research, 3) marine species from the Eastern United States (Atlantic), marine species from Florida and the Caribbean, 4) Behavioral and/or Chemical Ecology. - The decisions of the Committee are final.

\*Application: \* Must include 3 components: a proposal, budget, and CV. \*(6 pages at most)\*

- \*Proposal\* (4 pages at most): title, abstract of project, not to exceed 150 words, body including background information necessary to understand the project and its significance, materials and methods, and proposed plan of research, and illustrations if necessary, literature cited (included in page count, may be of slightly smaller font), single-spaced, 12 point font - \*Budget \*(1 page): list of estimated expenses, and if applicable, a list of grants applied to for the same/similar project. Reasonable per diem costs and housing are eligible expenses. - \*CV/Academic Biography \*(1 page): include address, phone number, email address, academic and/or relevant professional history

\*Suggestions:\* Keep the introduction short and relevant; consider that all committee members are broadly trained invertebrate zoologists. Provide justifications and details of analytical procedures including statistical analysis (which tests will be used and why those tests). Provide evidence that the techniques proposed are relevant and reasonably mastered. The inclusion of preliminary data is helpful, when applicable.

Applications are judged by the COA Grants Committee. Awardees will be notified via email in (or before) May 2019, then announced at COA's annual convention. Awardees need not be present at the convention.

THE DEADLINE FOR APPLICATIONS IS FEBRUARY 28 All application and recommendation (for degree-seeking students) must be emailed, preferably, as pdfs to: \*jannvendetti@yahoo.com

Jann Elizabeth Vendetti, Ph.D.

Assistant Curator & Twila Bratcher Chair in Malacology

\*Natural History Museum of Los Angeles County\*

900 Exposition Blvd., Los Angeles, CA 90007

—

\*The Western Society of Malacologists\* (WSM) is proud to offer a financial stipend for students to study fossil or recent malacological collections to further their research. This award honors the late James H. McLean, Curator of Malacology at the Natural History Museum of Los

Angeles County from

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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>

ology, University of Virginia 064C Gilmer Hall, P.O. Box 400327 Charlottesville, VA 22904-4327 USA +1-434-243-4989 o | +1-434-906-3122 c enagy@virginia.edu bio.as.virginia.edu/people/esn8n | mlbs.org

“Nagy, Eric S (esn8n)” <esn8n@virginia.edu>

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## MountainLakeBiologicalStation SummerReuProgram

[MLBS REU Program] < <https://mlbs.us14.list-manage.com/track/-click?udd2397558126f5ceb0c7824&id=Ee8ec01c8&ep206c726c> >  
2020 Summer NSF-REU Program at Mountain Lake Biological Station

Research Experiences for Undergraduates Become a National Science Foundation REU. Join undergraduates from around the country for a unique 10-week learning and living research experience in the southern Appalachians. Students conduct independent research in field ecology, evolution, behavior, and physiology under the supervision of resident scientists. REUs are internships that include all station costs, travel, and a \$6,000 stipend.

Program dates: May 25 - July 31 Application deadline: February 20

Learn More and Apply < <https://mlbs.us14.list-manage.com/track/-click?udd2397558126f5ceb0c7824&id8731c156c&ep206c726c> >

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Eric S. Nagy, Ph.D., Associate Director & Professor  
Mountain Lake Biological Station & Department of Bi-

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## NavjotSodhi ConservationStudentAward

Are you a passionate student from a developing country conducting research in tropical conservation biology?

Every year the Association for Tropical Biology and Conservation presents the Navjot Sodhi Conservation Research Award to a student from a developing country conducting research in tropical conservation biology. This award is in remembrance and recognition of the contributions of our colleague and friend Navjot Sodhi, who inspired many students and colleagues with his passion for research and the conservation of tropical biodiversity. The selected recipient will receive a cash award (up to \$500) to be used towards research-related expenses. Nominees must be members of the ATBC.

Send your application (or nominate someone!) to Lisa Davenport ( [ldavenport@parkswatch.org](mailto:ldavenport@parkswatch.org)) by February 29th, 2020.

Application guidelines: <https://tropicalbiology.org/-navjot-sodhi-award/> [magei@gmail.com](mailto:magei@gmail.com)

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## PLE UPittsburg EarlyCareerFellowship

The University of Pittsburgh’s Pymatuning Laboratory of Ecology (PLE) is pleased to offer the Frank J. Schwartz Early Career Research Fellowship of up to \$10,000 plus up to three months of station fees and residency costs for the primary investigator (PI). PLE is a vibrant research and education facility located on Lake Pymatuning in Northwest Pennsylvania. PLE’s research facilities are spread across 350 acres and include access to a variety of aquatic and terrestrial ecosystems. Its 10,000+ square feet of laboratory facilities include a field laboratory adjacent to an open field that can be



used for large-scale replicated experiments, a modern molecular laboratory, and facilities for animal, plant and aquatic studies. The station has been a site for research in ecology and evolutionary biology for nearly 70 years.

This opportunity is open to researchers holding PhD degrees in any science discipline that can benefit from PLE's resources (<http://www.biology.pitt.edu/facilities/pymatuning>). The purpose of the fellowship is to permit researchers to explore new projects or collect preliminary data. Fellowship funds can be used at the PI's discretion to facilitate the research but not for PI compensation. Preference will be given to individuals and projects with the potential to develop into long-term research activities at PLE. We especially encourage applications from individuals in the postdoctoral or early faculty phases of their careers, but researchers holding PhD degrees at all stages of their careers are also encouraged to apply. We welcome projects related to the study of evolution.

"Zawacki, Corinne Lee" <cori.zawacki@pitt.edu>

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### Short Video Contest Success Stories In Conservation Biol

Short Video Contest: Success Stories in Tropical Biology and Conservation

In partnership with Mongabay, BAND Foundation, and the Smithsonian Earth Optimism Summit, the Association for Tropical Biology and Conservation is hosting the ATBC Short Video Contest on Science Communication with the theme "Success Stories in Tropical Biology and Conservation".

Deadline for submissions: \*\*\* FEBRUARY 10 \*\*\* Submit here: <https://filmfreeway.com/ATBCvideocontest>

Biodiversity refers to the variety of life on Earth in all of its levels, constituting an integral component of any ecosystem. Despite that, we are currently facing an alarming biodiversity loss due to species displacement or extinction, especially in the Tropical regions of the World. Humans are capable of incredible growth, learning, resilience, and change in the face of challenge. We need to tap into these core traits to step up to the growing challenges facing biodiversity and our ecosystems. \*Create a short video that shares your success conservation story, biodiversity research, opportunity, and/or optimism for tropical biology and conservation\*. Videos must be no longer than four minutes, including title and credits. Creativity is encouraged, and partici-

pants may use various forms of media, including slow motion, animation, illustration, and claymation, among others.

All three (3) winners will be notified by email on or around February 20, 2020. The winners will be invited to attend the Smithsonian Earth Optimism Summit <<https://earthoptimism.si.edu/>> in Washington, D.C. on April 23-25, 2020. Winners will also have a chance to attend the Earth Day Rally on the National Mall, which follows immediately after the end of the summit on April 25. The winner will have the opportunity to speak about their conservation work and show their video at a summit session organized by the Smithsonian Institution. Airfare, lodging, and registration fees will be fully covered but winners will be responsible for obtaining a visa to attend the summit.

communications@tropicalbio.org

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### SMBE Nominations President-Elect Treasurer 2 Councillors

Subject: SMBE - Nominations for President-elect, Treasurer and 2 Councillors

\*Nominations for President-elect, Treasurer \*\*and\*\* 2 Councillors\* \*due by Wednesday, March 11th, 2020\* Dear SMBE Members,

I am writing to solicit nominations for SMBE President-Elect, Treasurer and 2 Councillors, whose terms will begin on January 1, 2021. All of these positions are for a duration of three years. As the society grows and thrives, council members play important roles in guiding its development and in soliciting and implementing programs that support our members, enrich opportunities for young scientists from around the world, and oversee our two excellent journals (\*MBE\* and \*GBE\*) as well as our annual meeting and satellite meetings.

Nominations will be reviewed by the Nomination Committee\* who will then put forward a slate of two candidates for each position for membership vote. Past and current council members are listed at [\\*https://www.smbe.org/smbe/ABOUT/Council.aspx\\*](https://www.smbe.org/smbe/ABOUT/Council.aspx) <<https://t.e2ma.net/click/9m73qb/duvmg1/dqwkch>>

\*Please send nominations with a brief statement in support of your suggestion (self-nominations are accepted) to: M.Mar Albà (mar.alba@upf.edu <mar.alba@upf.edu>) and Nadia Singh (nsingh@uoregon.edu <nsingh@uoregon.edu>).\*

Nota bene: we ask the nominators to confirm \*explicitly\* that the person they are nominating has already confirmed their willingness to run for office.

\*Please send your nominations by Wednesday, March 11, 2020.\*

We look forward to hearing from you.

Yours sincerely,

Nadia Singh Secretary of SMBE, on behalf of the Nomination Committee\*

\*The Nomination Committee is composed as follows: M.Mar Albà (Chair), Universitat Pompeu Fabra, Barcelona Maria Anisimova, Zurich University of Applied Sciences Tom Gilbert, University of Copenhagen Nancy Moran, University of Texas, Austin Yoko Satta, Graduate University for Advanced Studies in Hayama Nadia Singh (\*ex officio\*), University of Oregon

Society for Molecular Biology & Evolution [smbe@allenpress.com](mailto:smbe@allenpress.com)  
[smbe@allenpress.com?subject=>](mailto:smbe@allenpress.com?subject=>) \*Share this email.\* \*Manage\* your preferences | \*Opt out\* using \*TrueRemove\* Got this as a forward? \*Sign up\* <<https://app.e2ma.net/app2/audience/signup/77681/-25123.88736291/>> to receive our future emails. View this email \*online\* <<https://t.e2ma.net/message/-9m73qb/duvmg1>>. 810 East 10th Street Lawrence, KS | 66044 US <#m.-3849504825005021107.> This email was sent to [smbe.contact@gmail.com](mailto:smbe.contact@gmail.com). \*To continue receiving our emails, add us to your address book.\*

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

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

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## SouthAfrica VolResAssist MoleRat

The Kalahari Mole-Rat Project run by the University of Cambridge (UK) is looking for several volunteer research assistants to carry out exciting experiments with captive Damaraland mole-rats, cooperatively breeding subterranean rodents, at the Kuruman River Reserve in the South African Kalahari Desert.

Our research broadly investigates the influence of genes, hormones, breeding and social factors on individual developmental, growth, behaviours and ageing.

This position is particularly suited, but not exclusively, for people aiming to carry on their academic education or hold a management position in a research project. Successful applicants can expect to gain invaluable experience in animal handling procedures and in conducting and managing experiments.

They will also gain database skills (MySQL) and will be provided with the opportunity to work on a personal analysis project. Costs of food and accommodation while at the project will be covered. A contribution towards travel costs will be made (300 Euros/Year) Applicants should be available for a period of 6 to 12 months, starting February-May 2020. They should be hardworking, enthusiastic, physically fit, and prepared for long hours in the laboratory. Successful applicants will be responsible to run experiments and will be involved in data collection (behavioural observations, collection of biological samples), data editing and animal handling.

If you are interested in this position send your CV and cover letter stating your availability to [molerat.volunteer@gmail.com](mailto:molerat.volunteer@gmail.com). Shortlisted applicants will be invited for a Skype interview.

Deadline: 28th February 2020 (spontaneous applications beyond this date are welcome)

Philippe Vullioud <[philippe.vullioud@gmail.com](mailto:philippe.vullioud@gmail.com)>

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## SouthAfrica Volunteer StripedMouseProject

Volunteers needed throughout 2020

Minimum stay 2 months

Evolution and Socio-Ecology of Small Mammals in the Succulent Karoo of South Africa

(NOTE: This is an unpaid volunteer position. We currently also advertise 2 paid positions as field managers for 1.5 to 3 years, and 1 postdoc position for 2 years. See other advertisements or ask via email [carsten.schradin@iphc.cnrs.fr](mailto:carsten.schradin@iphc.cnrs.fr))

**Opportunity:** This is a great opportunity for anybody who wants to get more experience in field work related to animal behavior, evolution, eco-physiology, and ecology before starting an MSc or PhD project.

**Project:** We study the evolutionary and ecological reasons as well as physiological mechanisms of group living, solitary living, and social flexibility in the striped mouse and the bush Karoo rat. One focus is on the adaptation to droughts, combining physiological, behavioral, ecological and evolutionary research. As these species are diurnal and the habitat is open, direct behavioral observations in the field are possible.

**What kind of people are needed?** Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5:30 and 7 AM), and stops its activity with dusk (7 PM). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40°C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

**Work of volunteer field assistants:** Trapping, marking and radio-tracking of small mammals; direct behavioral observations in the field. Volunteers will also see how blood samples are collected for physiological measurements and possibly (depending on the month) how we measure metabolic rate. Volunteers are expected to help with maintenance of the research station (water pump, solar power, etc.).

**Confirmation letter:** Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

**Costs:** Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1750 (around 110 Euro) must be paid for accommodation at the research station. Students must buy their own food in Springbok. Including extras (going out for dinner; shopping), you should expect costs of about 500

Euros or 600 US\$ per month.

German students can apply for a grant from the Deutsche Akademischer Auslandsdienst (DAAD, [www.daad.de](http://www.daad.de)). Here, commonly travel grants of 300 Euro are given to students. Students from other countries are encouraged to seek funding from their home institutions / home country. Students get an invitation letter which they can use to apply for funding in their home country.

**Place:** The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa close to Namibia. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

**When and how long:** We are looking for volunteers throughout 2020, though especially for the period January to July.

**How to apply?** Send a short motivation letter stating why and for which period you are interested and your CV via email to [carsten.schradin@iphc.cnrs.fr](mailto:carsten.schradin@iphc.cnrs.fr).

More information under

<http://www.strippedmouse.com/documents/-GeneralInformationResearchStationJan2018.pdf>

[http://strippedmouse.com/site1\\_3.5.htm](http://strippedmouse.com/site1_3.5.htm) Carsten Schradin <[carsten.schradin@iphc.cnrs.fr](mailto:carsten.schradin@iphc.cnrs.fr)>

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## SouthernAppalachianBotanicalSociety StudentGrants

The Southern Appalachian Botanical Society is now accepting applications from student members for the following awards. Note that students must be members of SABS to be eligible for these awards.

**Earl Core Student Research Award** - Up to \$1200 for research in plant taxonomy, systematics, or ecology. Deadline for applications is Feb. 21, 2020. More details can be found at [https://sabs.us/earl-core-student-research-award/?mc\\_cid=dbdfd89332&mc\\_eid=4dcd129a08](https://sabs.us/earl-core-student-research-award/?mc_cid=dbdfd89332&mc_eid=4dcd129a08) .

**John E. Fairey - Biological Field Station Scholarship** - Support for students to attend a botanical workshop or course at a field station of their choosing. Deadline for applications is March 23, 2020. More details can be found at [https://sabs.us/biological-field-station-scholarship/?mc\\_cid=3Ddbdfd89332&mc\\_eid=4dcd129a08](https://sabs.us/biological-field-station-scholarship/?mc_cid=3Ddbdfd89332&mc_eid=4dcd129a08) . Travel support to attend the Association

of Southeastern Biologists Meeting - \$300 award for support to attend and present at the ASB meeting. Deadline is Feb. 14, 2020. More details can be found at [https://sabs.us/student-awards-and-scholarships/?mc\\_cid=dbdfd89332&mc\\_eid=4dcd129a08#conference](https://sabs.us/student-awards-and-scholarships/?mc_cid=dbdfd89332&mc_eid=4dcd129a08#conference). Lisa Wallace, Ph.D. Associate Professor and J Robert Stiffler Professor of Botany Mailing Address: Old Dominion University Department of Biological Sciences Mills Godwin Building Rm. 110 Norfolk, VA 23529 Phone: 757.683.4947 Email: lewallac@odu.edu Website: <https://fs.wp.odu.edu/lewallac/> lewallac@odu.edu

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### SSE Diversity Committee New Members Deadline Extended

The deadline to apply to join the SSE Diversity Committee has been extended due to the Martin Luther King Jr. holiday coinciding with the previous deadline. The new deadline is this Friday, January 24.

The SSE Diversity Committee (DC) seeks to add two new members starting in 2020. The DC works to create a professional society that is supportive of members from all backgrounds through several main actions: by broadening representation to the SSE Executive Council, by pursuing initiatives that support underrepresented groups, and by creating an inclusive, accessible environment at the Evolution conference.

Applicants should submit a brief (1-2 page) statement of interest outlining their experience with Diversity, Equity, and Inclusion (DEI) service, and the ideas, events, and perspective they plan to contribute during their 3-year term. The DC seeks diverse members who represent different backgrounds and perspectives. Thus, we ask that applicants describe particular elements of their background and/or identity that will contribute uniquely to the composition of the DC. Applicants should also identify their career stage and affiliation, as we welcome participation from members of the community across all stages of their training, and in all career paths.

Applicants must be members of SSE (join or renew your membership here: <http://bit.ly/joinSSE>) and have attended at least one Evolution conference in the past. These items should also be mentioned in the application statement.

Many of the DC's initiatives are created and operated with the DCs of our sister societies, the American Society of Naturalists and the Society for Systematic Biologists. Past or ongoing efforts of the SSE DC include:

- Data collection and analysis regarding the demographic composition of SSE
- Creation of guidelines on best practices for awards procedures
- Events at the Evolution meeting including Story Collider and mixers to build community among LGBTQ+ biologists, biologists with disabilities, biologists of color, biologists at PUIs, and parents
- Improving accessibility at the Evolution conference for scientists with disabilities, scientists of marginalized genders, and scientists who are nursing/caretaking

More information about the SSE DC and our prior initiatives can be found on our web page: <http://bit.ly/SSE Diversity>. Please submit your application by January 24, 2020 to [diversity@evolutionsociety.org](mailto:diversity@evolutionsociety.org). Questions may also be directed to this email address.

\*Kati Moore\*she/her/hers \*Communications Manager\*  
\*Society for the Study of Evolution\*  
[communications@evolutionsociety.org](mailto:communications@evolutionsociety.org)  
[www.evolutionsociety.org](http://www.evolutionsociety.org) SSE Communications  
<[communications@evolutionsociety.org](mailto:communications@evolutionsociety.org)>

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### Symposia Funding Call New Phytologist

Funding of up to 43k is available to run New Phytologist Symposia and Workshops, with slots available for 2022 onwards. The application deadline for Symposia proposals is 29 February 2020.

The internationally renowned series of New Phytologist Symposia supports emerging and key areas of research. These meetings usually last between one and three days, with invited speakers and a maximum of 120 delegates. In this way we hope to provide an informal atmosphere for the stimulation and exchange of ideas and the building of collaborations. We particularly encourage the involvement of early career researchers, and as such a number of travel grants will be awarded in association with each meeting.

If you are interested in organising a New Phytologist Symposium, please complete the proposal pro forma <<https://www.newphytologist.org/news/view/145>> and email this to Freja ([np-symposia@lancaster.ac.uk](mailto:np-symposia@lancaster.ac.uk)) by 29 February 2020. Feel free to get in touch with any queries or for guidance on completing the proposal.

We also welcome workshop proposals throughout the



ful especially for future Master or PhD student §this work can be part of a small project to get credit points from an university.

How to apply: If you are interested in this position or need more information, you can send an email to [nolwenn.fresneau@gmail.com](mailto:nolwenn.fresneau@gmail.com). Application should be sent by the 1st of March 2020 the latest to this email address with “Volunteer position application” as the subject. It should contain a CV including the name and e-mail contact of at least two referees as well as a cover letter.

We will notify the successful shortlisted candidates on the 6th of March 2020 the latest and job interview by skype meeting will be held during the week of the 9th of March 2020. Decision will be made around the 13th of March 2020. \*Nolwenn Fresneau\* \*PhD\* \*University of Pannonia, Veszprém, Hungary\* \*Twitter: @NolwennFresneau\*

[nolwenn.fresneau@gmail.com](mailto:nolwenn.fresneau@gmail.com)

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## UIdaho-Galapagos SummerREU EvolutionaryEcol

The Parent lab (<http://parentlab.weebly.com>) is looking for undergraduate students to assist with field research in the Galapagos Islands. The undergraduate students will spend approximately 10 weeks (May 25 - July 31 2020) conducting research in collaboration with a research team composed of 3 Faculty, 1 postdoc, 2 graduate students and at least 1 additional undergraduate student. Various research projects are possible, including population genomics, island biogeography, invertebrate physiology, biomechanics, morphometrics, etc.

The research involves traveling to the Galapagos Islands, hiking long distances carrying field equipment on difficult terrain, backpacking and camping in remote locations, and working long hours in the laboratory to generate genomic data or measure physiological response and biomechanical variables in terrestrial invertebrates. The students will also participate in outreach activities in local schools in Galapagos.

We are looking for applicants with at least some of the following experience and skills: - Good communication skills and desire to work as part of a team - Patience and attention to details - Prior research in biology (e.g., genomics, genetics, physiology, biomechanics, ecology, etc.) - Ability to travel internationally (current valid

passport is required) - Ability to speak Spanish - Experience backpacking and camping in remote locations

Please contact Dr. Christine Parent at [ceparent@uidaho.edu](mailto:ceparent@uidaho.edu) with any questions.

To apply, follow instructions here: <https://www.uidaho.edu/sci/biology/research/summer-reu/application-process> The deadline to submit an application is Feb 14, 2020.

“[ceparent@uidaho.edu](mailto:ceparent@uidaho.edu)” <[ceparent@uidaho.edu](mailto:ceparent@uidaho.edu)>

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## UIowa REU Evolution

Please share with undergraduates who would stand to benefit from research experiences in areas related to evolution, including anthropology and paleontology.

The University of Iowa is offering ten NSF-funded Research Experiences for Undergraduates (REU) opportunities during the summer of 2020. Research projects span a range of topics, including evolution of behavior, origin of species, cancer evolution, evolution of sex, evo-devo, and paleontology. REU students work on one project, but through interactions with their cohort ultimately receive a broad exposure to evolutionary science. As part of the program, students: receive training in research best practices, participate in career workshops, create a digital exhibit based on their research for the University of Iowa Natural History Museum, and make formal research presentations based on their work. Free housing, a meal allowance, a \$6000 stipend, and a travel allowance will be provided to all participants. Students from underrepresented minority groups and/or who have limited research opportunities at their home institution are especially encouraged to apply.

The REU program website and application form can be found here: <https://biology.uiowa.edu/reu> If you have questions, contact Andrew Forbes ([andrewforbes@uiowa.edu](mailto:andrewforbes@uiowa.edu)) or Maurine Neiman ([maurine-neiman@uiowa.edu](mailto:maurine-neiman@uiowa.edu)).

Maurine Neiman Associate Professor Department of Biology & Department of Gender, Women’s and Sexuality Studies, University of Iowa Editor & Preprint Editor, Proceedings of the Royal Society of London B [maurine-neiman@uiowa.edu](mailto:maurine-neiman@uiowa.edu) <http://bioweb.biology.uiowa.edu/-neiman/> Twitter @mneiman

[maurine-neiman@uiowa.edu](mailto:maurine-neiman@uiowa.edu)

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## UMaine UndergraduateSummerRes EvolBiology

The University of Maine Initiative for One Health and the Environment is excited to announce an NSF-funded Research Experience for Undergraduates (REU) program for summer 2020. Our fully paid summer program will focus on Accelerating New Environmental Workskills (REU ANEW). From June 1 to August 8, 2020, we will invite 10 motivated undergraduate students to join our faculty and graduate students to conduct cutting-edge research at the intersection of human, animal, and environmental health. REU ANEW students will have the opportunity to work directly with faculty research mentors, as well as Broader Impacts mentors who are working in the field to apply One Health research to real world problems. Through our program, students will develop critical research and thinking skills that are directly relevant to future career success, and build lasting professional relationships with their undergraduate peers, graduate students, and faculty and broader impacts mentors. All REU participants will receive a generous stipend and living expenses, including partial travel expenses and housing at the University of Maine in Orono.

This year, several faculty mentors have projects of potential interest to students studying evolutionary biology, including research into the genetic basis for disease in wild and domestic animals, host-pathogen co-evolution, and adaptation to other environmental stressors. For more information about these projects and several others, and to apply, visit <https://nsfa.umaine.edu/one-health/REU>. Students should apply by January 31 for full consideration. Direct any questions you have about the program or the application process to [anne.lichtenwalner@maine.edu](mailto:anne.lichtenwalner@maine.edu).

Kristina Cammen <[kristina.cammen@maine.edu](mailto:kristina.cammen@maine.edu)>

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## Yukon KluaneRedSquirrelProject FieldInterns

\*Field Assistants Required for 2020 Kluane Red Squirrel Project, Yukon, Canada\*

\* We are looking for field technicians to assist with fieldwork that will run from February 8 to Oct 10 2020. We are looking for technicians for the following different time periods: (a) February 7 to May 31 (b) March 1 to May 31, (c) May 1 to July 1, or (d) Aug 15 to Oct 10. \*

\* The positions are part of a long-term study of red squirrel ecology, evolutionary biology and physiology. As a member of the study, technicians will be involved with monitoring the reproduction and survival of individual squirrels. Fieldwork will involve live-trapping and handling of squirrels, radio-telemetry, behavioural observation, and locating young in their nests. This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal.\*

\*All fieldwork is carried against the beautiful backdrop of southwestern Yukon, Canada. We will be staying at a rustic field station two hours from Whitehorse, and ~30 min to the nearest town (Haines Junction). All food and accommodation are provided and technicians are provided with transportation to and from the field site either through airfare or vehicle.\*

Training will be provided and no experience is necessary. Candidates should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. The field camp is remote and low tech (no showers, cell phone service, or internet), so successful applicants must enjoy the outdoors and be able to remain a positive and responsible team member under relatively isolated and demanding conditions. Candidates must be in good physical condition and have an enthusiasm for learning as well as a strong work ethic. KRSP aims to be a welcoming, safe, and inclusive research group and we strongly encourage applications from underrepresented groups. If you wish to apply for one of these posts then please fill out those Google Form (<https://forms.gle/gV3b9tHNAPN6rj367>) by \*January 31 2020\* for the spring positions (Feb-May). Application deadline for the autumn (Aug-Oct) positions is rolling. Please feel free to contact us at [kluanered squirrels@gmail.com](mailto:kluanered squirrels@gmail.com) if you have any questions.

[kluanered squirrels@gmail.com](mailto:kluanered squirrels@gmail.com)

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### AarhusU BiodiversityBioinformatics

3-year postdoc position in environmental DNA analyses of biodiversity with strong focus on bioinformatics

The Department of Bioscience, Aarhus University, Den-

mark, invites applications for a 3-year postdoc position in environmental DNA analyses. The position is available from 1st of April 2020.

We are seeking a highly-motivated postdoc to work with high-throughput eDNA analyses from a range of different environmental samples - water, soil, plants and faecal samples - collected along latitudinal and environmental gradients. Samples will be analysed using a Tree-of-Life metabarcoding framework in association with environ-



mental variables to test fundamental assumptions about the distribution of biodiversity. A major component of the work will be development and improvement of bioinformatics pipelines to analyse eDNA data from next-generation sequencing. There will also be opportunities for developing own research ideas related to environmental DNA and molecular ecology in collaboration with the group.

Applicants must have a PhD degree or equivalent, or have submitted their PhD thesis for assessment before the application deadline. We seek a candidate with expertise in: -Bioinformatics and statistical analyses of next-generation sequencing data. -Ecological data analyses, hereunder experience with R -DNA laboratory work (preferably eDNA) -Field work The candidate is expected to have good collaborative skills and proven abilities to publish at a high international level as well as experience in project management. The successful candidate will also be responsible for the daily management of his/her research project in coordination with other members of the group, and will be actively involved in the training and co-supervision of other staff members and students.

Applications must be submitted online and received by 20th of February 2020. Apply here: <https://international.au.dk/about/profile/vacant-positions/job/3-year-postdoc-position-in-environmental-dna-analyses-of-biodiversity-with-strong-focus-on-bioinform/> Philip Francis Thomsen, ph.d. Associate Professor Department of Bioscience Section for Genetics, Ecology and Evolution University of Aarhus Ny Munkegade 116 Building 1540 8000 Aarhus C Denmark email: pftthomsen@bios.au.dk phone: +45 27142046 skype: philip.francis.thomsen

Philip Francis Thomsen <pftthomsen@bios.au.dk>

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## ArizonaStateU GenomicsOfDogAging

Dr. Noah Snyder-Mackler at Arizona State University is looking for a postdoctoral researcher to join the Dog Aging Project, a large-scale nationwide longitudinal study of aging in companion dogs, to explore epigenomic and metabolomic aging.

Our goal is to understand how DNA methylation and chromatin accessibility change in dogs during the aging process, to identify specific loci that are altered dur-

ing the aging process, and to establish an “epigenetic clock” for aging in companion dogs. To this end, we seek a postdoc who will be part of our team and lead the molecular and computational components of this project. Working closely with our research technician who will prepare the samples, the postdoc will lead the analysis and interpretation of epigenomic and/or metabolomic data.

We are seeking someone with a PhD in biology, genomics, computational biology, or a related field, and who has strong molecular wet lab and computational skills. Experience with epigenomics and, in particular, next-generation sequencing data generation and analysis are essential. Strong organizational skills are a must, as this project comprises thousands to tens of thousands of samples.

The Postdoctoral Researcher will:

Design and carry out pilot experiments under the supervision of Dr. Snyder-Mackler and Dog Aging Project PI, Dr. Daniel Promislow (University of Washington). Coordinate the epigenomic and metabolomic data generation and analysis. Data will be generated by our research technician Establish a robust and standardized pipeline for the above steps, including an efficient and well-organized workflow for scaling up the project to ~1,100 samples per year. Analyze epigenomic and metabolomic data generated from ~1,100 dogs per year. Write up and publish results. Contribute to regular lab meetings and one-on-one discussions about project design and progress. REQUIREMENTS: PhD in biology, genomics, computational biology, or a related field.

If interested, please send your CV and a cover letter to Dr. Snyder-Mackler: nsnyderm@asu.edu.

Noah Snyder-Mackler

Assistant Professor School of Life Sciences Center for Evolution and Medicine Arizona State University 214 Life Sciences C <http://smack-lab.com/> Co-director, Simien Mountains Gelada Research Project <https://geladaresearch.org/> Please join me and my family in our fight against ALS write to me or log on to: The ALS Association of Philadelphia

Noah Snyder-Mackler <nsnyderm@asu.edu>

## Barcelona ChromatinEvolution

Postdoctoral Fellow: Evolution of Chromatin Architecture

The role: The successful candidate will comparatively study the regulatory genome architectures of phylogenetically diverse animal species (and closely related unicellular allies) to understand the evolution of multicellular gene regulation. The position will entail both performing chromatin profiling experiments (mostly HiC/HiChIP), as well as analysing and integrating this data to derive evolutionary insights. The work will be part of our ERC-funded project EvoCellMap, which aims at understanding how animal cell type and the associated genome regulation originates and evolves. The candidate will be part of a highly interdisciplinary, international and dynamic team composed by the Sebe-Pedros and Marti-Renom groups, which include developmental, computational, evolutionary and molecular biologists.

About the teams: The Sebe-Pedros Group (<https://www.crg.eu/en/programmes-groups/sebe-pedros-lab>) studies genome regulation from an evolutionary systems perspective. In particular, we are interested in deciphering the evolutionary dynamics of animal cell type gene regulatory networks and in reconstructing the evolution of genome regulatory mechanisms (from transcription factor binding through chromatin states to the physical architecture of the genome). To this end, we combine phylogenetics tools with functional genomics and proteomics methods (chromatin profiling, single-cell genomics) in order to characterize and compare cell types and epigenomic landscapes in non-model animal and other eukaryotic species. The Marti-Renom Group (<http://marciuslab.org>) at the National Center for Genomic Analysis - Centre for Genomic Regulation (CNAG-CRG) develops and uses experimental and computational approaches for characterizing the molecular regulation of cells by studying the structure of macromolecules and their complexes. In particular, we focus on regulatory molecules such as RNA and chromatin.

Additional details: <https://recruitment.crg.eu/content/jobs/position/evolution-chromatin-architecture-postdoctoral-fellow> Dr. Arnau Sebe-Pedros Group Leader, Systems Biology Program Centre for Genomic Regulation (CRG) Barcelona Spain

Arnau Sebe Pedros <arnau.sebe@crg.eu>

## Budapest 2 EvolutionaryGenomics

ERC.2.EvolutionaryGenomics

Postdocs in evolutionary genomics and phylogenomics are available to join the ERC 'GENECLOCKS' project (<http://cordis.europa.eu/project/rcn/207593.en.html>) headed by Gergely Szollosi (<http://solo.web.elte.hu>). Two positions are offered for 2 years with the possibility of a one year extension. The position comes with a salary of up to EUR 43,200 per year (approx. up to EUR 2,400-2,900 net per month after taxes), as well as a travel and research funds.

We are looking for an individual who received his or her PhD preferably within the last six years, who is highly self-motivated and can work independently on a project that he or she will help develop in the context of GENECLOCKS.

A central theme of GENECLOCKS is disclosing new sources of information for dating the first three-quarters of Earth's evolutionary history that are independent from both fossils and molecular clocks. Life's early history has remained terra incognita until now, because the fossils needed to calibrate standard evolutionary timescales are simply not available for microbial life. Microbial fossils are scarce and difficult to interpret in a phylogenetic context with confidence. In previous work we have shown that patterns of lateral gene transfer inferred from modern genomes encode a record of co-existing lineages throughout the history of life, and that we can use this record to reconstruct the relative ages of microbial groups from the three domains of life in deep time.

This discovery is a game changer for anyone interested in the history of life, from either a geological or genomic perspective. It demonstrates the existence of a new and abundant source of dating information that is inscribed in the genome of any organism, provided a gene transfer occurred in its ancestry. This constitutes the overwhelming majority of the diversity of life.

Postdocs will undertake projects together with international collaborators with the goal of either i) developing new methods that systematically extract information on the pattern and timing of genomic evolution by explaining differences between gene trees, or ii) apply existing methods to resolve the timing of microbial evolution and its relationship to Earth history and answer long stand-

ing questions. Possible collaborations and associated projects include:

Reconstructing a dated phylogeny of Eukaryotes including their position within Archaea in collaboration with Tom Williams at the University of Bristol.

Implementing and applying methods to include transfer derived relative age constraints in molecular clock estimates with Bastien Boussau and Vincent Daubin at the LBBE in Lyon.

Developing novel species-tree aware phylogenetic methods with the guys who make RAxML at Exelixis Lab in Heidelberg and Nicolas Lartillot at the LBBE in Lyon.

Developing new hierarchical probabilistic models of gene tree-species tree reconciliation with Sebastian Höhna at LMU in Munich.

Research visits of up to several months are foreseen as part of potential collaborations.

Recent GENECLOCKS publications:

AA Davín, E Tannier, TA Williams, B Boussau, V Daubin, GJ Szöllősi Gene transfers can date the tree of life *Nature ecology & evolution* 2 (5), 904 (2018) <https://doi.org/10.1038/s41559-018-0525-3> pdf: [http://ssolo.web.elte.hu/Davin\\_2018\\_NEE.pdf](http://ssolo.web.elte.hu/Davin_2018_NEE.pdf) TA Williams, C Cox, P Foster, GJ Szöllősi, T Embley Phylogenomics provides robust support for a two-domains tree of life *Nature Ecology and Evolution* (2019) <https://doi.org/10.1038/s41559-019-1040-x> pdf: [https://ssolo.web.elte.hu/Williams\\_2019\\_NEE.pdf](https://ssolo.web.elte.hu/Williams_2019_NEE.pdf) D Schrepff, N Lartillot, GJ Szöllősi Scalable empirical mixture models that account for across-site compositional heterogeneity *BioRxiv preprint* (2019) <https://doi.org/10.1101/794263>

GeneRax: A tool for species tree-aware maximum likelihood based gene tree inference under gene duplication, transfer, and loss B Morel, AM Kozlov, A Stamatakis, GJ Szöllősi *BioRxiv preprint* (2019) <https://doi.org/10.1101/779066> To be considered, please send a single merged PDF to [ssolo@elte.hu](mailto:ssolo@elte.hu) that contains your CV including publication list, preferably with a link to your google scholar profile, academic transcripts, a statement of research interests (3 pages or less) as well as three academic references. Please include 'GENECLOCKS2020' in the subject of your email. Applications will be considered until the position is filled with first round of selection

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## Caen France MicrobiomeDynamics

Postdoc position - Dynamic'H project Dynamic of respiratory Microbiome in Human Untangling the microbiome interplay with human respiratory viral infections

A two-year postdoctoral position, with an attractive salary, is available starting from January / February 2020 in the historical, cultural and university city of Caen, Normandy. The post-doc will be hosted in a young and dynamic team, the Virology Department of the University Hospital of Caen, Normandy (National Reference Center & WHO Coll. Center for Measles, Rubella and Mumps viruses). (Prof. Astrid Vabret & Dr. Meriadeg Le Gouil - <http://coronavirus.fr>) and at GRAM 2.0 (Group for Research on the Adaptation of Microbes, EA2656 UNICAEN/UNIROUEN), University of Caen, Normandy ; (Pr. Simon Le Hello). The position is part of a research project (Dynamic-H / RIN) funded by the region Normandy and European Commission (Feder).

Responsibilities: Leading and collaborating the research involved in the above-mentioned project under the supervision of Dr. Meriadeg Le Gouil ([https://www.researchgate.net/profile/Meriadeg\\_Ar\\_Gouilh](https://www.researchgate.net/profile/Meriadeg_Ar_Gouilh)).

The project includes the implementation and analysis of short and long reads sequencing / transcriptomics / targeted and untargeted sequencing of respiratory samples originating from 2 pre-characterized and rare human collections (n = 2000). The main objectives is to decrypt the species composition and the expression profile of the microbiome associated with respiratory viruses (Coronaviruses, RSV, Rhinoviruses, Influenza, Parainfluenza, Metapneumoviruses, Adenovirus, Bocavirus ...) and to model the dynamics and expression of microbial communities. This will allow a better understanding of the microbial interactions and evolution of the healthy - sick continuum for patients infected (or not) by respiratory viruses and will enhance our knowledge of the biological landscape and evolution of viral infections.

Prerequisites for an application include : 1. - A doctoral degree in natural sciences (biology, chemistry, biochemistry, etc.), with above-average grades and an interest in independent scientific work. 2. - Strong abilities to team co-working, networking, collaboration and socializing.

3. - Preferably, strong knowledge and skills in : virology, mixed approach of high-throughput sequencing (short

and long reads), analysis of NGS data (bioinformatics) and evolutionary analysis (phylogenetics) is desired. Scripting skills in bash, R and/or python would also be highly appreciated. 4. - We expect a very good command of English; French will be much appreciated.

For informal enquiries about the position, please get quickly in touch with : Meriadeg Le Gouil (meriadeg.legouil@unicaen.fr / meriadeg.legouil@normandie-univ.fr or Astrid Vabret (vabret-a@chu-caen.fr).

Deadline for applications: 17 January 2020 more infos : <https://euraxess.ec.europa.eu/jobs/471068> Application documents (CV, 1 page research statement, Publications) should be sent by PDF to the above contacts, or by post to:

Dr. Meriadeg Le Gouil GRAM 2.0 Service de Virologie, CHU de Caen Avenue Georges Clémenceau 14000 Caen FRANCE

Meriadeg Le Gouil, PhD, HDR

GRAM - Groupe de Recherche sur l'Adaptation Microbienne EA 2656 UNICAEN / UNIROUEN Normandie Université meriadeg.legouil@normandie-univ.fr

&

Service de Virologie, CHU de Caen CNR ROR - Centre National de Référence pour les Virus de la Rougeole, Rubéole et Oreillons Av. Georges Clémenceau, 14033 Caen, Cedex tel. : 0231272554 - Fax : 0231272557

Meriadeg research@Pasteur < <http://research.pasteur.fr/en/member/meriadeg-le-gouil/> > / Meriadeg@researchgate < [https://www.researchgate.net/profile/Meriadeg\\_Le\\_Gouil](https://www.researchgate.net/profile/Meriadeg_Le_Gouil) > / Coronavirus.fr / Chiroptera.fr < <http://chiroptera.fr/communaute/chiroblog/> >

Meriadeg Le Gouil <meriadeg.legouil@normandie-univ.fr>

## CAU Kiel Comparative Genomic-Metaorganisms

The Institute of Clinical Molecular Biology (IKMB) at Christian-Albrechts-University of Kiel (CAU) offers 1 position for a scientist/postdoc in bioinformatics (Biologist, informatician, bioinformatician) (TV-L E13)

The IKMB, together with the DFG-funded Collaborative Research Centre 1182 "Metaorganisms" (CRC 1182; "Sonderforschungsbereich'Ä), is looking for a motivated

bioinformatician with a PhD in bioinformatics, molecular biology, genetics, informatics, bioinformatics or a related field to join our interdisciplinary research group. A key goal of the CRC is to understand the molecular underpinnings that govern the interaction of host organisms with their associated microbiomes. To this end, a central task of the position will be to develop and implement comparative genomics approaches to enable analyses of multi-level omics data across diverse model organisms 'V ranging from plants to human. The ideal candidate should have experience in pipeline development, analysis of next-generation sequencing data and an interest in contributing this skillset to support diverse research projects. As the CRC is highly international, very good knowledge of the English language, both written and orally, is expected.

The position will be hosted at the Institute of Clinical Molecular Biology (IKMB), which hosts one of the four national German DFG-funded sequencing centres and is embedded in multiple high-profile research efforts, including the two DFG Excellence Clusters "Precision Medicine in Chronic Inflammation (PMI) and ROOTS. Through this stimulating working environment, the candidate will have an opportunity to interact with colleagues both nationally (e.g. through our membership in the German Network for Bioinformatics, de.NBI) and internationally working on diverse bioinformatic challenges, including genome projects and complex data integration as well as related soft-ware/infrastructure, to further improve her/his professional profile in these areas. Courses for additional certificates and visits of international conferences are supported.

We offer:

The position is immediately available until 31.12.2023 with the prospect of continuation. The salary will be paid in accordance with remuneration group E 13 TV-L (Public Sector Collective Agreement). Part-time employment is also possible. The preferred starting date is as soon as possible.

The UKSH has been certified as a family-friendly institution and is committed to further improve the compatibility of work and family life. The University supports the employment of disabled persons. Persons with disabilities will, with appropriate qualifications and aptitudes, be employed preferentially. The UKSH has set the goal to reach professional equality between men and women. The University aims to increase the number of women among the faculty staff and therefore explicitly encourages the application of female scientists.

Additional Information:

For questions about the position, please contact Prof.

Andre Franke of the IKMB at a.franke@ikmb.uni-kiel.de. Please contact for any further questions kariere@uksh.de. The deadline for this job offer is January 29th 2020. Please refer to the job ID 20190873.013.CK in your application. You can also submit your application online under: [www.uksh.de/Bewerbung.html?nr190873](http://www.uksh.de/Bewerbung.html?nr190873) (Interface in German only).

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## ClemsonU OralMicrobeEvolution

Clemson.OralMicrobeEvolution

Vincent Richards' lab in the Department of Biological Sciences at Clemson University is accepting applications for a post-doctoral position.

The overarching research theme will focus on the dental microbiome and the relationship between the bacterial and fungal components of this community. Specific questions include how these taxa respond and adapt to this dynamic environment. Operating over numerous time scales, multiple host factors such as diet, health, disease, and host genotype can impact the oral environment and hence are strong evolutionary forces that can shape and select for changes within the community. We are particularly interested in the interplay and co-evolution of bacterial and fungal components of the community and how these processes are impacted by immunosuppression. Multiple omic approaches such as comparative genomics, metagenomics, and metatranscriptomics will be coupled with network analyses to address these questions.

Similar projects focusing on the oral microbiome in general are possible and the postdoc will be free to explore and lead such projects. The postdoc will take a senior position within the laboratory and contribute to the mentoring of graduate and undergraduate research. The candidate should have a strong publication record and a background in microbial community dynamics. Ideally, the candidate should have experience analyzing next-generation sequence data and be versed in Linux/bash. Although desirable, experience with metatranscriptomics and network analyses are not required. The successful applicant will be trained in multiple bioinformatic approaches.

The position is available immediately and review of applications will continue until the position is filled. Up to four years of support are available (with the possibility for extension). Starting salary is \$50,000/year plus

benefits. Applicants should contact Vincent Richards directly at vpricha@clemson.edu. Please provide a cover letter (describing research interests, experience, and career goals), a CV that includes links to authored publications, and contact information for three references.

Clemson University is ranked 27th among national public universities by U.S. News & World Report and is located on Lake Hartwell near the Blue Ridge Mountains in beautiful Upstate South Carolina.

Vincent P. Richards, PhD Assistant Professor Department of Biological Sciences Clemson University Clemson, SC 29634 Email: vpricha@clemson.edu Lab website: <http://www.vprichards-lab.com> Vincent Paul Richards <vpricha@clemson.edu>

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## Cologne NematodeGenomics

The previously advertised position in the newly established Worm Lab at the University of Cologne has now been officially announced.

The newly established Worm Lab at the University of Cologne is looking for a postdoc to join their team in a project funded by the DFG. The project will analyse evolutionary developmental constraints on the highly conserved nematode Bauplan using DNA and RNA sequencing methods, as well as molecular gene knockout assays. The postdoc will be focussing on computational analysis (e.g. assembly, annotation, orthology searches, genome comparison) and writing software tools. However, the postdoc will also be involved in nematode sampling, and - importantly - lab work. The postdoc will co-supervise BSc, MSc and PhD students, and will be encouraged to develop their own research programme through independent grants.

At the Worm Lab we are fully committed to diversity and gender equality. Come as you are and bring whom you want. We also know how difficult it is to work in a job like ours when having kids. Thus we offer very flexible working models and regardless of their gender, all parents will be encouraged to take parental leave.

The official job advert can be found here

<https://www.stellenwerk-koeln.de/jobboerse/-wissenschaftl-stellen-postdoc-position-worm-lab-ag-schiffer-k-2020-01-24-297367> Looking forward to

read your applications

Philipp

Philipp Schiffer <philipp.schiffer@gmail.com>

db Sloan <db Sloan@rams.colostate.edu>

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## Colorado State University Organelle Mutation Rate Evolution

The Sloan Lab at Colorado State University is looking for a postdoctoral researcher with experience in plant molecular biology to join an ongoing NIH-funded project to understand the mechanisms responsible for extreme variation in mutation rates in plant mitochondrial and plastid genomes. The broader focus of our research is on the evolution of plant organelle genomes and their co-evolution with the nucleus. More information about our research projects and publications is available at our lab website: <https://sites.google.com/site/danielbsloan/>. We seek someone who is excited about addressing evolutionary questions at the molecular level and wants to contribute to a positive and collaborative intellectual environment. May 1, 2020 is the target start date, but this is flexible.

Applicants should have expertise in:

- Molecular biology techniques
- Plant (preferably Arabidopsis) genetics, transformation, and/or genome editing

Additional relevant skills and experience could include one or more of the following areas:

- Mechanisms of mutation, DNA damage/repair
- Mitochondrial and chloroplast biology/biochemistry
- Library construction for next-generation sequencing
- Comparative genomics and bioinformatics

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

Interested researchers should e-mail Dan Sloan (db-sloan@rams.colostate.edu) and include a CV, along with a brief statement of research/career goals and how they pertain to the position. Review will begin January 25, 2020, but inquiries are still very much encouraged after that date.

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## Cornell University Machine Learning Metabolomics

Postdoctoral Associate Machine Learning Genetics of Oat Composition School of Integrative Plant Science Cornell University

Please apply via <https://academicjobsonline.org/ajo/jobs/15773>. The position is in the Plant Breeding and Genetics Section at Cornell University, and is part of a USDA Agriculture and Food Research Initiative grant to breed more nutritious oat. Oat is uniquely valued among grain crops for the health-promoting composition of its seeds. This position seeks to apply novel machine learning methods to extensive genomic, transcriptomic, and metabolomic datasets. Results should generate effective methods to improve the composition of oat seed.

The Plant Breeding & Genetics Section, within the School of Integrative Plant Science, trains interdisciplinary scientists in the elaboration of new breeding methods, the discovery of genetic mechanisms important for economically important traits, and the creation of genetic stocks, germplasm, and varieties. We promote a collaborative and interactive workspace to improve learning, cross connectivity, and mutual support between basic and applied researchers. Cornell University plant breeders are world leaders in innovative plant breeding research, teaching, and extension, and we collaborate globally.

The Jannink lab works with several crop species (wheat, oat, barley, cassava, and the brown algae sugar kelp) to develop genomic prediction methods and integrate them optimally into breeding schemes. We work together to discover, build on, and share new ideas and tools from across computational disciplines that lead to successful applied breeding outcomes. With the Jannink lab, Dr. Michael Gore and Dr. Mark Sorrells provide leadership on the multiomic oat selection project.

In research for this project, the postdoc will collaborate with oat breeders at Universities in Minnesota, Wisconsin and South Dakota, as well as a postdoctoral associate currently working on the project. We have characterized an oat diversity panel of 384 genotypes with high-density DNA marker data, RNA-seq gene expression data, and non-targeted LC-MS, GC-MS, and targeted fatty acid methyl ester data of mature oat seed. We will analyze

these data to identify important genomic drivers of the mature oat seed metabolome. We will test whether results from this analysis can improve prediction accuracy in a series of 18 biparental crosses. We will also sequence a population of 1,500 oat TILLING (Targeted Induced Local Lesions In Genomes) lines at putative causal loci to determine if their metabolomes are indeed affected.

We seek a candidate with machine learning expertise, specifically deep learning neural network methods, and interest in applications relating to genetic variation and complex biological systems. The datasets described have rich structure and are amenable to machine learning analyses to identify patterns eluding linear models. Aided by other project personnel, the postdoc will identify patterns in the metabolomic and transcriptomic assays and their associations with genetic variation. The postdoc will construct learning models to identify multifactorial causes of seed composition variation, enabling the prediction of the impact of genetic perturbation on seed composition and suggesting effective breeding strategies to leverage this ability.

Anticipated Division of Time Field work, sample prep, data collection - 25% Machine learning analysis and interpretation - 30% Writing - 30% Training of lab members and collaborators in machine learning - 15%

Position Requirements Ph.D. in engineering, statistics, or computer science focused on machine learning, with experience or interest in genetic or complex biology applications, or Ph.D. in genetics with emphasis on machine learning analysis of genetic data. Proven scientific writing ability and communication skills.

Preferred Specific Skills Knowledge of genetics and genetic data types and analysis. Knowledge of biochemistry, metabolomics or systems biology methods. Basic bioinformatics skills (sequence alignment, use of gene annotations). Basic notions of plant or animal breeding.

How to Apply Candidates should send a statement of interest, curriculum vitae, contact information for three references and a statement of diversity, equity and inclusion (<https://cals.cornell.edu/faculty-staff/human-resources/policies-resources/statement-contribution-diversity-equity-and-inclusion>). Submit all application materials to Academic Jobs Online (<https://academicjobsonline.org/ajo/jobs/15773>).

Questions about the position can be addressed to Dr. Michael Gore at: [mag87@cornell.edu](mailto:mag87@cornell.edu). Review of applications will begin immediately and continue until the

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[mcmaster.ca/~brian/evoldir.html](http://mcmaster.ca/~brian/evoldir.html)

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## CRG Barcelona Modeling Cancer Evolution

Postdoctoral researcher position in the group  $\hat{\Delta}$ Evolutionary Processes Modeling $\hat{\Delta}$  at the Centre for Genomic Regulation (CRG), Barcelona, Spain

Application portal and more information here: <https://recruitment.crg.eu/content/jobs/position/postdoctoral-researcher-position-group-%E2%80%99Evolutionary-processes-modeling> The Institute

The Centre for Genomic Regulation (CRG) is an international research institute based in Barcelona, Spain, with more than 400 scientists from 44 countries. The CRG shares principles of an interdisciplinary and creative scientific team that is supported by high-end and innovative technologies and a flexible and efficient administration.

In 2013, the CRG received the 'HR Excellence in Research' logo from the European Commission. This is in recognition of the institute's commitment to developing an HR Strategy for Researchers designed to bring the practices and procedures in line with the principles of the European Charter for Researchers and the Code of Conduct for the Recruitment of Researchers.

The Group

Cancer is a genetic disease, subject to population genetics forces like mutation, selection and stochasticity. Our lab has recently demonstrated that coding sequences of cancer tumors not only exhibit positively selected mutations that drive cancer ([www.biorxiv.org/content/10.1101/485292v1](http://www.biorxiv.org/content/10.1101/485292v1)), but that there exist genes that the tumor cannot afford to lose to the mutational pressure ([www.nature.com/articles/ng.3987](http://www.nature.com/articles/ng.3987)). In addition to genes, we have also identified cancer driver loci in the non-coding part of the genome ([www.nature.com/articles/s41467-017-00100-x](http://www.nature.com/articles/s41467-017-00100-x)). Both coding and non-coding selection can act to promote cancer defense mechanisms against therapy, which can be unveiled through the analysis of time-sequence data of cell-free DNA and of patient survival data.

Our lab is particularly interested in how the evolution and survival of cancer cell populations relies on mutation influx and in the selection inference from allele

frequency information. To this end, we develop statistical and computational approaches to estimate mutation rates and selection. We use whole-exome sequencing and whole-genome data repositories to analyze selection on coding and non-coding sequences. In addition, we analyze cell-free DNA from tumors and their temporal evolution in response to therapy. Estimates of the strength of selection in cancer allow for a prioritization of genes and non-coding regions by their disease relevance, with the ultimate goal of promoting therapeutic advances.

The Evolutionary Processes Modeling lab was established in October 2018 and is part of the "Bioinformatics and Genomics" program at the CRG. Further information can be found at <https://weghornlab.net/> and at [www.crg.eu/en/programmes-groups/weghorn-lab](http://www.crg.eu/en/programmes-groups/weghorn-lab). The Role

We are looking for a postdoctoral researcher to join the "Evolutionary Processes Modeling" group to help elucidate cancer evolutionary dynamics using population genetics predictions and statistical modeling, together with computational analysis of recently published and unpublished cancer sequencing data. The ideal candidate should be highly motivated and eager to work on evolutionary and biological problems through the use and development of theoretical and computational approaches.

Whom would we like to hire?

- PhD degree in population genetics, physics, statistics, genetics, bioinformatics, computer science or a related discipline.
- Familiarity with principles of population genetics and statistical analysis.
- Experience with computational analysis of sequencing and other biological datasets.
- Fluency in English.

The Offer

- Contract duration: 1 year (with possibility of extension).
- Estimated annual gross salary: Salary is commensurate with qualifications and consistent with our pay scales.
- Target start date: Immediately.

We provide a highly stimulating environment with state-of-the-art infrastructure and unique professional career development opportunities. We offer and promote a diverse and inclusive environment and welcome applicants regardless of age, disability, gender, nationality, race, religion or sexual orientation.

Application Procedure

Applications should be addressed to Dr. Donat Weghorn and include:

1. A letter of motivation.
2. A complete CV, including a list of publications.
3. A brief statement of research

interests. 4. Contact details (or reference letters) of at least two referees.

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## EPFL Switzerland TheoEvolBiology

Dear colleagues,

I am pleased to announce openings for two postdoc positions funded by an ERC Starting Grant in my new group at EPFL (Ecole Polytechnique Federale de Lausanne, Switzerland). Both positions will be initially for 1 year, with the possibility of renewal. Start dates are March 1st, 2020 or later. For full consideration, please apply by January 20, 2020.

1- Post-doctoral researcher in statistical physics / stochastic processes applied to evolutionary biology. Topic: Characterizing the exploration of rugged fitness landscapes by subdivided populations. Full information: <https://recruiting.epfl.ch/Vacancies/1175/-Description/2> 2- Post-doctoral researcher in computational biology, working on protein sequence data. Topic: Sequence-function relationship in proteins. Full information: <https://recruiting.epfl.ch/Vacancies/1173/-Description/2> Best regards, Anne-Florence Bitbol

"anne-florence.bitbol@epfl.ch"

<anne-florence.bitbol@epfl.ch>

florence.bitbol@epfl.ch

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## GeorgiaTech 2 HumanEvolutionaryGenomics

Multiple Postdoctoral Positions in Human Evolutionary Genomics

Description: TheLachance Lab at Georgia Institute of Technology is recruiting two postdocs in human evolution genomics. Our lab uses computational approaches to understand how genetic disease risks have evolved over recent human history. Additional projects include



improving the generalizability of polygenic risk scores to diverse populations. The first postdoctoral position will focus on evolutionary medicine and anthropological genetics. The second postdoctoral position will focus on genetic epidemiology and public health genomics. Both of these positions are NIH funded (R35GM133727).

Environment: The Lachance Lab contains a diverse set of scientists and we foster an inclusive research environment. Additional information about our lab's research can be found at: <https://popgen.gatech.edu>. We are part of the Center for Integrated Genomics at Georgia Tech - which includes the labs of Greg Gibson, Soojin Yi, and King Jordan. Opportunities to develop collaborations with African colleagues will also be available.

Qualifications: - PhD in evolutionary biology, genetic epidemiology, human genomics, bioinformatics, or anthropology - Evidence of research productivity, including first author publications - Ability to work independently - Strong writing skills - Coding skills (R, Python) and previous experience working with large genome-scale datasets - A desire to mentor graduate and undergraduate students

Salary and duration: As per NIH guidelines, salaries will be commensurate with qualifications and experience. Subject to yearly review, both appointments are renewable and funding is available for multiple (3+) years.

Informal inquiries are welcome. Please contact me at [joseph.lachance@biology.gatech.edu](mailto:joseph.lachance@biology.gatech.edu) if you have any questions.

Joseph Lachance Assistant Professor School of Biological Sciences Georgia Institute of Technology [joseph.lachance@biology.gatech.edu](mailto:joseph.lachance@biology.gatech.edu) <https://popgen.gatech.edu> "Lachance, Joseph L" <[joseph.lachance@biology.gatech.edu](mailto:joseph.lachance@biology.gatech.edu)>

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## Ifrermer France ToxicityMicroalgae

Dear colleagues,

Could you please—share the attached—offer for a postdoc in my lab at Ifremer, Concarneau, France,—to assess the ichthyotoxicity of French marine microalgae using bioassays targeting cultured cells of fish and shellfish. We are looking for a candidate with an international experience (PhD or postdoc out from France), who was awarded his/her PhD for less than 4 years. Deadline for application is March 1st, 2020. Many thanks and

happy new year!

Malwenn

Malwenn Lassudrie (PhD)IFREMER ODE/UL/LER Bretagne Occidentale Station de biologie marine Place de la Croix BP 4053729185 Concarneau France Tél: +33 2 98 10 42 96 (52 96)

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[gueveloueric@yahoo.fr](mailto:gueveloueric@yahoo.fr)

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## IowaStateU ComparativeMethods

Postdoctoral Associate: morphometrics and phylogenetic comparative methods

The Adams laboratory, Department of Ecology, Evolution and Organismal Biology (EEOB) at Iowa State University, is seeking applicants for a fulltime postdoctoral position in geometric morphometrics and phylogenetic comparative methods. This position is for a maximum of two years and is part of an NSF collaborative CIBR project. The postdoctoral associate will contribute to ongoing macroevolutionary studies in vertebrates, will coordinate the development of tutorials and code profiling in geomorph, and will mentor undergraduates in quantitative morphology studies. Successful applicants are encouraged to develop their own independent empirical research in multivariate macroevolution.

Additional details about the position, as well as a link to apply, may be found on the ISU HR website: [https://isu.wd1.myworkdayjobs.com/IowaStateJobs/-job/Ames-IA/Postdoctoral-Research-Associate—Ecology–Evolution-and-Organismal-Biology\\_R1519](https://isu.wd1.myworkdayjobs.com/IowaStateJobs/-job/Ames-IA/Postdoctoral-Research-Associate—Ecology–Evolution-and-Organismal-Biology_R1519) Questions about the position should be directed to Dean Adams ([dcadams@iastate.edu](mailto:dcadams@iastate.edu)).

Dean

Dr. Dean C. Adams Director of Graduate Education, EEB Program Professor Department of Ecology, Evolution, and Organismal Biology Iowa State University <https://www.eeob.iastate.edu/faculty/adams/> phone: 515-294-3834

“Adams, Dean [EEOB]” <[dcadams@iastate.edu](mailto:dcadams@iastate.edu)>

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## KielU MPI EvolBio MicrobiomeEvolution

The Section of Evolutionary Medicine at Kiel University and the Max Planck Institute for Evolutionary Biology is seeking a postdoc to work on ongoing projects applying ecological and evolutionary approaches to gut microbiome-mediated treatment strategies for inflammatory bowel disease (IBD). The work consists of experimental mouse models of IBD, including gnotobiotic humanized mice, computational analyses of microbiome sequencing data, and ultimately the possibility to translate results to clinical settings.

The candidate should have experience in one or more of the following: mouse experimental disease models, computational analysis of next generation sequencing data, evolutionary biology, microbiology. Candidates willing to complement their existing skill set with any of the above are encouraged to apply.

The position is embedded in the German Research Foundation (DFG)-funded Excellence Cluster “Precision Medicine in Chronic Inflammation” (PMI) and will involve work at both the University Medical Center Schleswig-Holstein (UKSH, Campus Kiel) and the Max Planck Institute for Evolutionary Biology in nearby Plön. The candidate will interact with an interdisciplinary team of evolutionary biologists, microbiologists and clinicians and make use of state of the art in-house facilities for gnotobiology and next generation sequencing.

Kiel and Plön

The city of Kiel is located directly at the Baltic Sea and the smaller town of Plön is located nearby in the popular vacation region “Holsteinische Schweiz” (approximately 30 minutes by car or train from Kiel main station). Both areas offer beautiful natural settings including access to a variety of beaches and lakes, outdoor activities as well as cultural events. The major city of Hamburg is located 60-90 minutes away from either location and is well connected by train.

Application

The position is initially limited to 2 years, with the possibility of extension. The salary will be according to the German public service pay scale (TvöD Bund 13-14 scale, depending on experience). Social benefits are granted in accordance with the regulations for the

public sector.

Interested candidates should send their application (motivation letter that describes their interest in the position and their relevant background (max. one page), CV, copies of certificates, contact details of two references) by email to [baines@evolbio.mpg.de](mailto:baines@evolbio.mpg.de).

The Max Planck Society strives for gender and diversity equality. We welcome applications from all backgrounds. The Max Planck Society is committed to employing more disabled individuals and especially encourages them to apply. The Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply.

The initial application deadline is February 12th, 2020, but the position will remain open until filled by a qualified candidate.

For further information, please contact John Baines.

Contact: Prof. Dr. John Baines Section of Evolutionary Medicine Institute for Experimental Medicine Kiel University and Max Planck Institute for Evolutionary Biology August-Thienemann-Str. 2 24306 Ploen Germany [baines@evolbio.mpg.de](mailto:baines@evolbio.mpg.de) <https://www.evolbio.mpg.de/-2169/en> <http://www.evolbio.mpg.de/evolgenomics/> “[baines@evolbio.mpg.de](mailto:baines@evolbio.mpg.de)” <[baines@evolbio.mpg.de](mailto:baines@evolbio.mpg.de)>

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## LundU ModelingEvolutionFlower- ingPhenology

Postdoctoral fellow in Environmental Science

Lund University, Centre for Environmental and Climate research

Lund University was founded in 1666 and is repeatedly ranked among the world’s top 100 universities. The University has 40 000 students and 7 600 staff based in Lund, Helsingborg and Malmo. We are united in our efforts to understand, explain and improve our world and the human condition.

The Faculty of Science conducts research and education within Biology, Astronomy, Physics, Geosciences, Chemistry, Mathematics and Environmental Sciences. The Faculty is organized into nine departments, gathered in the northern campus area. The Faculty has approximately 1500 students, 330 PhD students and 700 employees.

The Centre for Environmental and Climate Research, CEC (<http://www.cec.lu.se>) conducts research, education and communication on environmental science and climate research at Lund University.

The postdoctoral position is funded by BECC (Biodiversity and Ecosystem services in a Changing Climate), an interdisciplinary strategic research area based on collaboration between more than 250 researchers at the universities of Lund and Gothenburg. BECC develops research that contributes to the visualization and generation of knowledge to predict and manage the combined effect of climate change and land use on biodiversity, ecosystems and ecosystem services. BECC's strength is its existing and successful research leaders from many different disciplines such as biology, political science, geology, mathematics, physical geography and economics that together develop BECC. The Center for Environmental and Climate Research, CEC, hosts BECC. CEC is both a physical and a virtual center at Lund University. CEC conducts research, education and communication about environmental science and climate research.

#### HOW WILL SEASONAL CLOCKS IN WILD AND AGRICULTURAL PLANTS ADAPT TO CLIMATE CHANGE?

Shifts in the seasonal timing of flowering is a commonly observed effect of climate change. Flowering time is primarily controlled by temperature and day length and, as a result of evolution, plant responses to these cues are often genetically adapted to the local climate. Will future climates render such evolved controls suboptimal and if so, what will evolution replace them with? As part of an ongoing interdisciplinary collaboration, the postdoc will develop and test ecological and genetically informed life-history theory to understand how plants should adapt their flowering time strategies to climatic changes. The project focuses on annual plants which, due to their short generation times, are particularly likely to exhibit rapid evolutionary responses to environmental change. Annual plants furthermore include important crops, invasive weeds and pollen-allergy causing plants. The theoretical work will be related to data from barley growth experiments at different latitudes across Europe and to data on plant phenology from the Swedish Phenology Network. By improving our understanding of flowering time adaptations in annual plants the results of this project may find applications in for example plant breeding to address food security and in predicting and managing invasive species in a changing climate.

#### Duties

The main duties involved in a post-doctoral position is to conduct research. Teaching may also be included,

but up to no more than 20% of working hours. The position shall include the opportunity for three weeks of training in higher education teaching and learning. - development and analysis of eco-evolutionary plant life history models using mathematical tools and computer simulations - model validation based on statistical analyses of plant phenology and growth data. - simulation of plant performance in future climate change scenarios.

#### Qualifications and requirements

Appointment to a post-doctoral position requires that the applicant has a PhD, or an international degree deemed equivalent to a PhD, within the subject of the position, completed no more than three years before the last date for applications. Under special circumstances, the doctoral degree can have been completed earlier.

- applicants should have completed a PhD in ecology, mathematics, environmental sciences or similar. - keen interest in general evolutionary ecology - solid background in quantitative or theoretical ecology - excellent programming skills - ability to work both independently and in teams with other researchers. - excellent communication skills in written and spoken English.

#### Merits

- publications in internationally recognized scientific journals - experience in plant ecology, plant genetics and eco-evolutionary modelling.

#### Assessment criteria and other qualifications

This is a career development position primarily focused on research. The position is intended as an initial step in a career, and the assessment of the applicants will primarily be based on their research qualifications

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## LundU ModellingPlantPollinators

Postdoctoral fellow in Eco-Evolutionary modelling, Environmental Science Lund University, Centre for Environmental and Climate research:

Lund University was founded in 1666 and is repeatedly ranked among the world's top 100 universities. The University has 40 000 students and 7 600 staff based in

Lund, Helsingborg and Malm?. We are united in our efforts to understand, explain and improve our world and the human condition.

The Faculty of Science conducts research and education within Biology, Astronomy, Physics, Geosciences, Chemistry, Mathematics and Environmental Sciences. The Faculty is organized into nine departments, gathered in the northern campus area. The Faculty has approximately 1500 students, 330 PhD students and 700 employees.

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The postdoctoral position is funded by BECC (Biodiversity and Ecosystem services in a Changing Climate), an interdisciplinary strategic research area based on collaboration between more than 250 researchers at the universities of Lund and Gothenburg. BECC develops research that contributes to the visualization and generation of knowledge to predict and manage the combined effect of climate change and land use on biodiversity, ecosystems and ecosystem services. BECC's strength is its existing and successful research leaders from many different disciplines such as biology, political science, geology, mathematics, physical geography and economics that together develop BECC. The Center for Environmental and Climate Research, CEC, hosts BECC. CEC is both a physical and a virtual center at Lund University. CEC conducts research, education and communication about environmental science and climate research.

Eco-evolutionary models of plant-pollinator communities ? community response to landscape structure:

Sustainable agriculture is promoted by mutualistic?plant-pollinator interactions,?services that may increase?economic and societal value.?The aim is to study such services by?formalising plant-pollinator community response to landscape structure and agricultural intensity using trait-based and eco-evolutionary models. The applicant should have experience in modelling and knowledge of ecological interactions, evolution, and dispersal processes in the context of population and community dynamics. An important component is to test models against data on?bees, bumblebees, and butterflies to study how insects may respond to agricultural intensification and landscape simplification, considering both short and long-term effects by focusing on a historical and contemporary adaptation of functional. By fitting models to data, we aim to quantify active processes in the study system and to communicate ways of optimizing ecosystem services to stakeholders and

policymakers.

Duties:

The main duties involved in a post-doctoral position is to conduct research. Teaching may also be included, but up to no more than 20% of working hours. The position shall include the opportunity for three weeks of training in higher education teaching and learning.

\* formalisation of the complexity in which ecological interactions, evolution, and dispersal of organisms affect mutualistic interactions, and population and community dynamics \* design and implementation of spatial, trait-based and eco-evolutionary models of mutualistic interactions \* model validation given available data, using computational and statistical approaches.

The candidate should have a Ph.D. in Environmental science/ Ecology/ Evolution/ Physics/ Mathematics or Computer science. Knowledge of ecological, evolutionary and spatial processes is required. Candidates should be proficient in modelling dynamic systems (e.g. ODE-models or IBM?s) with experience in programming (e.g. Matlab, Python, C++, etc). Experience in numerical methods, model validation and Bayesian statistics are desirable. Important qualities are outgoing, problem-solving, independent and persistent.

Qualification requirements:

Appointment to a post-doctoral position requires that the applicant has a PhD, or an international degree deemed equivalent to a PhD, within the subject of the position, completed no more than three years before the last date for applications. Under special circumstances, the doctoral degree can have been completed earlier.

Assessment criteria and other qualifications:

This is a career development position primarily focused on research. The position is intended as an initial step in a career, and the assessment of the applicants will primarily be based on their research qualifications and potential as researchers. Particular emphasis will be placed on research skills within the subject. ? Terms of employment:

This is a full-time, fixed-term employment of a maximum of 2 years. The

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## MaxPlanckInstEvolBiol EvolutionaryGenomics

Postdoc - Theoretical evolutionary biology and evolutionary genomics

A position for postdoctoral researchers with a PhD age of 2-10 years is available for three years in the field of evolutionary genomics with the Max Planck research group "Environmental Genomics" headed by Prof. Eva H. Stukenbrock (see more: <http://web.evolbio.mpg.de/envgen/> < <http://web.evolbio.mpg.de/envgen/> >). The Max Planck group is affiliated with the Max Planck Institute for Evolutionary Biology in Plön and the Christian-Albrechts University of Kiel in the North of Germany. The position is compensated at TV-L 14 (depending on qualifications), covers 39h/week. Start of the position is June 1st 2020.

### Background

Research in the Environmental Genomics group focuses on adaptive evolution and speciation of fungal plant pathogens. A key question in our research is the impact of plant domestication and agro-ecosystem structure on plant pathogen evolution. To this end we study large-scale datasets of fungal plant pathogens from different crop plants and their wild relatives. Research in the group is highly interdisciplinary and integrates computational and experimental approaches.

### Position

The successful candidate will lead analyses of multiple population genomic datasets, including changes in diversity, admixture, signatures of selection, comparisons of impacts and changes across species, and conduct analyses to understand processes of speciation. The post doc will supervise student projects at various levels and have the possibility of contributing to teaching in evolutionary biology and population genetics at Kiel University. The position furthermore provides extensive opportunities for collaboration within our own interdisciplinary team, as well as at the Max Planck Institute for Evolutionary Biology (<https://www.evolbio.mpg.de/2169/en> < <https://www.evolbio.mpg.de/2169/en> >) and Kiel Evolution Center (<http://www.kec.uni-kiel.de>).

The candidate should have a PhD in the field of population genetics/evolutionary biology. No experience in fungal biology or genetics is required, though experi-

ence with population genomic modeling, Approximate Bayesian Computation, and database management is a plus. Proficiency in Linux scripting, in a major programming language and in handling large datasets is a requirement. A promising record of publication is expected. The successful applicant will be an independent, motivated problem solver who communicates well and enjoys working in a collaborative setting.

### Application

Depending on qualification and professional experience, payment is made according to TVöD Bund up to remuneration group E14. In addition, social benefits are granted in accordance with the regulations for the public sector. Interested candidates should send their application (motivation letter that describes their interest in the position and their relevant background, CV, copies of certificates, contact details of two references) by email to [stukenbrock@evolbio.mpg.de](mailto:stukenbrock@evolbio.mpg.de). Please use the respective code 01/2020 in the subject line. The Max Planck Society strives for gender and diversity equality. We welcome applications from all backgrounds. The Max Planck Society is committed to employing more disabled individuals and especially encourages them to apply. The Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply. For further information, please contact Eva Stukenbrock ([stukenbrock@evolbio.mpg.de](mailto:stukenbrock@evolbio.mpg.de)). The application deadline is March 15th, 2020, however the position will remain open until filled by a qualified candidate.

Contact: Prof. Dr. Eva Stukenbrock Max Planck Fellow Group Environmental Genomics Max Planck Institute for Evolutionary Biology, Plön, Germany  
Website: <http://web.evolbio.mpg.de/envgen/> <https://www.evolbio.mpg.de/2983911/environmentalgenomics>  
Email: [stukenbrock@evolbio.mpg.de](mailto:stukenbrock@evolbio.mpg.de)

"Eva H. Stukenbrock" <[estukenbrock@bot.uni-kiel.de](mailto:estukenbrock@bot.uni-kiel.de)>

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## McGillU BioinformaticsEnvironmentalGenomics

McGill University; Bioinformatics and Environmental Genomics

Preferred Disciplines: Biology, Bioinformatics (Postdoc position) Project length: 2 years, renewable for 3rd year  
Approx. start date: February 15, 2020 Location: McGill

University, Montreal, QC

**Summary of Project:**The Postdoctoral Fellow will be involved in long-term and highly replicated laboratory and field experiments on the effect of multiple stressors on the structure and function of aquatic communities. The research will involve developing and implementing bioinformatic tools for analysing metabarcoding, metagenomics and transcriptomics data sets and assessing biodiversity trends for broad taxonomic groups (bacterial, phytoplankton, zooplankton). The fellow will compare biodiversity estimates obtained from traditional sampling techniques with estimates based on refined metabarcoding approaches to describe the biodiversity of contaminated aquatic habitats. The project involves the biodiversity group at McGill University and collaborators from the Biodiversity Institute of Ontario (BIO), University of Guelph, University of Quebec at Montreal and University of Montreal.

**Research Objectives/Sub-Objectives:** 1) Develop sensitive metabarcoding bioinformatics protocols to describing aquatic communities; 2) Investigate the impact of multiple stressors on complex aquatic communities.

**Methodology:** 1) Use high-throughput sequencing to develop metabarcoding and metagenomics protocols for describing aquatic communities in complex environmental samples; 2) Validate protocols; 3) Apply protocols on highly replicated field experiments.

**Expertise and Skills Needed:**Experience with next generation sequencing or large sequence data and related bioinformatics / computational / programming skills is required. Familiarity with one or more of the following would be an advantage: genomics, transcriptomics, phylogenetic analyses, genome evolution / programming language (R/Unix/Python or Perl). Experience working with aquatic organisms would be an asset. The candidate should have a PhD in evolution / genetics / computational biology, a good publication record and the ability to work well in a collaborative research environment.

Applicants should send a curriculum vitae, short statements of research interests, and 3 representative publications to Melania Cristescu [melania.cristescu@mcgill.ca](mailto:melania.cristescu@mcgill.ca). The application deadline is January 31, 2020.

McGill University is strongly committed to diversity and equity within its community. McGill University is among Canada's leading research-intensive universities with students from over 140 countries. The university is located in Montreal, a cosmopolitan city with great cultural and linguistic diversity.

Melania Cristescu <[melania.cristescu@mcgill.ca](mailto:melania.cristescu@mcgill.ca)>

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## MichiganStateU ModelingRangeShifts

Postdoctoral Position, Integrative Modeling of Species Range Shifts, Department of Fisheries and Wildlife, Michigan State University

A postdoctoral research associate position in population genetics and demographic modeling is available in the Department of Fisheries and Wildlife at Michigan State University. The successful applicant will join an established collaborative network of researchers across five institutions (Michigan State University, the Morton Arboretum, the College of Charleston, the Missouri Botanical Garden, Mount Royal University) and contribute to an NSF-funded data integration project focused on quantifying species' historical range shifts and population sizes using multiple data types (for more information see: [https://www.nsf.gov/awardsearch/showAward?AWD\\_ID=1759759](https://www.nsf.gov/awardsearch/showAward?AWD_ID=1759759)). Although multiple data types contain information on species' range shifts (i.e., fossil pollen data, occurrence data and ecological niche models, and population genetic data) these datasets do not always result in equivalent inferences (e.g., on the speed of range shifts). This project seeks to integrate these data types in a coherent analytical framework to infer demographic parameters (migration rates, population sizes, etc.), the location of glacial refugia, and the pace of post-glacial range movement (see Hoban et al 2019 *Ecography*). The statistical framework provided by Approximate Bayesian Computation (ABC) is a major component of the integrative modeling approaches we are developing. Our project team currently includes individuals with expertise in Mathematics, Statistics, Ecology, Biogeography, and Population Genetics, and we look forward to welcoming a new collaborator to the project.

Applicants must have a Ph.D. in Genetics, Ecology, Evolutionary Biology, Bioinformatics, or a similar field with demonstrated experience in population genetics and a robust computational skillset. In particular, experience with programming (R, Python, C++), Approximate Bayesian Computation, cluster computing, and analysis of population genomic data is desirable. Other desired qualifications include a strong work ethic, problem-solving and time management skills, and experience communicating scientific results. Applicants should demonstrate an interest in joining an established

interdisciplinary research team working at the interface of statistics and ecology, and in contributing to an open-source software development project. This position includes opportunities (and funding) to engage in a wide variety of professional development activities (depending on areas of interest) and to participate in planned outreach efforts associated with this project.

Interested applicants should submit a cover letter, statement of research interests, and contact information for three references via the Careers @ MSU website (job posting #632351): <https://careers.msu.edu/en-us/job/-503149/research-associatefixed-term> In addition to the materials above, code (e.g., link to a GitHub repository) and writing samples (i.e., one or more recent publications) are also strongly encouraged, and will be considered during review. Questions about the position can be directed to Dr. John Robinson, [jdrob@msu.edu](mailto:jdrob@msu.edu). The initial appointment for this position is for a period of one year, with the possibility of renewal for a second year pending satisfactory performance. Start date is no later than July 1, 2020. Review of applications will begin March 15, 2020 and will continue until the position is filled.

“Robinson, John” <[jdrob@msu.edu](mailto:jdrob@msu.edu)>

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## MIZ Poland Dolphin Evolutionary Genomics

Dear EvoDir subscribers,

A postdoctoral research assistant position is available at the research group led by Dr Andre E. Moura at the Museum and Institute of Zoology of the Polish Academy of Sciences (MIZ-PAS). The research group is focused on cetacean ecology and evolution, and this position will focus on genomic analyses of striped dolphin in relation to Morbillivirus infection.

The position is available for 33 months, and includes a three month probation period. The expected start date is early April 2020, or sooner if the successful candidate is available. The research group is based at the Research Station of the MIZ-PAS in Gdańsk, and maintains strong links with the main research facilities of the MIZ in Warsaw. Therefore, research visits at the main MIZ facilities in Warsaw may be required as part of the job duties. The Research Station also hosts groups working on canid genomics and avian immunogenetics.

The post-doctoral assistant will possess expertise in

evolutionary genomics, population genomics or bioinformatics. Candidates can have a background (BSc or MSc degree) in biology, zoology, bioinformatics, computer science, or related fields, and a PhD degree (awarded or to be awarded soon) in a relevant area. The PhD degree should have been awarded no earlier than 7 years before the start of employment. The candidate must be eligible to work in Poland at the time of appointment. A list of required skills can be seen at the end of this message.

To apply, the following documents should be sent to Andre Moura at [avmoura@miiz.waw.pl](mailto:avmoura@miiz.waw.pl) no later than 28.02. 2020:

1. Copy of a PhD certificate
2. Curriculum vitae including a publication list, with the following statement provided at the end and signed:

“I give my consent to the processing of personal data provided in my application documents by the Museum and Institute of Zoology PAS for the purpose of the recruitment process, pursuant to the Personal Data Protection Act of 10 May 2018 (Journal of Laws 2018, item 1000) and in agreement with Regulation (EU) 2016/679 of the European Parliament and of the Council of 27 April 2016 on the protection of natural persons with regard to the processing of personal data and on the free movement of such data, and repealing Directive 95/46/EC (General Data Protection Regulation; L 119 from 04.05.2016)”.

IMPORTANT: Applications that do not include this statement cannot be processed.

3. Motivation letter (maximum one page)
4. A copy of one research paper to be evaluated in the recruitment process
5. Contact details of two persons who can be contacted for references.

The interviews of shortlisted candidates will take place in early March at the Research Station of the Museum and Institute of Zoology PAS in Gdańsk-Górki Wschodnie. A Skype interview can be arranged. Informal inquiries can also be addressed to Andre Moura.

Essential skills:

1. Experience with preparing NGS libraries and processing NGS data
2. Good knowledge of evolutionary theory and/or population genetic theory
3. Experience of Linux/Unix environment;
4. Experience with at least one coding language (e.g. Python, Perl, Unix Shell scripts);
5. Good organisational skills;
6. Experience with large databases;
7. Ability to work independently and to communicate with a multi-disciplinary team;

Desirable skills:

8. Experience with analysing whole-genome datasets,

aligning to reference genomes, SNP detection; 9. Experience with software for evolutionary genomic analyses; 10. Experience with online genomic databases; 11. Good understanding of natural selection theory; 12. Good understanding of mammalian immune system; 13. Experience of working in an international team.

**Research environment** The research at the MIZ is focused on a broad range of themes in animal biology, including systematics, biogeography, evolutionary biology, ecology and population genetics. Andre Moura research group is part of the Laboratory of the Molecular and Biometric Techniques led by Prof. Wieslaw Bogdanowicz, grouping researchers focused on population genetics, phylogeography and evolutionary genomics of a broad range of animal taxa. MIZ laboratories contain modern equipment for genomic analyses, including Pacific Biosciences RSII long-read sequencer and Illumina MiSeq System. The state-of-the-art ancient DNA laboratory carries out work on mammalian palaeogenetics. The Museum zoological collection is among the largest and most valuable in Europe.

“Andre E. Moura” <avmoura@miiz.waw.pl>

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## Montpellier Butterfly Population Genomics

2-year Postdoc in population genomics - CNRS Montpellier, France

A 2-year post-doctoral fellowship is available to work on the evolutionary genomics and demography of inversion polymorphism in tropical butterflies (*Heliconius*), in the group of Mathieu Joron (<http://joron.cefe.cnrs.fr>) at the Centre for Evolutionary and Functional Ecology (CNRS CEFÉ) in Montpellier, France

Inversion polymorphisms often act as Mendelian loci (or supergenes), switching between different ecological strategies coexisting within populations, such as alternative social organisations in ants, mate acquisition tactics in birds, pollination syndromes in flowering plants, or mimicry associations in butterflies. Our research focuses on the spectacular wing pattern polymorphism of the tropical butterfly *Heliconius numata*, famous for its distinct mimetic forms controlled by a series of adjacent chromosomal inversions. We study the evolution of this genetic architecture using theoretical, genomic, and ecological approaches.

The postdoc will lead genomic research aiming at under-

standing how inversions establish and spread through populations across the distribution range. The project allows for much flexibility in the direction taken depending on the skills and interests of the person hired. Major objectives include, for instance, deciphering how supergene evolution affects population demography and differentiation, the dissection of deleterious mutations and antagonistic fitness effects associated with inversions, and the factors underlying disassortative mating, etc. Datasets available include 120 resequenced genomes, multiple independent reference assemblies, transcriptomes and annotations, and will be expanded during the project.

The postdoc will join a lively consortium of teams (CEFE Montpellier and Museum of natural history in Paris) and will interact with team members working on the ecology of inversion polymorphism, the modelling of balancing selection, or the functional dissection of wing-patterning. Our partner institution INRIA Genscale in Rennes is a major bioinformatics institute, so the postdoc will enjoy direct support from a bioinformatics team.

The CEFÉ is a major institute in Europe for evolutionary ecology and genetics. Within CEFÉ, our team comprises 12 CNRS researchers whose research combines genetics and evolutionary ecology to address a diversity of topics on adaptation and natural variation. Our group focuses on butterfly wing patterns as a model to decipher how diversity is shaped by natural selection and other processes at the phenotypic and genomic level. Montpellier is a major hotspot for evolutionary and environmental research worldwide and has a vibrant research community with several hundred researchers in this domain, and highly praised graduate programmes. The University of Montpellier ranked 1st in the 2018 and 2019 Shanghai ranking in Ecology. Montpellier lies near the Mediterranean region in the South of France and enjoys pleasant weather, fantastic nature and great cultural and city life.

Starting date : ideally before the summer 2020, and no later than Oct. 2020. Net salary: between 25 k€/year and 35 k€/year depending on experience, including social benefits and public health insurance.

Candidates should have a PhD or equivalent in biological sciences or computational biology (by the starting date), advanced knowledge of population genetic theory, a keen interest in understanding biodiversity. Candidates should have experience with genomic datasets, population genomics and/or demographic inferences using genomic data.

Applications : Informal enquiries are highly encouraged. Please contact Mathieu Joron,



mathieu.joron@cefe.cnrs.fr. Website: <http://joron.cefe.cnrs.fr>. Formal applications must be done through the CNRS portal (<http://bit.ly/2tGenlZ>). Applicants should upload a letter of application with details on their motivation and achievements and including proposed research directions, a full CV, the names and contact details of two references, and their date of availability.

Application deadline 23 February

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

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### NHM London SoilMicrobiologyBioinformatics

Dear all,

We are offering a 26-month Postdoc position at the Life Sciences Department, Natural History Museum.

This position is available in the field of soil microbiology, plant diseases and the application of bio-inoculants in horticulture within the H2020-funded EXCALIBUR (<https://www.excaliburproject.eu/>) project in Dr Jungblut's and Dr David Bass's research teams at the Life Sciences Department, Natural History Museum, London (<https://www.nhm.ac.uk/our-science.html>).

Full job description: [https://careers.nhm.ac.uk/templates/CIPHR/jobdetail\\_1848.aspx](https://careers.nhm.ac.uk/templates/CIPHR/jobdetail_1848.aspx) The project aims to gain a better knowledge of underground soil biodiversity including prokaryotes, microbial eukaryotes, and microfungi, and their synergistic effects with prebiotic and probiotic approaches in horticulture. Soil microbial bio-inoculants and bio-effectors will be tested on three model crops of economic importance such as tomato, apple, and strawberry under different experimental and open-field conditions across Europe, and the feedback effect of and on native soil biodiversity will be monitored.

The work will provide an excellent opportunity for a post-doctoral research scientist to apply cutting-edge microbial community analysis techniques to investigate the relationship between soil microbial communities, plant diseases, microbial inoculants, environmental drivers and biogeography in horticulture.

The postdoctoral research scientist will take a leading role in the assessment of soil microbiology, microbe-plant interactions and plant diseases across study sites, as well as in the monitoring of the response of soil microbial as-

semblages, plant endophytes and rhizosphere in tomato, strawberries and apples on microbial inoculants during the field trials and contrasting agricultural management practices.

The successful candidate will have Bachelor or Masters Degree in sciences, PhD in relevant discipline and knowledge of fundamental microbiological and molecular biological techniques, experience in working with environmental samples including DNA extraction and PCR, as well as bioinformatics tools for microbial community structure analysis.

Best wishes

Anne

Dr. Anne D. Jungblut Research Scientist Algae, Fungi and Plants Division Life Sciences Department The Natural History Museum Cromwell Road London SW7 5BD United Kingdom

Anne Jungblut <a.jungblut@nhm.ac.uk>

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### QMUL London AncientGenomicsDomestication

Dear all,

A 24 month Postdoctoral Research Assistant position is available at Queen Mary University of London (QMUL) in Dr. Laurent Frantz's group, investigating the evolutionary history of domestic animals using ancient genomes.

Candidates for this position must have a strong experience in population genomics, and ideally [but not necessarily] in ancient genomics. They should have a PhD (awarded or reasonably expected to be awarded within 3 months) or equivalent qualification/experience in an area of molecular evolution, genomics, bioinformatics or a related discipline. They will engage with the analyses of ancient pigs, chickens (and potentially dogs) genomes. A track record of peer-reviewed publications is essential.

The post holder will be integrated into Dr. Frantz's group of several PhD students/postdocs and work closely with the team of Prof. Larson (University of Oxford). Potential projects involve analysing ancient pig genomes to establish the spatial and temporal differences in the proportion and genomic location of the incorporation of wild boar genes into domestic stocks in order to assess how domestic pigs adapted to novel environments.

The post is funded by the NERC and is a full-time position. The start date is mid-February or as soon as possible thereafter. The salary is dependent on qualifications, skills and experience and is in the range of 31,613-36,098 per annum, inclusive of London allowance. Benefits include 30 days annual leave and a pension scheme.

Candidates must be able to demonstrate their eligibility to work in the UK in accordance with the Immigration, Asylum and Nationality Act 2006. Where required this may include entry clearance or continued leave to remain under the Points Based Immigration Scheme.

To apply: <https://webapps2.is.qmul.ac.uk/jobs/-job.action?jobID=5010> Application enquiries should be directed to [laurent.frantz@qmul.ac.uk](mailto:laurent.frantz@qmul.ac.uk)

The closing date for applications is 21 February 2020. Interviews will be held shortly thereafter.

Laurent Frantz <[l.frantz@qmul.ac.uk](mailto:l.frantz@qmul.ac.uk)>

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## Roscoff France EvolutionaryGenomics

### BIOINFORMATICS POSTDOC IN EVOLUTIONARY GENOMICS

Roscoff Marine Station, France

A postdoctoral position (1 year with possible renewal for 3 years) is available immediately in the Algal Genetics group at the Roscoff Marine Station, Brittany, France (<http://www.sb-roscoff.fr/en/team-algal-genetics>).

We are seeking highly qualified and enthusiastic applicants with strong skills in computational biology/bioinformatics, ideally also with experience in data mining and comparative or evolutionary genome analyses.

We have been interested in a range of topics related to the evolution of sexual reproduction across the brown algal group. In the framework of our research, and together with collaborators at Genoscope (Paris) we have generated full genomes of 48 lines of brown algae and comprehensive sets of RNA-seq data for a range of life cycle stages from representatives of all major brown algal lineages and evolutionary outgroups. We perform integrated analyses to study the evolution of brown algal genomes across lineages, life cycle stages, chromosomes and sexes.

The postdoctoral fellow will be funded by an awarded

ERC Starting Grant (SEXSEA) and perform integrated evolutionary/bioinformatics analyses based on data produced in our lab and available genomic data. The project will focus on analyses of the 'omics' datasets generated in the framework of the ERC Grant and Phaeoexplorer (France Genomique), including high quality genomes, HiC datasets, genetic maps, transcriptomes, etc. More precisely the postdoc will use bioinformatics and comparative evolutionary genomic approaches to identify sex chromosomes and investigate their evolution.

The language of the institute is English and its members form a highly international group. The Roscoff Marine Station is located in Brittany at the sea Front, and Roscoff is a picturesque city close to Brest, 3h away from Paris.

Please submit a CV, statement of research interest, and names of three references to: Susana Coelho ([Coelho@sb-roscoff.fr](mailto:Coelho@sb-roscoff.fr)).

We are always interested in applications from highly qualified and motivated bioinformatics postdocs, experimental (genomics/molecular/ developmental biology) postdocs and bioinformatics PhD students. Please send applications and other requests to Susana Coelho ([Coelho@sb-roscoff.fr](mailto:Coelho@sb-roscoff.fr)).

Note that three postdocs and one PhD studentship in evolutionary genetics/genomics/epigenetics will be advertise this Spring for a start from September 2020 (in the context of a recently awarded ERC Consolidator grant).

Susana Coelho Algal Genetics Group Integrative Biology of Marine Organisms Department (UMR8227) Station Biologique CNRS UPMC Place Georges Teissier CS 90074 29688 Roscoff cedex France tel: +33 (0)2 98 29 23 60 <http://www.sb-roscoff.fr/en/algal-genetics-0> <https://www.embo-embl-symposia.org/symposia/2020/EES20-09/index.html> Susana Coelho <[coelho@sb-roscoff.fr](mailto:coelho@sb-roscoff.fr)>

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## SouthAfrica EvolutionSocialityOrStress

Postdoc Project either on Reproductive Competition and Sociality or alternatively on Environmental harshness and social stress

(NOTE: We also advertise 2 paid positions as field managers for 1.5 to 4 years, and unpaid volunteer positions for 2-12 months. See other advertisements or ask via

email [carsten.schradin@iphc.cnrs.fr](mailto:carsten.schradin@iphc.cnrs.fr))

We are looking for a highly motivated postdoc to join the striped mouse project [www.strippedmouse.com](http://www.strippedmouse.com) and our group at the University of the Witwatersrand (Johannesburg). The postdoc is paid via a grant of the South African NRF for two years from Prof. Neville Pillay at the University of the Witwatersrand. The postdoc is expected to spend most of the time at the Succulent Karoo Research Station, conducting field work, analysing and publishing data.

We have two possible projects for a postdoc. Both projects are of similar interest to us. When applying, please state for which of the two projects you apply.

**Project 1: Reproductive Competition (Seasonal Unpredictability and Social Flexibility)**

For this project, a long-term dataset on social organisation of striped mice will be available for analyses (from 2003 to present) and further data collection will extend to 2021. Sociality (% of solitary versus group-living striped mice) will be studied in relation to population density and the intensity of reproductive competition, which is (i) very high during the spring breeding season when all females breed, (ii) absent during most summer dry seasons, (iii) low during summers with unexpected rains when few females breed (6 out of 17 summers in the current data set).

**Questions and predictions:** We expect that reduced reproductive competition during summer breeding will lead to more social instability in spring compared to summer, i.e. groups to be more stable in summer. We will also study which factors differ between females that breed during the summer vs. females that don't. Finally, the impact of rare summer breeding on population dynamics will be studied.

**Time planning:** Preferred start is June / July 2020 and the position must be started in 2020. The postdoc is expected to be in the field for most of the time but can plan two slots of 3 months each to spend at the University of the Witwatersrand.

**Project 2: Environmental harshness and social stress in a biodiversity hotspot: corticosterone might not be the only nor the best measure**

Animals have to cope with harsh environments and with stress but these phenomena are not synonymous. Stress is the activation of the sympathetic nervous system (SNS) and the hypothalamic-pituitary (HPA) axis, leading to the secretion of catecholamines and glucocorticoids, providing extra energy to overcome the stressor inducing stress. Environmental conditions are termed harsh when they are long-lasting and life threatening,

such as seasonal food shortage. Thus, while harshness demands energy saving, stress demands increased energy expenditure, predicting that the stress response will change as environmental harshness changes. In our study model, the African striped mouse *Rhabdomys pumilio*, we will measure several indicators of stress under varying conditions of harshness, some for the first time in an eco-physiological framework. We will evaluate three different aspects to differentiate between effects of harshness (dry season) and social stress (reproductive competition during the moist season) on survival, and fitness. These include: 1) neuropeptide y as an indicator of sympathetic activity and thus short-term stress; 2) corticosterone as an indicator of mid-term investment in increased energy expenditure; 3) Measures of resting metabolic rate and how these are related to corticosterone levels. Our study will be the first to assess how the stress response adapts to environmental harshness, predicting that in the harsh dry season, the HPA axis will be downregulated, while the response of the SNS will not change seasonally, allowing for an immediate response to life threatening events such as predation. Thus, we predict an adaptive desynchronization of the SNS and the HPA axis, a phenomenon so far only described as pathology in humans. This project will contribute fundamentally to our understanding of how to distinguish harshness from stress and how animals can cope with these two phenomena adaptively via different mechanisms.

**Time planning:** Preferred start is June / July 2020 and the position must be started in 2020. The postdoc is expected to be in the field for most of the time but can plan to spend 1-2 months in Strasbourg (France) for laboratory analyses and 4 months at the University of the Witwatersrand.

**Key requirements:** Strong statistical skills. Strong CV with 3 publications from the PhD and at least 1 publication per year from postdoc studies, some of them in high ranking journals (impact factor >3). Willingness to spend considerable time in the field in South Africa. Ability to analyse data and

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## StockholmU Paleotranscriptomics

Postdoctoral Fellow in Paleotranscriptomics

Stockholm University (Department of Molecular Biosciences, The Wenner-Gren Institute).

Closing date: 31 January 2020.

The interdisciplinary post doctorate position is shared between the groups of professor Love Dalén, affiliated with the Swedish Museum of Natural History and the Centre for Palaeogenetics ([www.palaeogenetics.com/LD](http://www.palaeogenetics.com/LD)) and associate professor Marc Friedländer, affiliated with The Department of Molecular Biosciences, Wenner-Gren Institute at Stockholm University ([www.su.se/mbw](http://www.su.se/mbw)) and SciLifeLab ([www.friedlanderlab.org](http://www.friedlanderlab.org)).

The Centre for Palaeogenetics (CPG) is a joint venture between Stockholm University and the Swedish Museum of Natural History. The overall objective of the centre is to bring researchers from different disciplines, such as biology, archaeology and geology, together into a state-of-the-art research environment dedicated to ancient DNA analyses.

The Science for Life Laboratory (SciLifeLab) is a national center for large-scale biosciences with a focus on health and environmental research. The center combines advanced technical know-how and state-of-the-art equipment with a broad knowledge in molecular biosciences. Read more about SciLifeLab at [www.scilifelab.se](http://www.scilifelab.se).  
**PROJECT DESCRIPTION** The project will focus on the discovery and characterization of RNA complements of ancient tissue samples of extinct animal species, with emphasis on regulatory microRNA molecules. The post doctorate position is funded by a SciLifeLab-SU grant (SU FV-5.1.2-0523-19).

**MAIN RESPONSIBILITIES** The successful applicant will spearhead and coordinate the paleotranscriptomic project. Specific tasks will depend on the expertise of the applicant (wet-lab or dry-lab) but can include: field work, RNA extraction and sequencing, computational quality control and characterization of detected sequences, homology analyses and wider interpretation of findings.

**QUALIFICATION REQUIREMENTS** 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.

**ASSESSMENT CRITERIA** The degree should have been completed no more than three years before the deadline for applications. An older degree may be acceptable under special circumstances, which may involve sick leave, parental leave, clinical attachment, elected positions in trade unions, or similar. In the appointment process, special attention will be given to research skills. We are looking for candidates with wet-lab and/or dry-lab skills in the fields of evolutionary biology, RNA biology or computational sequence analysis. Specific experience with palaeogenetics or microRNA annotation constitutes an advantage, but is not necessary. The candidate must be highly motivated, creatively thinking and have a record of high-quality scientific 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, with the possibility of extension under special circumstances. Start date 2020-03-01 or as per agreement. Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

**FURTHER INFORMATION AND HOW TO APPLY:**

<https://www.su.se/english/about/working-at-su/-jobs?rmpage=job&rmjob=11001&rmlang=UK>

Love.Dalen@nrm.se

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## Syngenta MalariaVectorResistanceModelling

PostDoc position: Syngenta.Basel.Malaria-VectorResistanceModelling

Syngenta is committed with sustainability and open to collaborate with external partners to develop solutions aligned with this commitment. In Syngenta Professional Solutions R&D, we are particularly interested in developing solutions for vector control. To be able to deploy these solutions in a sustainable way, we are expanding our predictive resistance management capabilities with this open position.

If you are a theoretical/computational biologist looking to make an impact on real-world problems and you have experience in building and using computational models in population biology or related fields, this role may be for you.

The position is for a postdoctoral researcher (2-year contract) to work on resistance-evolution models applied

to a malaria vector control project. The basic principle is to work in the area of insecticide resistance in the malaria vectors, *Anopheles* spp., using computer models to aid in developing a new technology and optimize resistance-management efforts.

This role offers abundant possibilities of collaborations with both our internal experts in vector-control biology and chemistry and any academic partners with a shared interest in the question of predictive resistance management.

You will also be expected and supported to contribute to scientific publications, participate in conferences and collaborate with academic partners. While still being able to investigate fundamental questions in resistance evolution, you can also expect to see your work have a positive impact out there by influencing the industry's resistance-management strategies with the ultimate goal of eradicating malaria.

For more details and to apply, follow this link:

<https://syngenta.taleo.net/careersection/switzerland/-jobdetail.ftl?job=18014647> Thanks again. Best regards, Ricardo Kanitz, PhD

Senior Scientist Resistance Modelling Global Product Biology Syngenta Crop Protection Ricardo.Kanitz@syngenta.com

Kanitz Ricardo CHBS <ricardo.kanitz@syngenta.com>

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## TempleU InvasionLandscapeGenomics

POSTDOC POSITION: Landscape genomics, Temple University, Philadelphia, USA

The Integrative Ecology Lab (iEcoLab) at Temple University is seeking creative and productive applicants for a postdoctoral researcher to lead research into the landscape genomics of the invasive spotted lanternfly pest (*Lycorma delicatula*). The spotted lanternfly is an Asian planthopper that was first introduced to the US just outside of Philadelphia, Pennsylvania in 2014, and has since spread to five nearby states. In addition to natural dispersal, human-assisted dispersal occurs during all lanternfly life stages: adults and nymphs hitchhike on cars and it can spread long distances in the egg stage because it lays eggs on mobile outdoor objects like trains and landscaping materials. It feeds on over 70 plant species, sometimes at very high densities, including eco-

nomically important species like maples, apples, hops, and grapes. Invaded vineyards have lost entire crops, affecting wine production. We are just beginning to understand its ecology and potential to cause economic and ecological impacts, but there is still more to learn. You can be at the forefront of cross-disciplinary research on this emerging invasion.

The postdoctoral researcher will be mentored by Jocelyn Behm (<https://www.iecolab.org/jocelyn-e-behm/>) and will be part of a larger collaborative team of postdocs, graduate students, and faculty at Temple University studying and modeling spotted lanternfly spread and impacts from the labs of Matt Helmus (Biology) and Benjamin Seibold (Math) (for a brief overview of the project see: <https://www.iecolab.org/projects/spotted-lanternfly/>).— The postdoc will also interact with a USDA-funded multi-university team of cross-disciplinary scientists and public stakeholders and will regularly attend working groups and meetings on this invasive pest.— The anticipated start date for the landscape genetics postdoc position is May 2020. The position is for one year, with the possibility for renewal upon satisfactory performance and funding. Salary is commensurate with experience and benefits are included.

The role of the landscape genetics postdoc will be to develop research using genomic techniques to explore the relative contributions of human-assisted versus natural dispersal to spotted lanternfly spread, as well as elucidate dispersal corridors and pathways in its invaded range, and other noteworthy spatial genomic patterns. There will be opportunities for the postdoc to develop and pursue additional research questions based on their interests.

Qualifications: A PhD in Biology, Ecology, Evolution, Genetics or other related field Expertise in landscape genetic and/or genomic lab and statistical methods and associated software A competitive publication record appropriate for career stage Well-organized and able to work both independently and in a team setting

Applications should be emailed to Jocelyn Behm (jebehm@temple.edu). Please send as a single PDF: Cover letter outlining qualifications, experience and why you are interested in the position Curriculum vitae including links to authored publications Name, phone number, and email addresses of three references

Review of applications will begin February 3 and will continue until the position is filled.

iEcoLab is in a new LEED-Gold certified building in historic Philadelphia. iEcoLab is part of the Center for Biodiversity, which provides state-of-the-art biodiversity research facilities along with support staff with

expertise in media development, GIS technology, high-performance computing, and genetics. Temple University, founded in 1884, is a public R1 university with a diverse student body of ca. 40,000 students. It is the sixth-largest provider of graduate school education in the U.S., is within the top 4% of research institutions in the U.S. and is in the top ten of the fastest gainers in ranking by the U.S. News & World Report Best Colleges.

Philadelphia is the birthplace of the United States and the first of only two UNESCO world heritage cities in the United States. It is filled with numerous attractions (e.g., Philadelphia Museum of Art, Philadelphia Zoo, Academy of Natural Sciences), amazing food, and it is a quick train ride to New York City and Washington DC. Philadelphia is nestled within an extensive national/state trail and park system and is very close to Valley Forge National Park, the Pocono Mountains, the unique Pine Barren ecosystem, and beaches of the Atlantic shore.

Temple University is an equal opportunity, equal access, affirmative action employer committed to achieving a diverse community. iEcoLab believes the crisis in biological diversity can only be addressed by scientists from diverse backgrounds and with diverse viewpoints. iEcoLab



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## The Jackson Laboratory Evolutionary Genomics

The Dumont Lab at The Jackson Laboratory is seeking a Postdoctoral Associate in the field of mammalian evolutionary genomics. The position is available initially for one year, but renewable for up to 4 additional years conditional on satisfactory performance and mutual agreement. Start date is negotiable, and as soon as March 2020.

The successful candidate will help lead a federally-funded research program investigating the evolution and genetic basis of species, population, and sex differences in meiotic recombination. The candidate will also be encouraged to develop independent research projects

that leverage the mouse model system, extensive JAX resources, and institutional expertise to address foundational questions about the mechanisms that generate genetic variation and how these mechanisms evolve.

Required qualifications include a recently obtained (2018 or later) PhD in Genomics, Evolutionary Biology, Genetics or a related field, and a genuine enthusiasm for basic biological research. The successful candidate must also have significant experience with the analysis of large genomic data sets. Expertise with mouse genetics is strongly desired, but not required. Ability to plan, execute, and analyze an independent research project is essential, as well as exceptional verbal and written communication skills. Preference will be given to self-motivated and career-oriented individuals.

The Jackson Laboratory (<http://www.jax.org>) in Bar Harbor, Maine, USA, is recognized internationally for its excellence in research, unparalleled mouse resources, outstanding training environment characterized by scientific collaboration, and exceptional core services - all within a spectacular setting adjacent to Acadia National Park. Translational research collaborations in genomics-based, personalized medicine are fostered through our JAX Genomic Medicine campus in Farmington, CT. In addition to lab-based training, JAX has developed a unique program for trainees to expand their professional skills in science communication, entrepreneurship, teaching, mentoring and laboratory management to best prepare postdocs for future career opportunities.

To apply, please submit (1) a cover letter describing past research accomplishments, research interests, and career goals, (2) a current CV, and (3) the contact information of three references, as one PDF file. Apply online at <https://careers-jax.icims.com/jobs/27498/-postdoctoral-associate/job>. All qualified applicants will receive consideration for employment without regard to race, color, religion, age, mental disability, physical disability, medical condition, sex, sexual orientation, genetic information, ancestry, marital status, national origin, veteran status, and other classifications protected by applicable state and local non-discrimination laws.

Beth Dumont <[Beth.Dumont@jax.org](mailto:Beth.Dumont@jax.org)>

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**TU Braunschweig LMU Munich**  
**Evolutionary Bioinformatics**

\*Postdoc position: Bioinformatic tools for integrative taxonomy\*

A postdoctoral researcher position in evolutionary bioinformatics (up to 3 years) is available at the Technische Universität Braunschweig, Germany (research group of M. Vences: <https://www.tu-braunschweig.de/en/-zoology/research/evolutionary-biology>) with collaborations at the Ludwig-Maximilians-Universität in Munich, Germany.

The aim of the postdoctoral project is the development of concepts and bioinformatic tools for taxonomic data, in the framework of the DFG-funded “Taxon-Omics” priority program (SPP 1991; [www.taxon-omics.com](http://www.taxon-omics.com)).

This encompasses

(1) developing and implementing tools for user-friendly archiving and retrieving of specimen-based information from data repositories, for taxonomic use and re-use; and

(2) developing a software pipeline that formalizes an integrative taxonomy workflow: using diverse kinds of data and combining various species delimitation approaches.

The research will be embedded in the DFG-funded Taxon-Omics priority program (SPP 1991), in which some 27 research projects are producing an array of data, from high-throughput imaging and chemotaxonomy to genomics, from protists, plants, fungi, and animals. The cutting-edge approaches to taxonomy in this program and the diversity of taxa and data, provide an ideal environment for collaborative research, and a unique opportunity to produce high-visibility methods. The research environment in this priority program is international and operates in English; international applicants are encouraged to apply.

The postdoctoral researcher will be based at TU Braunschweig, but will spend extended periods at the Ludwig-Maximilians University in Munich, working with biodiversity-informatics experts there. A close collaboration with the team of GFBio ([www.gfbio.org](http://www.gfbio.org)) is envisaged.

\*Main responsibilities\*

Research tasks:

- (1) Development of software pipelines and tools (90%)
  - Conceptual development
  - Implementation in a programming language, e.g. in R, C++, Python
  - Simulation studies
  - Collaboration with research groups in the Priority Program
  - Proof-of-principle studies with empirical data sets
  - Writing scientific publications

(2) Organizational tasks in the SPP (10%)\* \*

\*Applicant’s profile\*

We seek a highly motivated, scientifically excellent post-doctoral researcher with substantial programming skills.

\_Requirement: -

- a doctoral degree in a relevant discipline, e.g. biology, mathematics, physics, or informatics

\_Ideally, the researcher should combine as many as possible of the following skills:-

- expertise or interest in biological systematics, taxonomy, or another field of evolutionary biology

- familiarity with relevant programming languages

- experience with research data management and data repositories

- experience with machine learning approaches

- experience with analysis of genomic data

- excellent oral and written communication skills in English

- original research publications in peer-reviewed international journals

\*Remuneration\*

Salary will be paid according to Remuneration level 13 of the Wage Agreement for Public Service in the Federal States (TV-L). The position is available for 36 months.

Applications should be sent until 31st January 2020 to Miguel Vences (by email: [m.vences@tu-braunschweig.de](mailto:m.vences@tu-braunschweig.de)) and include (1) a cover letter explaining your background and motivation, (2) a CV, and (3) email addresses of two references.

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**UAntwerp**  
**EcologyInfectionsSmallMammals**

The Evolutionary Ecology Group at the University of Antwerp, Belgium ([www.uantwerpen.be/eveco](http://www.uantwerpen.be/eveco)) is starting three new projects on the ecology of infections carried by small mammals (use the links to see the project summaries)

\*BIODIV-AFREID: Biodiversity changes in African forests and Emerging Infectious Diseases: should we worry? (<https://www.uantwerpen.be/en/research-groups/eveco/research/main-ongoing-project/new-biodiv-afreid-/>) \*BioRodDis: Managing biodiversity in forests and urban green spaces. Dilution and amplification effects of rodent microbiome and rodent-borne diseases (<https://www.uantwerpen.be/en/research-groups/eveco/research/main-ongoing-project/new-bioroddis-mana/>) \*Co-infections, heterogeneity and behaviour: models and real rodents. (<https://www.uantwerpen.be/en/research-groups/eveco/research/main-ongoing-project/new-co-infections-/>)

We are looking for enthusiastic and competent postdocs to work in these projects. We can offer a position for a period between 1.5 and 4 years (the projects' salary budget is fixed, but monthly salary costs may vary considerably depending on seniority and, for foreigners, possible tax exemptions). Moreover, there will be opportunities every year to apply for competitive postdoc grants from the Flemish Research Foundation FWO <<http://www.fwo.be/>> ([www.fwo.be](http://www.fwo.be/)).

We are on the outlook for scientists with a proven record in ecology, epidemiology, modelling or other expertise relevant to these projects (preferably in some combination). Positions can start from March 2020 or soonest thereafter.

To apply, please send a cv and a brief motivation letter to [herwig.leirs@uantwerpen.be](mailto:herwig.leirs@uantwerpen.be) before 31 January.

"[herwig.leirs@uantwerpen.be](mailto:herwig.leirs@uantwerpen.be)"  
<[herwig.leirs@uantwerpen.be](mailto:herwig.leirs@uantwerpen.be)>

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**UArizona**  
**ComputationalPopulationGenomics**

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](mailto: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 Feb 3, 2020 and will continue until the position is filled. rgutenk@email.arizona.edu

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## UBasel SingleCellEvoDevo

A 4-years PostDoc position is available in the labs of Patrick Tschopp and Walter Salzburger at the University of Basel, Switzerland, to study the molecular and ontogenetic basis of dietary adaptations in vertebrates at the macro- and micro-evolutionary scale. This project is part of a Sinergia grant by the Swiss National Science Foundation (SNF) to H. Kaessmann (UHeidelberg), M. Clauss (UZurich), P. Tschopp (UBasel) & W. Salzburger (UBasel). Through a timely combination of state-of-the-art genomics technologies and a broad phylogenetic sampling, we will study the molecular and developmental underpinnings of dietary adaptations in vertebrates.

We are looking for a highly motivated young scientist, who holds a PhD in biology or related fields, and has a strong background in bioinformatics, single cell/transcriptome/genome analyses, as well as in evolutionary and/or developmental biology. She/he should have experience in supervising and project management. We offer a highly interactive, stimulating and interdisciplinary research environment, state-of-the-art technology platforms and research infrastructure, attractive employment conditions with a competitive salary, and career development opportunities.

The University of Basel ([www.unibas.ch](http://www.unibas.ch)) is the oldest university in Switzerland, located in one of Europe's most important life science hubs at the border between Switzerland, France and Germany. The Tschopp lab ([www.evolution.unibas.ch/tschopp/research/](http://www.evolution.unibas.ch/tschopp/research/)) studies the gene regulatory mechanisms of cell type specification and evolution in vertebrates. The lab of Walter Salzburger ([www.salzburgerlab.org](http://www.salzburgerlab.org)) studies the dynamics of adaptation and organismal diversification in cichlids from African Lake Tanganyika and other exceptional groups of fishes.

Applications should include a motivation letter, a CV, a list of publications, a statement about research interests, as well as the names and contact details of at least two referees. Applications (in the form of a single .pdf file) should be sent to Patrick Tschopp ([patrick.tschopp@unibas.ch](mailto:patrick.tschopp@unibas.ch)) and Walter Salzburger

([walter.salzburger@unibas.ch](mailto:walter.salzburger@unibas.ch)) until February 7th, 2020.

Prof. Dr. Walter Salzburger

Zoologisches Institut, Universität Basel Vesalgasse 1, 4051 Basel, Switzerland

phone: +41 (0) 61.207.0303; fax: .0301  
 eMail: [walter.salzburger@unibas.ch](mailto:walter.salzburger@unibas.ch) web:  
<http://www.salzburgerlab.org> fb: [http://-](http://www.facebook.com/waltersalzburgerlab)  
[www.facebook.com/waltersalzburgerlab](http://www.facebook.com/waltersalzburgerlab) Walter  
 Salzburger <[walter.salzburger@unibas.ch](mailto:walter.salzburger@unibas.ch)>

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## UCambridge AvianMacroevolPalaeontology

Post-doctoral research associate in avian macroevolution and vertebrate palaeontology (Fixed Term)

The Department of Earth Sciences, University of Cambridge, is seeking a Post-doctoral research associate (PDRA) in avian macroevolution to join the project “Modernization, diversification, and domination: Macroevolutionary origins of living bird diversity”, funded by UK Research and Innovation. The PDRA is for 2 years in the first instance with a possible extension for a third year. Ideally the candidate would start in 2020.

The scope of the project is broad, and it is anticipated that the successful candidate will have flexibility to pursue research questions aligning well with their interests. It is expected that the candidate will have experience and interest in at least one of the following areas: 3D morphological analysis and anatomical description, palaeoneurology (cranial endocast reconstruction and analysis), computational biomechanics, 3D geometric morphometrics, divergence time analysis, phylogenetic inference and study of diversification rates, phylogenetic comparative methods, ecological niche modelling, and/or historical biogeography.

Applications are invited from candidates with relevant expertise in fields such as vertebrate palaeontology, vertebrate morphology, molecular and morphological approaches to phylogenetics, and/or phylogenetic comparative methods, preferably including knowledge of avian diversity. The successful candidate will work as part of a wider team of vertebrate palaeontologists and evolutionary biologists working with a range of data types to study the origins of modern avian biodiversity, including questions related to how, when, and where extant avian diversity arose.

The candidate will have (or be about to obtain) a PhD and possibly some postdoctoral experience in a relevant area. They will have significant experience in macroevolution and/or vertebrate palaeontology, good communication skills, the ability to work as part of a team, good IT and data handling skills, and preferably a track record of publication in peer-reviewed journals.

Fixed-term: The funds for this post are available for 2 years in the first instance.

Click the 'Apply' button below to register an account with our recruitment system (if you have not already) and apply online.

Enquiries concerning this position should be directed to Dr. Daniel Field ( [djf70@cam.ac.uk](mailto:djf70@cam.ac.uk)), and applicants are encouraged to contact Dr. Field regarding the position. More information about our research group can be found here: <http://danieljfield.com/Home/People.html> Please quote reference LB22145 on your application and in any correspondence about this vacancy.

The University and the Department are committed to equality and diversity and inclusion and encourages applications from all sections of society. The University holds an institutional Athena-SWAN silver award and the Department is a bronze award holder. Details of some of the family-friendly policies operated by the University are at: <http://www.hr.admin.cam.ac.uk/pay-benefits/cambens-employee-benefits/family-friendly> .

The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

Apply online here: <https://hrsystems.admin.cam.ac.uk/-recruit-ui/pages/auth/login.xhtml> – Daniel Field, PhD

University Lecturer Department of Earth Sciences, University of Cambridge Downing Street | Cambridge | CB2 3EQ | United Kingdom [djf70@cam.ac.uk](mailto:djf70@cam.ac.uk) | Tel: +44 (0)7413 231913 [danieljfield.com](mailto:danieljfield.com) | <https://www.esc.cam.ac.uk/directory/daniel-field> Fellow in Natural Sciences Christ's College, University of Cambridge St Andrew's Street | Cambridge | CB2 3BU | United Kingdom <https://www.christs.cam.ac.uk/-person/dr-daniel-field-phd> UK Research and Innovation Future Leaders Fellow

Daniel Field <[djf70@cam.ac.uk](mailto:djf70@cam.ac.uk)>

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## UChicago Evolutionary Genetics Complex Traits

The Berg lab (<http://www.jjbpopgen.org/>) at the University of Chicago is looking to hire a postdoctoral researcher to join our group in the Department of Human Genetics at the University of Chicago (<https://genes.uchicago.edu/>). Broadly, our research focuses on problems in population and quantitative genetics, via a combination of mathematical theory, statistical method development, and data analysis. In particular, we are interested in learning about how factors like mutation, natural selection (positive, negative, direct, pleiotropic...), epistasis, and demographic history combine to shape patterns of genetic variation among individuals and populations. A major focus of the lab is on understanding the forces shaping genetic variation for complex traits and diseases. However, our general interest in population genetics is fairly broad, and I am open to exploring other project directions if an applicant has an interesting idea. Applicants could have a background in statistical, population, quantitative or evolutionary genetics, physics, computer science, mathematics or statistics.

Post-docs in our group will have the opportunity to be part of a fantastic community of human geneticists and evolutionary biologists at the University of Chicago. Other labs on the same floor include those of Maanasa Raghavan, Anna Di Rienzo, John Novembre, Matthew Stephens, and Xin He. Faculty in the Ecology and Evolution department < <https://pondside.uchicago.edu/-ee/> >, including Matthias Steinruecken, are located in nearby buildings.

I am committed to ensuring a safe, friendly, and inclusive workplace for all lab members, regardless of personal background, nationality, race or ethnicity, religion, sex, gender identity, sexual orientation, age, veteran status or medical condition. I especially encourage applications from persons traditionally underrepresented in the sciences.

If you are interested, you can apply by email to [jjberg \[at\] uchicago \[dot\] edu](mailto:jjberg@uchicago.edu). Please include a brief cover letter describing your research interests, a current CV, and contact information for at least two (and up to three) references with the email subject line "POSTDOC APPLICATION: [FULL NAME]".

The start date is flexible. The initial appointment is for one year, with the understanding that eventual renewal for additional years would be ideal for most applicants. The position can be renewed up to a maximum of five years of total career time as a postdoc. Applications will be considered on a rolling basis after that until the position is filled.

A version of this posting can be found at: <http://www.jjbpopgen.org/pdoc-ad.html>. The University of Chicago is an Affirmative Action/Equal Opportunity/Disabled/Veterans Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, age, protected veteran status or status as an individual with disability.

Jeremy J Berg Assistant Professor Department of Human Genetics University of Chicago

Jeremy Berg <jjberg@uchicago.edu>

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## UCopenhagen MicrobialEvolutionaryMedicine

### Postdoc position

Section of Microbiology, Department of Biology, Faculty of Science at University of Copenhagen is offering a postdoc position in microbe-host interactions commencing 1 May 2020 or as soon as possible thereafter.

### Project description

This postdoc project examines the effects of microbial interactions on host fitness, within an Evolutionary Medicine framework. The postdoc will test whether the bacterium *Helicobacter pylori* can protect against malaria complications in a mouse model. *H. pylori* is renowned for causing stomach ulcers and -cancer, but can also protect against the development of asthma and allergies. This complex relationship is shaped by thousands of years of co-evolution. Infection affects immune system development and has systemic anti-inflammatory effects if established early in life. The postdoc will explore the effects of early life *H. pylori* infection on development of malaria later in life, with a particular focus on identifying the role of immunoregulation by *H. pylori*, and microbiome interactions. Techniques include mouse experimental work with *Plasmodium chabaudi* and *P. berghei* infection, flow cytometry and host tissue transcriptomics.

The position is for 17 months with support for application for additional funding. The project will be carried out at Section of Microbiology, Department of Biology, University of Copenhagen, where you will engage in teamwork within the group and with national and international collaborators. The position is funded by a Sapere Aude grant from the Independent Research Council Denmark to PI Sandra Breum Andersen with the objective of studying intra- and interspecies interactions involving *H. pylori*.

### Qualifications:

We are looking for a highly motivated and ambitious researcher in evolutionary microbiology. Applicants should have some of the following qualifications, and an interest in acquiring the rest:

Ph.D. degree in microbiology, evolutionary biology, biotechnology, immunology or a closely related field, completed after March 2015 (discounting periods of leave) Experience with basic microbiological and molecular techniques Certification for mouse experimental work Bioinformatics skills for analysis of transcriptome data Experience with flow cytometry Fluency in English For further information, contact: Assistant Professor Sandra Breum Andersen at [sbandersen@bio.ku.dk](mailto:sbandersen@bio.ku.dk).

### Terms of employment

The position is covered by the Memorandum on Job Structure for Academic Staff.

Terms of appointment and payment accord to the agreement between the Ministry of Finance and The Danish Confederation of Professional Associations on Academics in the State.

The starting salary is currently at a minimum DKK 434,179 including annual supplement (+ pension up to DKK 74,244). Negotiation for salary supplement is possible.

### Application Procedure

The application, in English, must be submitted electronically by clicking APPLY NOW below.

### Please include

- Motivated letter of application, - Curriculum Vitae - Diploma and transcripts of records (Master and PhD) - Other information for consideration, e.g. list of publications (if any), - Full contact details (Name, address, telephone & email) of 1-3 professional referees

The University wishes our staff to reflect the diversity of society and thus welcomes applications from all qualified candidates regardless of personal background.

The deadline for applications is 25 February 2020, 23:59

GMT +1.

#### Procedures

After the expiry of the deadline for applications, the authorized recruitment manager selects applicants for assessment on the advice of the Interview Committee. Afterwards an assessment committee will be appointed to evaluate the selected applications. The applicants will be notified of the composition of the committee and the final selection of a successful candidate will be made by the Head of Department, based on the recommendations of the assessment committee and the interview committee.

The main criterion for selection will be the research potential of the applicant and the above mentioned skills. You can read more about the recruitment process at <http://employment.ku.dk/faculty/recruitment-process/> . General information about the Section is available at [www1.bio.ku.dk/microbiology](http://www1.bio.ku.dk/microbiology).

If you consider applying from abroad, you may find useful information on how it is to work in Denmark and at UCPH in this links: <http://ism.ku.dk>, <https://www.nyidanmark.dk/en-us/frontpage.htm> and <https://www.workindenmark.dk/> Part of the International Alliance of Research Universities (IARU), and among Europe's top-ranking universities, the University of Copenhagen promotes research and teaching of the highest international standard. Rich in tradition and modern in outlook, the University gives students and

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### UEdinburgh Bioinformatics

We are seeking a highly motivated bioinformatics or evolutionary genetics post-doc to work with Darren Obbard, Peter Keightley and Susan Johnston at the Institute of Evolutionary Biology, University of Edinburgh.

This post forms part of a project that aims to quantify variation in mutation rate and other evolutionary parameters across multiple species of Drosophilidae. It is funded by the BBSRC for 3 years from 1st June 2020.

The work will involve the development and implementation of bioinformatics pipelines and the evolutionary analysis of population-genomic data from multiple species, and applicants should have (or be about to complete) a PhD in bioinformatics, evolutionary genomics, population genetics, or similar. A successful candidate is likely to have experience with sequence-based bioinformatics (e.g. genome assembly, annotation and/or resequencing data), including a good knowledge of relevant scripting languages (e.g. Python and/or R, Bash, Snakemake etc) and software (e.g. read-mappers, genome-assemblers, variant-callers).

Please email [darren.obbard@ed.ac.uk](mailto:darren.obbard@ed.ac.uk) with informal enquiries

The full advert and a link for formal applications can be accessed here: [https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq\\_jobspec.version.4.jobspec?p\\_id=051172](https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec.version.4.jobspec?p_id=051172) For more information about what we do, see

Obbard <http://obbard.bio.ed.ac.uk/> Keightley <http://www.homepages.ed.ac.uk/pkeightl/> Johnston <https://sejohnston.com/> – Darren Obbard [darren.obbard@ed.ac.uk](mailto:darren.obbard@ed.ac.uk) The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

OBARD Darren <[darren.obbard@ed.ac.uk](mailto:darren.obbard@ed.ac.uk)>

### UGeorgia GenomicsEcophysiologyAbioticStress

We anticipate the availability of two postdoctoral positions as part of a collaborative project between the labs of John Burke and Lisa Donovan at the University of Georgia. These positions will involve the genomic and physiological analysis of abiotic stress responses in cultivated sunflower and related wild sunflower species. The ideal candidates will have a strong background in one or more of the following areas: population/quantitative genetics, genomics, bioinformatics, plant ecophysiology, and/or stress physiology. Funds are expected to support these positions over multiple years with a preferred start date of April 2020. Review of applications will begin immediately and will continue until the positions are filled.

To apply, please send your CV, a brief statement of research interests, and the names and contact information for three references to: [jmburke@uga.edu](mailto:jmburke@uga.edu) and [ldono](mailto:ldono)

van@uga.edu. Informal inquiries are also encouraged.

For more information about the UGA Department of Plant Biology, please visit:

<http://www.plantbio.uga.edu/> Information on the Burke lab can be found at:

<http://www.theburkelab.org/> Information on the Donovan lab can be found at:

<https://www.plantbio.uga.edu/directory/people/lisadonovan> John M. Burke, Ph.D. Tel: 706.583.5511 Fax: 706.542.1805 <http://www.theburkelab.org/> University of Georgia Department of Plant Biology Miller Plant Sciences Athens, GA 30602

jmburke@uga.edu

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## UGeorgia SpeciationGenetics

Post-Doctoral Position in the Sweigart Lab at the University of Georgia

A post-doctoral position in evolutionary genetics is available in the lab of Andrea Sweigart in the Department of Genetics at the University of Georgia. Our lab is broadly interested in the genetics of speciation in the model flowering plant *Mimulus* (monkeyflower). Funded projects include: 1) Evolutionary/genetic investigation of hybrid seed failure across *Mimulus*, 2) Molecular genetic analysis of interspecific incompatibilities that cause hybrid sterility, and 3) Development of functional genetics to link genotypes with ecologically important phenotypes. The postdoctoral researcher would have opportunities to contribute to any of these ongoing projects, but would also be encouraged to develop new research directions.

This position is ideal for someone with training or interest in quantitative genetics, population genomics, evolutionary ecology, and/or comparative genomics. We use computational and experimental approaches, and our studies often include a combination of genetic analysis, molecular biology, bioinformatics, and field experiments.

The Sweigart lab values diversity and aims to create a welcoming and inclusive lab environment. We are located at the University of Georgia, which has an exceptionally strong group of plant geneticists and evolutionary biologists. Greenhouse, laboratory, and computational facilities are also excellent. UGA is located in Athens, a vibrant college town with a low cost-of-living, wonderful community spirit, and lively arts/music scene. There is also easy access to Atlanta and to di-

verse outdoor recreational opportunities (e.g. Great Smoky Mountains NP, Savannah/GA Coast, Okefenokee Swamp).

The position is available for up to three years, with a \$47,000 salary and full benefits. The position is available immediately, but the start date can be flexible for the right candidate. To apply, please email a CV, a brief statement of research accomplishments and future goals, and contact information for three academic references to: sweigart@uga.edu. Informal inquiries are very welcome.

For more information about research in our lab, go to: <http://www.genetics.uga.edu/sweigartlab>. Andrea L. Sweigart Department of Genetics 120 East Green Street Davison Life Sciences Building, C218 University of Georgia Athens, GA 30602-7223

office phone: (706)-542-7001 sweigart@uga.edu

Andrea Sweigart <sweigart@uga.edu>

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## UJohannesburg Genomics

Postdoctoral fellowship in genomics of marine and/or sub-Antarctic island fauna, University of Johannesburg, South Africa

The Centre for Ecological Genomics and Wildlife Conservation at the University of Johannesburg (<https://molzoolab.co.za/>) invites applications for a Global Excellence and Stature (GES 4.0) postdoctoral research fellowship to the value of R 220 000 p.a. (US\$: 15 446, EUR: 13 830).

Suitable applicants should have been awarded their PhD no earlier than 2016, and should have experience in data generation, analysis and publication in any area of next-generation sequencing (e.g. WGS, RADseq, transcriptomics, metagenomics). Familiarity with R, unix and/or python are highly desirable, as is experience using a unix server.

The position involves both work on one of a number of new studies on coastal southern African or sub-Antarctic fauna as the lead researcher, and collaboration with post-graduate students on ongoing projects. An enthusiastic applicant will thus receive a career boost by gaining experience as an officially registered co-supervisor, and by being involved in the publication of numerous scientific papers as a first or contributing author.

The most suitable applicant will be selected on January

24. The successful applicant is then expected to work with the hosts on a project proposal that will be submitted to the University of Johannesburg's GES panel no later than January 31. The actual commencement of the position is flexible, but should be no later than 3 months after the outcome of the GES application has been announced. Depending on performance, the position may be renewed for up to two additional years.

Interested candidates should please send the following documents to Prof. Peter Teske (pteske101@gmail.com) and Prof. Bettine van Vuuren (bettinevv@uj.ac.za): \* Motivation letter not exceeding 1 page in which the applicant briefly summarises his/her skills and interests, and explains why they constitute a good match for this position \* A short CV \* Proof of having completed a PhD in 2016 or more recently (e.g. a scan of the PhD certificate or academic record) \* Pdf of at least one published (or in press) scientific paper; first authorships are preferred \* Contact details of three references

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Prof. Peter Teske Department of Zoology University of Johannesburg, Kingsway Campus Auckland Park 2006 South Africa Tel 27 (0)11 559 3373 <https://sites.google.com/view/peterteske/> –

For courier shipments: D3 LAB 339 (D LAB building on the far right (seen from D RING), two floors up, turn right through the glass door, last entrance on the left) Department of Zoology University of Johannesburg, Kingsway Campus (APK) Corner Kingsway and University Rd. Auckland Park 2092 Email: pteske101@gmail.com Tel.: 011 559 3373

Peter Teske <pteske101@gmail.com>

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## UKent UK GenomeEvolution

We are seeking to recruit an enthusiastic postdoctoral Research Associate to join the Ellis laboratory. The successful applicant will join an established research group working on fundamental and applied aspects of male reproductive biology. Ellis group lab interests encompass mechanisms of chromosome segregation during meiosis, cytoplasmic and nuclear remodelling during haploid germ cell development, and how DNA damage in developing male germ cells affects the quality of the resulting gametes.

You will work on a three-year project funded by the Leverhulme Trust that seeks to understand how trans-

mission ratio distorters manipulate the processes of gametogenesis and/or fertilisation so that they are passed on to more than 50% of offspring. You will work in close collaboration with the evolutionary and functional genomics lab, led by Dr Farré, to develop new approaches to answer how individual genes cause “drive”, how genome rearrangements contribute to drive, and the evolutionary consequences of drive for genome structure.

Techniques to be used will include cutting-edge single-cell genomics, RNA-Seq and ChIP-Seq techniques; therefore, candidates with experience analysing these types of data are encouraged to apply. Although the position is mainly focused on bioinformatics, depending on the candidate's interests there will be significant opportunities for you to participate in benchwork and gain appropriate lab skills.

To be successful in this role you will have:

- \* a PhD degree in Biology, Biochemistry or related discipline or equivalent
- \* bioinformatic analysis of genomics data, particularly RNA-Seq and ChIP-Seq
- \* a good understanding of evolutionary genetics and phylogenetic reconstruction
- \* at least one publication in a peer-reviewed journal

More information and how to apply here: <https://jobs.kent.ac.uk/vacancy.aspx?ref=STM-100-19> Deadline: Friday 31st January 2020

Marta Farré, PhD | Lecturer in Genomics School of Biosciences, University of Kent Stacey Building G17 Canterbury, Kent, CT2 7NJ, UK

ORCID: <https://orcid.org/0000-0001-9170-5767> Lab web: <http://www.farre-evogenomicslab.com/> "M.Farre-Belmonte" <M.Farre-Belmonte@kent.ac.uk>

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## ULiverpool SexRoles

How is behaviour constrained within typical sex roles?

A PDRA with expertise in behavioural or evolutionary ecology is required to join the research team of Prof Paula Stockley, Prof Jane Hurst and Prof Steve Pateron (University of Liverpool, Department of Evolution, Ecology & Behaviour), to investigate how behaviour is constrained within typical sex roles using wild house mice.

Utilising natural behavioural variation we will use an experimental approach, manipulating social environments under carefully controlled naturalistic conditions to: 1)

quantify how increased investment in competition affects parental behaviours in either sex, according to competitive phenotype, and 2) assess how parental responses to competition are mediated in either sex, to test for evidence of predicted physiological constraints on behaviour and trade-offs with costly competitive signalling. We will also utilise behavioural variation to compare genome-wide gene expression patterns, determining: 3) if a high level of parental care by males is associated with 'de-masculinisation' of gene expression, constraining the ability to successfully compete, and 4) if a high level of competitive behaviour by females is associated with 'de-feminisation' of gene expression, constraining the ability to successfully care for young.

The successful applicant will contribute to experimental design and run behavioural experiments within the Mammalian Behaviour and Evolution Group's custom-built research facilities (<https://www.liverpool.ac.uk/mammalian-behaviour-and-evolution/research/research-facilities/>). Working with laboratory and animal technicians, you will collect samples for hormone assays and gene expression studies, co-ordinate with the Centre for Genome Research in Liverpool to schedule genome-wide gene expression analyses, and interpret the resulting data. Good experimental and communication skills are essential, and an established interest in reproductive competition or parental care would be beneficial. You should have a PhD in Biological Sciences relevant to behavioural research.

This NERC-funded 3-year post is available to start from April 1st 2020. Salary range: 34,805 - 40,322 pa.

Informal enquires to [p.stockley@liv.ac.uk](mailto:p.stockley@liv.ac.uk).

Further details via <https://recruit.liverpool.ac.uk> (job ref 013294).

Closing date 21/1/2020.

Prof Paula Stockley Mammalian Behaviour & Evolution Group Institute of Integrative Biology University of Liverpool Leahurst Campus Chester High Road Neston CH64 7TE, UK

Tel: +44 151 794 6103 Mail: [p.stockley@liv.ac.uk](mailto:p.stockley@liv.ac.uk)  
Web:<https://www.liverpool.ac.uk/mammalian-behaviour-and-evolution/> Twitter: @MBE\_liv

“Stockley, Paula” <[P.Stockley@liverpool.ac.uk](mailto:P.Stockley@liverpool.ac.uk)>

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## UManchester PDF 2PhD ComputationalBiol

Postdoc position: Title: Manchester, evolution, microbiology, synthetic biology

Unravelling genotype-phenotype mapping in promoters and transcription factors that drive the evolution of resistance to multiple antibiotics. Specific focus of the project is on implementing synthetic/molecular biology in order to develop predictive understanding of multi-drug resistance evolution. We are looking for a wet lab scientist, with a keen interest in developing their own ideas, collaborating with theoretical biologists, and working independently. More information can be found at:<https://www.jobs.manchester.ac.uk/-displayjob.aspx?jobid=18478> The funding for this position is not dependent on the outcomes of Brexit, and as such UK's decision to leave the EU will not directly impact any of these positions.

For any interest or queries, please do not hesitate to contact me ([mato.lagator@manchester.ac.uk](mailto:mato.lagator@manchester.ac.uk))

PhD position 1: title: Manchester, computational biology PhD position in Predictive Genotype-Phenotype-Fitness mapping in E.coli- this collaborative project will combine several modelling approaches in order to develop a comprehensive genotype-phenotype-fitness map of metabolic networks in E.coli, capable of predicting the effects of individual single point mutations. Achieving such a mapping (which, in simple terms, means understanding what mutations do) would provide critical novel insights into bacterial evolution. The project is largely based around modelling, but will also involve getting your 'hands wet' in the lab. It is an ideal opportunity to cross the barrier between more formal sciences and biology, and as such we are ideally looking for people with background and experience in computer science, physics, mathematics, bioinformatics or a related discipline. More information can be found at: <https://www.findaphd.com/phds/project/bbsrc-dtp-predictive-genotype-phenotype-fitness-mapping-in-e-coli/?p113802> The PhD position is available only to candidates from the UK/EU, due to funder restrictions. The funding for this position is not dependent on the outcomes of Brexit, and as such UK's decision to leave the EU will not directly impact any of these positions.

For any interest or queries, please do not hesitate to

contact me (mato.lagator@manchester.ac.uk)

PhD position 2: Title: Manchester, antibiotic resistance evolution PhD position in Evolution of resistance to RNA Polymerase-targeting antibiotics - antibiotic resistance is becoming one of the largest problems for global health. The goal of this project is to improve our ability to predict antibiotic resistance evolution to a major class of drugs (those that target RNA polymerase), by linking mutations in RNA polymerase to their effect on 3D structure, and then understanding how those changes in the 3D structure impact the ability to evolve resistance to other antibiotics. The project will involve working with clinical samples of antibiotic resistant strains, and experimentally evolving resistance in them. The project is a collaboration with Prof. Benjamin Howden at the University of Melbourne, and will involve some time in Australia. More information can be found at: <https://www.findaphd.com/phds/project/-evolution-of-resistance-to-rna-polymerase-targeting-antibiotics-manchester-melbourne-dual-award/?p118037>

The PhD position is available only to candidates from the UK/EU, due to funder restrictions. The funding for this position is not dependent on the outcomes of Brexit, and as such UK's decision to leave the EU will not directly impact any of these positions.

For any interest or queries, please do not hesitate to contact me (mato.lagator@manchester.ac.uk)

Mato Lagator <mato.lagator@manchester.ac.uk>

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## UManitoba SeaLampreyPopGenomics

POSTDOCTORAL FELLOW POSITION IN POPULATION GENOMICS: POSITION NUMBER 28700

DEPARTMENT OF BIOLOGICAL SCIENCES, UNIVERSITY OF MANITOBA, CANADA

POSITION START DATE: We're targeting a start between March and July 2020, but we may be able to be flexible with start dates. Funding is for two years

CLOSING DATE FOR APPLICATIONS: We will begin review of applications 9 Feb 2020 and the position will remain open until filled

RANK: Post-doctoral fellow

SALARY RANGE: \$45,000-\$55,000 per annum (plus benefits), commensurate with qualifications and experience

PROJECT OVERVIEW: Sea lamprey (*Petromyzon marinus*) are native to the Atlantic Ocean and invasive in the Great Lakes, where they cause significant damage to the ecosystem and fishery. The objectives of this project are to use whole genome re-sequencing data to 1) model the invasion history of the Great Lakes system and 2) search for signatures of selection in the freshwater populations. Sea lamprey likely moved into Lake Erie and the upper Great Lakes following completion of the Welland Canal which allowed passage around Niagara Falls. Current population connectivity among the upper Great Lakes, Lake Erie, and Lake Ontario, and between the marine and invasive freshwater populations is not well characterized. Our goal is to use whole genome re-sequencing of individuals sampled across 20 sample sites within the Great Lakes, the Finger Lakes, and Lake Champlain, and along the Atlantic coast to model the demographics of the invasion history and gene flow within this system.

The primary management tool currently in use to control the invasive sea lamprey populations is lampricide treatment. The use of lampricides has reduced and held adult sea lamprey abundance to ~10% of that observed prior to the start of control efforts thus potentially exerting strong selection. We are in the position to test for the evolution of lampricide resistance at a suite of candidate genes associated with physiological and transcriptomic responses to experimental lampricide applications identified in ongoing related work. Given the very different environmental conditions experienced in marine and freshwater environments, we also may find evidence for selection associated with selection pressures other than lampricide applications (e.g., associated with osmoregulation and life history trait variation).

Please send any additional questions about the position to [colin.garroway@umanitoba.ca](mailto:colin.garroway@umanitoba.ca)

JOB DESCRIPTION: The primary task of this position will be to model gene flow and the demography of the invasion at the best resolution our data affords, and to test for signatures of selection associated with candidate loci for lampricide resistance. We also want to stress that the PDF will have the opportunity to develop and pursue other research questions of their own interests. You will be joining a well funded sea lamprey research program that is jointly led by Margaret Docker, Ken Jeffries, and myself Colin Garroway, and comprised of 2 postdocs, 2 PhD students, and 2 MSc students with additional students working on related questions in other species.

RESPONSIBILITIES: To contribute significantly to and lead experimental design, data interpretation, and statistical analysis related to the above described research



objectives. To trial new techniques and assay systems as required and keep abreast of the research literature relevant to the project. Disseminate research through publications in peer reviewed journals. To attend and contribute to research seminars, departmental meetings, and international conferences. Carry out administrative roles as required, e.g. organising physical or remote meetings with collaborators and arranging travel to meetings. Perform professional activities such as refereeing papers, editing journals, refereeing research grants, external examining, organising conferences, committee membership, and involvement with professional bodies.

**QUALIFICATIONS:** PhD (current or expected at commencement of contract) in evolutionary biology, computational biology, or genetics. Proven ability to process and analyse next-generation sequencing data. Proficiency with analysis software and programming languages, as well as ability to write or adapt scripts and pipelines for in silico genetic analysis. Ability to work both collaboratively and independently Well-developed leadership and management skills

**CONTACT:** Applicants should send their curriculum vitae, a cover letter expressing their research experience and research interests, and the names of three referees by email to:

Colin Garroway

Assistant Professor Department of Biological Sciences,  
University of Manitoba garroway-lab.com

Colin.garroway@umanitoba.ca

The University of Manitoba is strongly committed to equity and diversity within its community and especially welcomes applications from women, racialized persons/persons of colour, Indigenous peoples, persons

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and the ways that selection acts on new genetic material. Our lab will survey genome structure changes in *Drosophila* and other organisms, to determine how these mutations shape evolutionary outcomes.

The ideal candidate will have a thorough understanding of genetics, statistics, and bioinformatics. Working knowledge of one or more major programming languages will be essential. Experience working with Illumina short read sequencing and PacBio long molecule sequencing will be advantageous. Experience working with *Drosophila* will be beneficial. Candidates interested in learning programming are encouraged to contact the PI to discuss their skills and interest.

Applications must be submitted via [jobs.uncc.edu](http://jobs.uncc.edu). Candidates are strongly encouraged to contact the PI before submission to discuss their fit for the position. Candidates should include a CV, a brief summary of research interests including how their work will fit with the lab, and three references to be contacted on request. The position will remain open until filled. A copy of materials should be emailed to [Rebekah.Rogers@uncc.edu](mailto:Rebekah.Rogers@uncc.edu). Minimum salary will follow NIH recommendations.

Target start date is Spring 2020, with flexibility depending on circumstances. Initial contract will be for 1 year with potential for renewal for up to 4 years. The Rogers lab supports diversity in science. We are committed to a positive working environment for LGBTQ individuals, underrepresented minorities, and women in science.

Charlotte, NC is a diverse city with an excellent symphony, theater, and performing arts scene. Charlotte also offers a thriving arts scene and live music in NoDa and Ovens auditorium, farm-to-table restaurants, and family-friendly programs at local museums. A light rail connects UNCC campus to downtown and other neighborhoods. The cost of living is affordable, offering a comfortable lifestyle for postdocs.

Rebekah Rogers Assistant Professor Department of Bioinformatics UNC Charlotte

“rroger26@uncc.edu” <rroger26@uncc.edu>

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**UNorthCarolina Charlotte**  
**GenomeEvolution**

The Rogers lab at UNC Charlotte is hiring a postdoc to work on evolutionary genetics of genome structure. The lab is interested in duplications and chromosomal rearrangements, their role in creating new gene sequences,

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**UNorthCarolinaGreensboro**  
**DiseaseEvolution**

Postdoc position available immediately in Infectious Disease Evolution and Ecology at the University of North Carolina Greensboro. We seek a researcher to work on phylogeography, evolution, and ecology of black-legged

ticks\*, *Ixodes scapularis*\* and Lyme disease bacterium, *Borrelia burgdorferi*\* in the Southeast United States. Candidates should have experience in molecular population genetics methods and analysis with interests and opportunities in landscape ecology. The candidate is expected to be independent and motivated to work in a team environment, collaborate with other scientists and state officials, and mentor graduate students and undergraduates as appropriate. Strong interpersonal skills are required as well as strong analytic, writing, and oral communication skills. Candidate will be expected to write manuscripts, deliver presentations, and assist with grant writing.

UNCG was founded in 1891 as the first college serving women in the University of North Carolina system. UNCG became co-educational in 1963, and the campus has rapidly grown to include more than 30 academic buildings with 79 undergraduate programs in more than 100 areas of study, 65 masters programs and 30 doctoral programs. With more than 19,600 students and 2,500 faculty and staff, UNCG is the largest state university in the Piedmont Triad region of North Carolina and has an annual economic impact of more than \$1 billion. UNCG holds two classifications from the Carnegie Foundation for the Advancement of Teaching, as a “research university with high research activity” and for “community engagement” in curriculum, outreach and partnerships. More than \$30 million in grants and contracts for research and creative activity are awarded to faculty members annually. UNCG Biology Department has 25 research faculty 19 faculty lecturers, a Ph.D. program in Environmental Health Sciences and MS in Biology with > 45 graduate students and a growing number of postdoctoral research scholars.

Minimum Qualifications: Ph.D. in Evolutionary Biology, Ecology, Molecular Biology, or related fields, with preferred background and technical experience in population/landscape/evolutionary genetics methods and analysis.

Applicants must apply through Spartan Talent position 2475 at <https://hrs.uncg.edu/spartantalent/> with a C.V. and letter of interests explaining qualifications and career plans. Position will remain open until filled. Inquiries about the position can be addressed to Malcolm Schug at the Department of Biology, UNC Greensboro ([mdschug@uncg.edu](mailto:mdschug@uncg.edu)).

– Malcolm Schug Head, Department of Biology 312 Eberhart Building University of North Carolina Greensboro Greensboro, NC 27402

(336) 334-4960 (office) (336) 334-5839 (FAX)

Malcolm Schug <[mdschug@uncg.edu](mailto:mdschug@uncg.edu)>

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## UNorthCarolina TheoreticalModelsSpeciation

Postdoctoral Position in Servedio Lab at the University of North Carolina, Chapel Hill

A position is available for a Postdoctoral Research Associate in the lab of Maria Servedio at the University of North Carolina, Chapel Hill, to work on an NSF funded collaboration between Maria Servedio and Reinhard Bürger (University of Vienna) on theoretical models of speciation. Prior experience with theoretical modeling techniques (especially population genetic modeling) and a strong mathematical background is preferred. A Ph.D., programming experience and a strong background in evolution is required.

Research in the Servedio lab (<https://sites.google.com/view/servedio-lab/home>) concentrates on developing mathematical models of speciation and mate choice. Please contact Maria Servedio ([servedio@email.unc.edu](mailto:servedio@email.unc.edu)) for more information on the project involved in this position and other projects ongoing in the lab.

The appointment is for 1-2 years with a flexible start date. Submit applications including a cover letter, a CV, a description of research experience and interests and brief description of background in theory and related skills, and names and email addresses of two references to <http://unc.peopleadmin.com/postings/175126>, and please also send a copy of the cover letter and CV directly to Maria Servedio at [servedio@email.unc.edu](mailto:servedio@email.unc.edu)

The University of North Carolina at Chapel Hill hosts an active group in speciation, and more generally in Evolution and Ecology (see [bio.unc.edu](http://bio.unc.edu)). UNC is part of North Carolina’s Research Triangle, home also to Duke University, and North Carolina State University. Chapel Hill has reasonable living expenses, many outdoor activities, and a warm climate.

Informal inquiries are welcome. Review of applications will begin on January 15 and continue until the position is filled.

Dr. Maria Servedio Professor, Department of Biology University of North Carolina CB# 3280, Coker Hall Chapel Hill, NC 27599 Phone: 919-843-2692 Fax: 919-962-1625 e-mail: [servedio@email.unc.edu](mailto:servedio@email.unc.edu) <https://sites.google.com/view/servedio-lab/home> “Servedio, Maria R” <[servedio@email.unc.edu](mailto:servedio@email.unc.edu)>

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## UOulu Finland ChromatinResponse- ToEnvironmentalChangeInTrees

[https://rekry.saima.fi/certiahome/-open\\_job\\_view.html?did=5600&lang=en&id=00008538&jc=1](https://rekry.saima.fi/certiahome/-open_job_view.html?did=5600&lang=en&id=00008538&jc=1) Post-doctoral Researcher, Chromatin level responses to environmental change in forest trees

The University of Oulu is one of the biggest and most multidisciplinary universities in Finland. We are an international science community working in close cooperation with research institutes, companies, and the public sector. Together we form a globally significant research hub, relentlessly pushing the boundaries of known for a more sustainable and intelligent future.

We are now looking for a

Post-doctoral researcher to study chromatin level responses to environmental change in forest trees

to join the Ecology and Genetics unit at the University of Oulu.

A postdoctoral position for 24 months is available in the Department of Ecology and Genetics, University of Oulu, Finland (<http://www.oulu.fi/english/>) to work with Dr Tanja Pyhäjärvi (<http://www.oulu.fi/pyhajarvilab>).

Environment

The Department of Ecology and Genetics has strong expertise and tradition in plant population genetics. Current research topics include evolutionary and population genomics of forest trees, quantitative genetics, conservation genetics and molecular evolution of insects. We offer a scientific environment that is enthusiastic about plant evolutionary genetics, a possibility to develop your genomics and bioinformatics skills and initiate international collaboration. Within Europe, we collaborate closely with other forests geneticists via the Horizon 2020 project B4EST.

The project

The post doctoral fellow will be part of a new FOREVER consortium, a collaboration between University of Oulu, University of Helsinki and Natural Resources Institute Finland. Its goal is to understand the role of regulatory genomic regions in forest tree adaptation and evolution.

Qualifications

The applicant should have a doctoral degree, recorded

scientific expertise and interest in plant molecular biology, genetics and/or ecophysiology. Experience in bioinformatics, gene expression analysis, population, evolutionary and quantitative genomics is an advantage. The successful applicant will contribute to design, implementation and supervision of controlled and field trial experiments of Scots pine and silver birch. Research questions can be adjusted according to applicants interests and skills. The duties include a small amount of teaching and supervising students. The post-doctoral position will also include a 2-month research visit to Michigan State University to initiate applying new molecular genetic methodology in forest trees.

The salary will be based on the levels 5 - 6 of the demand level chart for teaching and research staff of Finnish universities. In addition, a salary component based on personal work performance will be paid (maximum of 50 % of the job-specific component).

Applications and further information

Apply online latest on Friday 31st January 2020. Please include the following attachments in your application: a letter of motivation (maximum 1 page) and (2) a CV that includes a list of publications and the contact details of at least two referees. [https://rekry.saima.fi/-certiahome/open\\_job\\_view.html?did=5600&lang=en&id=00008538&jc=1](https://rekry.saima.fi/-certiahome/open_job_view.html?did=5600&lang=en&id=00008538&jc=1) The position is filled as of 1st March 2020 (negotiable). A trial period of 6 months is applied in the position.

Further details are available from Dr Tanja Pyhäjärvi ([tanja.pyhajarvi\[at\]oulu.fi](mailto:tanja.pyhajarvi[at]oulu.fi)).

About Finland

Finland is one of the most livable countries, with a high quality of life, safety and excellent education system. The successful candidate will receive the benefits provided by the University of Oulu to university employees, including free occupational health care services, and obtain access to high-quality public affordable childcare services and schools.

Tanja Pyhäjärvi <[tanja.pyhajarvi@oulu.fi](mailto:tanja.pyhajarvi@oulu.fi)>

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## UOxford 2 MicrobiomeEvolution

TWO POSTDOCTORAL POSITIONS IN MICROBIOME ECOLOGY

University of Oxford, UK

Two postdoctoral positions (both 3 years in the first

instance, with the possibility of extension) are available in the Knowles Lab ([www.knowleslab.com](http://www.knowleslab.com)) in the Department of Zoology, University of Oxford.

We are seeking two motivated and highly qualified full-time postdoctoral research associates to work on a new project funded by an ERC Starting Grant (MUSMICRO). This project aims to unpick the causes and consequences of natural variability in the mammalian gut microbiome, using an insular population of house mice as a tractable, wild, model system.

#### Post 1: PDRA in Host-Microbiome Ecology

This position will involve using quantitative genetic techniques and other statistical approaches to explore how host genetics and environmental factors combine to mould individual variation in the gut microbiome among free-living mice. It will involve a mix of fieldwork, molecular biology lab work and bioinformatics/statistical analyses. The postholder will be based at the University of Oxford (Dept. Zoology) and also work closely with Dr Susan Johnston (<https://sejohnston.com/>), based at the University of Edinburgh.

Candidates should hold a PhD (or be near to competition) in a relevant subject (e.g. ecology/microbiology/genetics) and have demonstrable experience in quantitative ecology/quantitative genetics/bioinformatics and the analysis of complex datasets. The successful candidate will be expected to submit publications to scientific journals, attend and present at conferences, contribute to research degree student supervision and engage with other research partners on the project.

Further details are on the University website, vacancy ID 144371 [https://my.corehr.com/pls/uoxrecruit/-erq\\_search\\_package.search\\_form?p\\_company=-10&p\\_internal\\_external=E](https://my.corehr.com/pls/uoxrecruit/-erq_search_package.search_form?p_company=-10&p_internal_external=E) Post 2: PDRA in Mammalian Host-Microbiome Interactions

This position will focus on asking how naturally occurring variation in the gut microbiome affects host physiology, and ultimately host fitness traits (survival and reproduction). It will involve both collecting and analysing observational data from a wild mouse population, and later in the project performing controlled gnotobiotic (microbiome transfer) experiments in the lab. The postholder will be based at the University of Oxford (Dept. Zoology).

Candidates will hold a PhD (or be near to completion) in a relevant biological subject (e.g. physiology/microbiology/ecology/immunology) and have experience in the design and analysis of animal experiments. The position is well-suited to applicants with research experience involving mice, particularly in the

context of physiology, infection or the microbiome. The successful candidate will be expected to submit publications to scientific journals, attend and present at conferences, contribute to research degree student supervision, and engage with other researchers that partner on the project.

Further details are on the University website, vacancy ID 144372 [https://my.corehr.com/pls/uoxrecruit/-erq\\_search\\_package.search\\_form?p\\_company=-10&p\\_internal\\_external=E](https://my.corehr.com/pls/uoxrecruit/-erq_search_package.search_form?p_company=-10&p_internal_external=E) Informal enquiries about both positions can be made to: [sarah.knowles@zoo.ox.ac.uk](mailto:sarah.knowles@zoo.ox.ac.uk) Applications should be made through the University of Oxford Jobs website and vacancy IDs as specified above. Closing date: 12.00 noon, Friday 20th February 2020

Sarah Knowles Associate Professor and Tutorial Fellow of Keble College Department of Zoology University of Oxford 11a Mansfield Road Oxford, UK OX1 3SZ Tel: (+44) 1865 271210

Sarah Knowles <[sarah.knowles@zoo.ox.ac.uk](mailto:sarah.knowles@zoo.ox.ac.uk)>

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## UOxford 2 TreeOfLife

### TWO POSTDOC POSITIONS, UNIVERSITY OF OXFORD

The Darwin Tree of Life is a large collaborative project funded to sequence, assemble, annotate and release high quality complete genomes of 2000 eukaryote species from the UK, in the first phase. This Wellcome Trust-funded project is currently recruiting postdocs and other researchers to join the project, with posts at several Universities and research institutions around the UK. At the University of Oxford, Department of Zoology, we are seeking to appoint two postdocs with interest in evolution, ecology and genomes, especially of terrestrial arthropods (application closing date 21 Feb 2020; enquiries [peter.holland@zoo.ox.ac.uk](mailto:peter.holland@zoo.ox.ac.uk)). Links to opportunities at <https://www.darwintreeoflife.org/jobs> Peter Holland <[peter.holland@zoo.ox.ac.uk](mailto:peter.holland@zoo.ox.ac.uk)>

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## UPennsylvania EvolutionaryGenetics

Postdoctoral Fellow Position in Evolutionary genetics and comparative neurobiology

### Job Summary

The laboratory of Dr. Yun Ding in the Biology Department at the University of Pennsylvania is seeking a highly motivated and creative postdoctoral researcher to study the genetic and neural mechanisms underlying animal behavioral diversity in *Drosophila* species. Our lab takes a highly integrative and innovative approach to bridge the knowledge gap between behavioral genetics/neurobiology and evolutionary biology, aiming for a mechanistic understanding of how animal behavior evolves at different levels of biological organizations. The project uses rapid evolving *Drosophila* courtship behaviors as the comparative model system, and involved various start-of-art techniques including CRISPR genome editing, optogenetic manipulation, quantitative behavioral analysis, and single-cell transcriptome.

Expertise in any of the following areas is highly valued though not necessary:

Molecular biology and *Drosophila* genetics

Quantitative genetics and genomics

Single-cell transcriptome analysis

*Drosophila* neurobiology

Qualified candidates should hold a Ph.D. in evolutionary biology, neurobiology, genetics, or related field, and have peer-reviewed publication(s) or preprint(s) related to their Ph.D. work. Strong communication skills including scientific reading and writing in English is necessary. Successful candidates should be motivated to address fundamental biological questions. Position is available now and the start date can be flexible.

To apply, please send a cover letter, your CV (with a list of publications), and contact details of three references to [yding19@sas.upenn.edu](mailto:yding19@sas.upenn.edu).

Yun Ding Assistant Professor Department of Biology University of Pennsylvania 221 Leidy Laboratories 3740 Hamilton Walk Philadelphia, PA 19104 [yding19@sas.upenn.edu](mailto:yding19@sas.upenn.edu) <http://dinglab.org> “Ding, Yun” <[yding19@sas.upenn.edu](mailto:yding19@sas.upenn.edu)>

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## UPittsburgh EvolutionarySpeciesCoexistence

Interested in how evolution impacts—biodiversity and vice-versa?

The Turcotte lab at the University of Pittsburgh ([www.martinturcotte.net](http://www.martinturcotte.net))—is looking—to hire a multi-year postdoc to experimentally test how competition drives—rapid evolution and feedbacks onto the—determinants of species coexistence. This—work will combine experimental evolution in field mesocosms with cutting edge—approaches in species coexistence research. The project is an extension of—our—recent work using duckweed (DOI:10.1073/pnas.1816298116). The postdoc will—conduct a combination of field sampling, field experiments, lab experiments,—genetic analyses, and the application—(or development) of tools from the modern—coexistence theory. Although supported by an NSF grant the postdoc will have—opportunities to develop additional research projects.

To apply for the position please send an email to me—(turcotte@pitt.edu) including: 1) Cover letter: brief summary of your past research experience and why you are—interested in the lab and the position 2) C.V. (or resume) 3) Contact information for three references 4) Up to 3 PDFs of relevant publications or manuscripts in prep.

Applicants should submit their materials by—January—31st—2020—to ensure full consideration.

Martin—Turcotte, Ph.D. ———[www.martinturcotte.net](http://www.martinturcotte.net)  
Assistant—Professor, Department of Biological Sciences  
University—of Pittsburgh

“Turcotte, Martin” <[TURCOTTE@pitt.edu](mailto:TURCOTTE@pitt.edu)>

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## UPittsburgh PolyploidySpeciesInteractions

Postdoctoral position on Plant polyploidy and Species interactions University of Pittsburgh

Postdoctoral position the ecological effects of plant polyploidy on species interactions in the lab of Dr. Tia-Lynn

Ashman and in collaboration with Dr. Martin Turcotte. The postdoc will assess consequences of plant polyploidy on biotic interactions in two model plant systems. The focus will be on the effects of polyploidy on interactions with microbes, pollinators, and/or herbivores, as well as competitive interactions between plants. Responsibilities include setting up experimental populations, collection and analysis of data on species interactions, including community composition and interaction networks, and characterizing fitness effects, and the preparation of manuscripts for publication.

Position affords opportunities for undergraduate mentoring, scientific outreach, and the design and implementation of allied projects tailored to the skills and interests of the postdoc.

An ideal candidate has the following characteristics: 1) is evolutionary-minded, creative and a collaborative spirit, 2) background in community ecology, population biology or microbial or plant biology, 3) experience with insect identification, techniques for characterizing microbial communities and/or willingness to expand expertise, 4) strong statistical and writing skills.

Position is for two years and will be based in the Department of Biological Sciences at the University of Pittsburgh, Pittsburgh, PA. Start date is negotiable, but expected Spring/Summer 2020.

TO APPLY: Please send a CV and a cover letter describing your experience and interests to [tial1@pitt.edu](mailto:tial1@pitt.edu) along with the names and contact information for three referees. Review of applications will commence immediately and continue until filled.

Dr. Tia-Lynn Ashman Distinguished Professor of Ecology & Evolution Department of Biological Sciences University of Pittsburgh Pittsburgh, PA 15260-3929 412-624-0984 <http://www.pitt.edu/~tia1/> "Ashman, Tia-Lynn" <[tial1@pitt.edu](mailto:tial1@pitt.edu)>

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## UppsalaU 2 PlantEvolutionaryGenetics

Two Postdoctoral in Plant Evolutionary Genetics, Uppsala University: ONE WEEK LEFT TO APPLY!

Two postdoctoral positions are available in the research groups of Martin Lascoux and Pascal Milesi at the Evolutionary Biology Centre in Uppsala, Sweden. Our two research groups work on plant population genetics and evolutionary biology with a special emphasis on

local adaptation and genome evolution. We work on two groups of organisms: forest trees (spruces, birches, larches and poplars) and weeds (mainly the tetraploid weed *Capsella bursa-pastoris* and its close relatives). Please note that for both positions advertised below a background in Plant Biology is not required.

For more information please contact Martin.Lascoux@ebc.uu.se Pascal.Milesi@scilifelab.uu.se

The environment. The Evolutionary Biology Centre (<http://www.ebc.uu.se/>) is one of the world's leading research institutions in evolutionary biology. It is part of Uppsala University which is considered one of Europe's leading universities in the subject of biology bridging a broad variety of disciplines. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. Our lab is part of the Department of Ecology and Genetics and of the program in Plant Ecology and Evolution (<http://www.ieg.uu.se/>), an active environment addressing fundamental evolutionary and ecological questions with a wide range of different approaches. As members of the Science for Life Laboratory (<http://www.scilifelab.se/>) we make extensive use of high performance computing resources (<https://www.uppmix.uu.se/uppnex>) and extended bioinformatic infrastructure (<http://www.scilifelab.se/platforms/bioinformatics/>). The lab is situated in the student town of Uppsala that offers rich opportunities in cultural and outdoor activities. Sweden's capital, Stockholm, is less than an hour's train ride away.

For both positions the deadline to apply is January 15, 2020.

1. Postdoctoral position in population genomics of forest trees (Milesi group)

The project. The development of next generation sequencing has just begun to shed light on the complexity of the genetic architecture of quantitative traits. However, the role of structural rearrangements in their control has received limited attention. Coniferous species being of economic interest, a lot of genomic resources were produced during the last decades in both western Europe and north America. These species are also known to show strong pattern of local adaptation and their genome is enriched in paralogous genes. The project aims at studying the role of structural variants in adaptation and convergent evolution in Coniferous species.

The position. The successful applicant will be responsible for gathering genomic data and analyzing them. There will be also possibility to participate in other

ongoing projects on local adaptation in spruce. The applicant is expected to have a solid background in population genomics, including associated lab work and be familiar with UNIX environments and have experience in standard bioinformatic approaches using high throughput DNA and RNA sequencing data from platforms such as Illumina. Proficiency in relevant programming languages (e.g. awk, bash, Perl, Python, C) will be a strong advantage. Skills in modelling and simulation would be considered a merit.

How to apply. Applicants with a proven record and with a PhD degree are encouraged to apply. To apply please go to the website of Uppsala University where you can login and submit your application: <http://www.uu.se/en/about-uu/join-us/jobs/> The position is Postdoctoral researcher in Evolutionary genomics (Published 2019-12-10): <https://www.uu.se/en/about-uu/join-us/details/?positionId=303623> 2. Postdoctoral position on evolution of polyploids (Lascoux group, <https://lascouxlab.wordpress.com>)

The project. The present position is associated with a newly funded Swedish Research Council project that focuses on the evolution of genomic polymorphism and gene expression in polyploids, and more specifically on the importance of parental legacy in the evolution of allopolyploid species. This work will be based on new genome and transcriptome sequencing in *Capsella bursa-pastoris*. It is a continuation of the work published in PLoS Genetics in 2019 (Kryvokhyzha et al. PloS Genetics 15(2): e1007949; Kryvokhyzha et al. PloS Genetics 15(5): e1008131)

The position. The successful applicant will be responsible for growing

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## UppsalaU MetagenomicsAntimicrobialResistance

A postdoctoral researcher position in metagenomics with focus on the evolution of antimicrobial resistance (AMR) in wild mammals is available in the group of Katerina Guschanski at the Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University,

Sweden. The project is funded by the Carl Tryggers Foundation and the Swedish Research Council, FORMAS.

Our group is broadly interested in understanding how long-term evolutionary and short-term human-mediated processes shape biological diversity. To achieve this goal, and in particular to quantify the human impact on the environment, we take a temporal approach, studying time-spaced museum-preserved specimens of focal animal species and their associated microorganisms.

Project: We aim to understand the effect of human activities on host-associated microbiomes of wild mammalian populations. This project focuses on identifying antimicrobial resistance factors from ancient microbial communities derived from host-associated oral microbiomes, as preserved in dental calculus, a bacterial biofilm that builds on the teeth of vertebrates. Only few decades after the advent of the antibiotics mass production in 1940s, AMR has become a major global health threat. Yet, we know very little about the role of wild animal populations in the global AMR dynamics and the potential of wildlife to act as reservoirs for AMR genes. To provide a baseline of natural AMR prevalence, we will characterize naïve host-associated bacterial communities from time periods that predate the mass production of antibiotics. Subsequently, we will evaluate in how far human-produced antibiotics have changed the composition, functional profiles and particularly antimicrobial potential of host-associated microbiomes using several Scandinavian mammals as models. The project has the potential to expand into the study of oral pathologies, diet and population genomics of wild mammals. Thus, depending on the candidate's interests and experience, links can be built to pathogen evolution, conservation biology and ecology.

Qualification: The successful candidate must have a doctoral degree, or a foreign degree equivalent, in evolutionary biology, metagenomics, medical microbiology, bioinformatics or a related field. We are looking for a highly motivated, creative and skilled postdoctoral scientist to drive large-scale metagenomic data generation and analysis. Large parts of the data are already available, but additional data needs to be generated. Therefore, the ideal candidate will have both wet lab and bioinformatics skills. Experience with ancient DNA techniques will be an important asset. The candidate should have a solid background in evolutionary metagenomics, familiarity with AMR databases, experience with AMR analyses from metagenomic datasets, and bioinformatics skills to handle large-scale genomic data. A passion for science, good interpersonal skills, and strong writing skills are prerequisites for the position. We are looking for a candidate with an open-minded,

cooperative attitude, who can work both independently and in a team, and is open to training junior group members. This project is carried out in collaboration with a number of researchers in Sweden and worldwide. Strong interpersonal skills and the ability to communicate clearly across disciplines are required. Proficiency in English is a requirement.

The environment: The Evolutionary Biology Centre is one of the world's leading research institutions in evolutionary biology and part of Uppsala University - the oldest university in Scandinavia. Uppsala University, ranked 7th in the world in evolutionary biology (CWUR 2017), attracts approximately 40,000 students from all over the world, creating an international and stimulating research environment. The research themes at the Department of Ecology and Genetics ([www.ieg.uu.se](http://www.ieg.uu.se)) spans the scope from evolutionary ecology to genetics and metagenomics to studies of ecosystems. The city of Uppsala is a vibrant college town, conveniently situated 40 minutes by train from Stockholm (and even closer to the Arlanda International Airport), with beautiful and easy accessible surroundings.

Appointment: The postdoc is funded by a tax-free 2-year scholarship from the Carl Tryggers Foundation, amounting to 25,000 SEK per month. It is a requirement from the funding agency that you are an incoming postdoc (i.e. that your Ph.D. is not from Uppsala University). Start date is negotiable, but strong preference will be given to candidates that can start by May 2020.

How to apply: The application should include (1) a cover letter of max 2 pages that clearly states the candidate's research interests, qualification, and relevant experience, (2) CV including a list of publications, (3) copy of the doctoral degree, and (4) contact information including email and phone number for three references. Please clearly indicate

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## URochester SpeciationGenetics

A postdoc position is available in the Presgraves Lab at the University of Rochester (<http://blogs.rochester.edu/-PresgravesLab/>). We are looking for a motivated post-

doctoral researcher to contribute to our studies of the roles of selfish genetic elements in speciation among closely related *Drosophila* species. The ideal applicant will have experience in molecular biology, genetics, genomics, and/or population genetics. The lab is part of a collegial community in the Department of Biology with particular strengths in evolutionary genetics, speciation, and genetic conflict.

EOE / Minorities / Females / Protected Veterans / Disabled The University of Rochester is an Equal Opportunity Employer committed to diversity, and we encourage applications of candidates from groups underrepresented in higher education. More information on the University's diversity and inclusion policies is available at <https://www.rochester.edu/diversity/>. If interested, please send via e-mail a CV; a brief statement of research experience and interests; and contact information for 2-3 academic references.

Daven Presgraves <[daven.presgraves@rochester.edu](mailto:daven.presgraves@rochester.edu)>

Daven Presgraves <[dcpresgraves@gmail.com](mailto:dcpresgraves@gmail.com)>

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## USouthBohemia ParasitePhylogenomics

\*Two-year postdoc position: Phylogenomics & population genomics\*

Laboratory of Molecular Ecology and Evolution (Biology Centre, Czech Academy of Sciences and University of South Bohemia, Czechia) has funding for a Junior Researcher (postdoc) in the fields of phylogenomics & population genomics.

We are looking for an independent junior researcher with interest in evolutionary biology and strong background in bioinformatics and analyses of phylogenetic and population genetic data. Knowledge of Linux/unix and experience with scripting & programming languages (Python, R) and phylogenetic inference using WG data is necessary. Experience with population genomic and genome assembly and annotation pipelines is beneficial. A good publication record is important. The applicant should be able to coordinate a team of 2-3 students and have well-developed communication skills.

\*Job description:\*

This research position will include (mainly drylab) work on two grant funded projects:

1)Phylogenomics (and species diversity survey) of



Dicyemida, an enigmatic group of parasites from cephalopods (60% job time allocation).

2) Population genomics of adaptation in parasites. The project studies an interaction between host specificity, genomic differentiation and adaptation in a freshwater parasite (*Ligula intestinalis*) (40% job time allocation).

On the 1st project, the postdoc will be responsible for designing the research strategy (amplicon sequencing design for species diversity survey, selection of tools for extracting data from wg datasets) and for analyses of obtained data (transcriptome assemblies, amplicon assemblies, mining and filtering genes into matrices, phylogenetic reconstruction). On the 2nd project, the postdoc will provide an assistance with analyses of population level NGS data (whole genome re-sequencing data, RADseq, SNP calling, demographic inference, analysis of selection, etc.).

The postdoc will co-supervise one phd student and will be free to supervise undergrad students if desired (a valuable experience). There is an opportunity to take part in teaching, in field collecting trips and in other popgen projects running in the laboratory (incl. publication output).

\*We offer:\*

We are a relatively young but quickly developing laboratory with interests in evolutionary and ecological interactions between organisms and their environment. We use genetic (increasingly more genomic) data to answer the questions (e.g. <https://youtu.be/xvHSjEi0c44?t=7051>).

We have advanced computing resources available both in-house (> 300 nodes) and via a connection to the national grid (> 20,000 CPUs). The lab collaborates with institutions/labs abroad (e.g. University of Alabama [Kocot lab], University of Illinois [Catchen lab], University of Saskatchewan & Cornell [J.A.Andres]) and we co-organise the biennial Workshop on Population and Speciation Genomics (<http://evomics.org/2020-workshop-on-genomics-cesky-krumlov-czech-republic/>).

Biology Centre is a dynamic institution with strong international community of junior researchers and an "HR Excellence in Research" awarded institution. It is located in the centre of a university campus. English is the working language at the institution. The city of Ceske Budejovice is a charming historical city, has great outdoors nearby and it is located within easy reach of the capital, Prague, and several cities abroad (Vienna, Linz, Passau).

Funding is guaranteed for 1 year, with extension for another year, based on performance. Salary is 30% above the Czech average income, it is sufficient to cover all

necessary living costs with a margin (Czechia is a developed, yet relatively cheap country to live in). Biology Centre offers multiple employee benefits (fully covered health insurance, subsidised lunches, cultural/health programmes, etc.).

In case of questions, enquire using the contact info below.

\*Applications:\*

Applications should be prepared as a single pdf containing:

a CV (with publication list)

a detailed statement of research interests

names and contact information for 3 references.

Applications are welcome before 29 February 2019, sent by email to Associate Prof. Jan Átefka at [jan.stefka@gmail.com](mailto:jan.stefka@gmail.com). Prospective candidates will be interviewed in early March.

The position can be filled starting 1 April 2020, but will remain open until a suitable candidate has been found.

Jan Átefka, PhD

Laboratory of Molecular Ecology and Evolution

Institute of Parasitology, Biology Centre, Czech Academy of Sciences

Branisovska 31, Ceske Budejovice, CZECHIA

<https://www.paru.cas.cz/en/> <http://jstefka.info> Jan Stefka <[jan.stefka@gmail.com](mailto:jan.stefka@gmail.com)>

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## USouthernCalifornia HumanMedicalPopulationGenetics

A postdoctoral research position is available in the lab of Dr. Charleston Chiang in the Center for Genetic Epidemiology, Department of Preventive Medicine at the University of Southern California, Keck School of Medicine. The Chiang lab utilizes cutting-edge analytic tools to address questions at the intersection of human medical and population genetics. In particular, we have a strong interest in using genomic data to understand the evolution and architecture of complex traits and the history of diverse human populations. These insights will be critical for future medical genetics studies and in practicing personalized medicine.

The successful candidate will have substantial input in

the nature and the direction of the ongoing research projects within the lab and will be encouraged to explore projects that broadly fit within the lab's goals of learning about demographic history or natural selection from genetic variation data, or understanding genetic architecture and evolutionary history of complex traits. Opportunities are available to analyze large-scale genotyping and next-generation sequencing data in humans from diverse populations. Additional information about our lab and research can be found at: <http://chianglab.usc.edu>. The Center for Genetic Epidemiology is closely linked with the Departments of Preventive Medicine, Translational Genomics, and Quantitative Computational Biology. The Department of Preventive Medicine is one of the nations leading research programs in epidemiology and biostatistics, with particular expertise in genetics research in diverse populations. The Departments of Translational Genomics and Quantitative Computational Biology provide key technological, methodological and statistical supports of genetics research. Together, these Departments offer exceptional resources and collaborative opportunities for postdoctoral fellows. In particular, we work closely with research groups focusing on genetic epidemiology (e.g. Drs. Haiman, Wiemels, and de Smith), statistical genetics (e.g. Drs. Mancuso and Conti), and population genetics (e.g. Dr. Edge).

The position is available for 1 year and renewable contingent on successful progress and available funding. Salary will be competitive. The University of Southern California offers a competitive benefits package including medical, dental, vision, life insurance, accidental death and dismemberment insurance, and short and long term disability insurance.

Candidates should have a recent Ph.D. in biology, genetics, computer science, bioinformatics, computational biology, or a related field. Proficiency in one or more programming languages (e.g. python, perl, C++, R, etc.) and in Unix-based computing environments is essential. Competitive applicants will also have extensive experience in conducting human genetics or population genetics research and analyzing large genetic datasets, and the desire to apply for external fellowship funding. Preference will be given to candidates with a strong publication record, evidence of substantial research productivity, and ability to successfully communicate scientific information.

Review of applications will begin immediately and will continue until the position is filled. The position is expected to start in Spring or Summer 2020, though specific dates are negotiable.

Interested candidates should submit a CV, short (1-2

pages) cover letter describing your research interests and fit within the lab, and contact information for 2-3 references. Informal inquiries are also welcomed and should be addressed to Dr. Charleston Chiang at [charleston.chiang@med.usc.edu](mailto:charleston.chiang@med.usc.edu).

– Charleston W. K. Chiang, Ph.D. Assistant Professor of Preventive Medicine Center for Genetic Epidemiology Keck School of Medicine Assistant Professor of Biological Sciences Quantitative and Computational Biology Section University of Southern California <http://chianglab.usc.edu> Twitter: @CharlestonCWKC

“Chiang, Charleston” <Charleston.Chiang@med.usc.edu>

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## UTuebingen InvasivePlants

The Plant Evolutionary Ecology group at the University of Tübingen is seeking a motivated

POSTDOC IN EVOLUTIONARY ECOLOGY OF INVASIVE PLANTS

to conduct common garden and field experiments and analyse global-scale ecological and environmental data on invasive knotweeds (*Reynoutria ssp.*). The postdoc will work in the German-Chinese project “Evolution of plant defenses during a plant invasion”, which, together with the closely associated “Make Our Planet Great Again” project “Genomics and Epigenomics of Plant Invasion”, attempts to understand large-scale variation and adaptation, and their underlying functional and genomic mechanisms, in native vs. introduced populations of invasive knotweeds.

The project is funded by the German and Chinese science foundations (DFG and NSFC), and is in close collaboration with Fudan University in Shanghai and other groups in China and Europe. The data generated by the postdoc will be linked to ecological, chemical and genomic data generated by other groups, so there will be excellent opportunities for collaborations and learning outside of one's own project.

We are looking for someone who loves experiments as much as we do, who likes to ask big questions and juggle with large data sets, and who is interested in spending a significant amount of time in China. Applicants should have a PhD in ecology, evolution, or a related field. Strong candidates will also possess: (1) creativity and independence, (2) excellent oral/written communication skills, and (3) a strong affinity to R.

The position is full-time and funded for 2 years. It will be based at University of Tübingen. The starting date is flexible, but ideally in spring/summer 2020. The payment will be at German payscale level E 13 TV-L. To apply, please email a cover letter, CV and the contact details of three references as a single PDF to Oliver Bossdorf ([oliver.bossdorf@uni-tuebingen.de](mailto:oliver.bossdorf@uni-tuebingen.de)). If you have questions about the position, please also contact Oliver. Review of applications will begin in mid February and will continue until we found a suitable candidate.

Tübingen is a beautiful university town with a high quality of life and one of the oldest universities in Germany. The Plant Evolutionary Ecology group ([uni-tuebingen.de/plantevoeco](http://uni-tuebingen.de/plantevoeco)) in Tübingen studies a broad range of questions on plant variation and adaptation in changing environments.

The University of Tübingen is committed to increase the proportion of women in science, and qualified women are therefore particularly encouraged to apply. Equally qualified applicants with disabilities will be given preference.

– Oliver Bossdorf Professor of Plant Evolutionary Ecology Institute of Evolution & Ecology University of Tübingen 72076 Tübingen, Germany [oliver.bossdorf@uni-tuebingen.de](mailto:oliver.bossdorf@uni-tuebingen.de) [www.uni-tuebingen.de/plantevoeco](http://www.uni-tuebingen.de/plantevoeco) Oliver Bossdorf <[oliver.bossdorf@uni-tuebingen.de](mailto:oliver.bossdorf@uni-tuebingen.de)>

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## UUtah EvolutionaryGenomics

Postdoc position: Convergent Evolution in Extreme Environments

The Clark Lab ([nclarklab.org](http://nclarklab.org)) is hiring post-docs to drive research in convergent evolution and evolutionary genetics. Current projects in the lab study the genetic basis of adaptation to extreme behaviors and environments, such as diving in marine mammals, regressive evolution of eyesight in subterranean species, and adaptations to high-altitude (relevant papers below). These projects require interplay between computation and experiments, involving comparative genomics, chromatin and gene expression analysis, zebrafish embryology, and cell culture. Project extensions into clinical genetics are also underway for congenital eye diseases.

We seek candidates motivated to study evolutionary phenomena and possessing computational genomics and/or

wet lab expertise in developmental biology and cell culture. We will consider candidates with experience in both of these areas and at their interface. Post-docs will also have the opportunity to study the evolution of systems of their choice and to participate in the sequencing and annotation of the marsupial mole genome. Applicants should send CV, publications, and letter of interest to [nclark@utah.edu](mailto:nclark@utah.edu).

The Clark lab is located in the Department of Human Genetics at the University of Utah. The Department is home to research in evolutionary genetics, evolution and development, model organism genetics, genomics, disease models, and clinical genetics. The Clark lab is also part of the Cluster in Evolutionary Genetics and Genomics (CEGG) that catalyzes collaboration and instruction between evolution researchers throughout the University. The environment in the lab and surroundings provides ample opportunities for training in related fields in addition to evolutionary genomics.

\* Chikina M, Robinson JD, Clark NL. Hundreds of genes experienced convergent shifts in selective pressure in marine mammals. *Molecular Biology and Evolution*. 2016. 33(9): 2182-2192. \* Partha R, Chauhan BK, Worman-Ferrera Z, Robinson JD, Lathrop K, Nischal KK, Chikina M\*, Clark NL\*. Subterranean mammals show convergent regression in ocular genes and enhancers, along with adaptation to tunneling. *eLife*. 2017; 6: e25884. \* Meyer WK, Jamison J, Richter R, Woods SE, Kronk C, Partha R, Kowalczyk A, Chikina M, Bonde RK, Gaspard J, Lanyon JM, Furlong CE, and Clark NL. Ancient convergent losses of Paraoxonase 1 yield deleterious consequences for modern marine mammals. *Science*. 2018; 361(6402): 591-594. \* Kowalczyk A, Meyer WK, Partha R, Mao W, Clark NL, Chikina M. RERconverge: an R package for associating evolutionary rates with convergent traits. *Bioinformatics*. 2019; 1-3: btz468. \* RERconverge Package @ GitHub

Job posting: <http://clark.genetics.utah.edu/post-doctoral-positions-in-evolutionary-genomics/>  
Nathan Clark <[nclark@utah.edu](mailto:nclark@utah.edu)> Nathan Clark <[nclark@utah.edu](mailto:nclark@utah.edu)>

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## UWyoming 4 MicrobialGenomics

Four postdoctoral positions in microbial ecology at the University of Wyoming: functional genomics, microbial biogeography, and paleoecology

Position descriptions available below and on the UW job

site (positions 19005029, 19005030, 19005031, 19005032) at <http://bit.ly/2Ikqrfo>. This search is part of a cluster hire of postdoctoral research associates, supported by a 5-year, \$20 million NSF EPSCoR RII Track-1 grant to the University. In this project we will study microbial life and its ecological consequences; additional details can be found at <http://www.uwyo.edu/epscor/microbial-ecology>. Postdoctoral research associate in Microbial Ecology and Genomics (position 19005029): The van Diepen Soil Microbial Ecology lab (<http://www.uwyo.edu/esm/faculty-and-staff/linda-van-diepen/index.html>) at the University of Wyoming is seeking a postdoctoral researcher with expertise in microbial ecology and genomics. Minimum requirements include a PhD in a relevant discipline, experience with omics methods including proficiency in bioinformatics analysis of omics data (specifically metagenomics and transcriptomics), and experience in R programming or other statistical software. Additional preferred qualifications include experience with microbial culturing techniques, biogeochemistry, field work, and method development.

Postdoctoral research associate in Microbial Biogeography (position 19005030): The Albeke Ecoinformatics Lab (<https://www.uwyo.edu/wygisc/people/-albeke.shannon/>), in collaboration with the Shuman Lab (<https://sites.google.com/site/shumanlab/Home>), at the University of Wyoming is seeking a postdoctoral researcher with expertise in computational/spatial modeling and biogeography. Minimum requirements include a PhD in a relevant discipline, proficiency in spatial analyses and statistics, and R programming or other statistical modeling software. Additional preferred qualifications include experience with microbial ecology, biogeographic or community assembly analyses, environmental metagenomics, individual-based modeling experiments, and field work.

Postdoctoral research associate in Microbial Functional Genomics (position 19005031): The Ward research group at the University of Wyoming (<http://www.naomiwardlab.com/>) is seeking a postdoctoral researcher with expertise in microbial functional genomics. Minimum requirements include a Ph.D. in a relevant discipline, and experience with omics methods including proficiency in bioinformatics analysis of omics data (specifically metagenomics and transcriptomics), and experience in R programming or other statistical software. Additional preferred qualifications include expertise in proteomic or metabolomic approaches to microbial ecology, as well as fieldwork experience.

Postdoctoral research associate in Paleocology, Paleoclimatology, and Organic Geochemistry (position 19005032): The Shuman Lab (<https://sites.google.com/->

[site/shumanlab/Home](http://sites.google.com/site/shumanlab/Home)) at the University of Wyoming is seeking a postdoctoral researcher with expertise in analyses of sedimentary biomarkers, such as GDGTs and alkanes, using HPLC or GC-IRMS. Minimum requirements include a PhD in a relevant discipline, experience with organic geochemistry lab techniques, and experience with statistical analyses using R or other similar platforms. Additional preferred qualifications include publication of paleoecological or paleoclimatic research, experience with sediment core collection and analysis, or microbial culturing techniques. The University of Wyoming is an Equal Employment Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability or protected veteran status or any other characteristic protected by law and University policy. Please see [www.uwyo.edu/diversity/fairness](http://www.uwyo.edu/diversity/fairness). To apply, please complete the online application through <http://bit.ly/2Ikqrfo> with the correct position number (positions 19005029, 19005030, 19005031, 19005032). Please upload a single PDF file containing a cover letter, CV, contact information for three references, and two papers describing recent research. Review of applications will continue until a suitable applicant is identified. Interested applicants may apply for more than one position as long as they meet the minimum and preferred qualifications.

Linda van Diepen Assistant Professor Soil Microbial Ecology

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## UZurich UHelsinki 2 PlantMicrobeInteractions

Two post doc positions on the Ecology of Plant-Microbe Interactions in Research Group of Prof. Anna-Liisa Laine

1. Post-doctoral position (2 years) in Ecology of Plant-Microbe Interactions at the University of Zürich

We are seeking a post doctoral researcher to work in a consortium project aiming to understand how biological diversity could be integrated into our food production systems to develop sustainable and climate-smart farm-

ing practices. Specifically, we are addressing questions regarding how above-ground plant diversity links with below-ground microbial diversity, and how these jointly affect plant fitness, resistance and resilience to both biotic and abiotic stress using experimental approaches. The consortium joins expertise in agriculture, plant ecology, soil microbial ecology and climate science. It is an exciting interdisciplinary effort addressing cutting edge scientific questions with direct applicability. For more information about the consortium, please visit: <https://carbonaction.org/en-stn-multa/> For more information, please contact prof. Anna-Liisa Laine (anna-liisa.laine(at)ieu.uzh.ch). For more information on the research group of Prof. Laine, please visit our website <https://lainelab.net/> . Postdoctoral position requirements:

- The successful applicant should have a doctoral degree in ecology, evolutionary biology, plant biology, microbial ecology or agricultural sciences (or similar) - Previous experience working with questions and methods related to plant diversity and ecology of plant associated microbes (mycorrhizae / plant pathogens etc.) - Previous experience in analysis of microbial community sequence data is not necessary but considered an advantage. - Excellent written and verbal communication skills - Ability to conceive, execute and complete research projects - Ability to think independently and creatively - Ability to work in a team and independently.

How to apply Send your application by 22 January 2020 as a single pdf file to Jacqueline Moser (jacqueline.moser(at)ieu.uzh.ch). Applications should include the following documents as a single pdf file: motivational letter (max 1 page), CV (max 2 pages), and publication list. Please also include contact information of two persons willing to provide a reference letter by separate request.

Starting date March 2020 but to be determined by mutual agreement.

2. Post-doctoral position (1.5 years) in Ecology of Plant-Microbe Interactions at the University of Helsinki

We are seeking a post doctoral researcher to work in a consortium project aiming to understand how biological diversity could be integrated into our food production systems to develop sustainable and climate-smart farming practices. Specifically, we are addressing questions regarding how above-ground plant diversity links with below-ground microbial diversity, and how these jointly affect plant fitness, resistance and resilience to both biotic and abiotic stress using experimental approaches. The consortium joins expertise in agriculture, plant ecology, soil microbial ecology and climate science. It is an exciting interdisciplinary effort addressing cutting

edge scientific questions with direct applicability. For more information about the consortium, please visit: <https://carbonaction.org/twinwin-project/> . The tasks of the post doc include:

- Participating in a multi-year field trial that manipulates above- ground plant diversity - Design and implementation of potential greenhouse/common garden experiments - Literature synthesis.

For more information, please contact prof. Anna-Liisa Laine (anna-liisa.laine(at)helsinki.fi).

For more information on the research group of Prof. Laine, please visit our website <https://lainelab.net/> Postdoctoral position requirements:

The successful applicant should have a doctoral degree in ecology, evolutionary biology, plant biology, microbial ecology or agricultural sciences (or similar), and previous experience working with questions and methods related to plant diversity and ecology of plant associated microbes (mycorrhizae / plant pathogens etc.). We seek candidates with excellent written and verbal communication skills, and the ability to conceive, execute and complete research projects, and to think independently and creatively. Previous experience in analysis of microbial community sequence data is not necessary but considered an advantage.

How to apply Applications should include the following documents as a single pdf file: motivational letter (max 1 page), CV (max 2 pages), and publication list. Please also include contact information of two persons willing to provide a reference letter by separate request.

Please submit your application using the University of Helsinki

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

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## Verbania Italy MicrobialEvolution

\*Postdoc Position in Microbial Ecology and Evolution, Metagenomics and the Environmental Antibiotic Resistance\*

The Molecular Ecology Group (MEG) of the Water Research Institute of the National Research Council of

Italy (CNR-IRSA) in Verbania is looking for a post-doctoral researcher in microbial ecology with specific interest in antibiotic resistance, community ecology and evolution, and experimental ecology.

Specific tasks will focus on the study of freshwater microbial communities, in their resistome and pathobiome, and in their responses to huge changes in the water quality and in physical and chemical parameters. Studies will be performed both, in situ, following a large project of lake restoration involving Lake Varese, and in lab, with experimental synthetic and natural communities.

Expected Profile: PhD or equivalent certified experience in biology, natural sciences, environmental sciences or in related topics. Good lab skills and experience in metagenomic- and metagenetic-based approaches. Strong independence and willingness in collaborating in researches covering multiple fields of microbial ecology.

The MEG is an exciting, interdisciplinary group with excellent facilities and a leading position in microbial ecology, biogeography and in the study of antibiotic resistance in the environment. The MEG is located in Verbania at the CNR-IRSA Institute, on the beautiful shore of Lake Maggiore in Italy at the border with Switzerland. The MEG is involved in several projects in partnership with more than 50 national or international leading research centres and universities. The selected candidate will (possibly) have free access for the first month to the Institute's guest house. The contract is for 1+1 year, extendable for a maximum of additional 4 years. Net salary is about 1500 euros/month for the first year, the position is not imposing the continuative presence of the researcher in the Institute.

Deadline for application: 7th of February 2017, interview: 24th of February 2020 (10:30 AM Italian time), expected starting date: end of March 2020.

To apply: Please contact Dr. Gianluca Corno (gianluca.corno@cnr.it) to get more information on the procedures (a couple of forms in Italian to be filled, CV and publications list are required).

Diego Fontaneto <diego.fontaneto@cnr.it>

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## WashingtonStateU MicrobialAdaptation

The labs of Maren Friesen (Washington State University, Pullman) and Stephanie Porter (Washington State University, Vancouver) are seeking a postdoctoral research associate to study the evolutionary and ecological genomics of environmental adaptation in wild Mesorhizobium bacteria. These Mesorhizobia are nitrogen-fixing bacterial symbionts that inhabit the root nodules of a native west coast legume. We have identified a Mesorhizobium genomic island associated with nickel tolerance in generalist lineages that grow on and off nickel-enriched serpentine soil (Porter et al. 2017 ISME), and have expanded this project to encompass ~700 strains. The system has multiple specialist and generalist clades and is poised to address questions about the ecological and genomic determinants of adaptation in wild microbes. This NSF project also includes Joel Griffiths (Brigham Young University) who is testing the molecular genetic basis of nickel tolerance.

Our ideal candidate would have a strong quantitative background, firm understanding of evolutionary ecology, excellent written and verbal communication skills, and ability to work well in a collaborative team. Training in at least one of genomics, bioinformatics, phylogenetic methods, and/or biostatistics is desirable. The position will be based in Pullman WA and the successful applicant will have access to the excellent facilities at WSU for plant growth, phenomics, genomics, biochemistry, and microscopy. There is a strong intellectual community in the Palouse spanning WSU and our neighbor 7 miles to the east, the University of Idaho in Moscow, ID. Pullman and Moscow are vibrant small towns with a strong sense of community and ready access to outdoor activities. The postdoc will have regular virtual meetings with co-advisor, Dr. Porter, and will visit collaborators at the Vancouver campus twice a year.

Start date is flexible and Maren is at the ASN meeting in Asilomar (Jan 2020) if you'd like to chat! For more information please contact Maren Friesen at m.friesen@wsu.edu and/or Stephanie Porter at stephanie.porter@wsu.edu.

< [https://inboxwhenready.org/?utm\\_campaign=signature&utm\\_medium=email&utm\\_source=signature](https://inboxwhenready.org/?utm_campaign=signature&utm_medium=email&utm_source=signature) > I'm using Inbox When Ready < [https://inboxwhenready.org/?utm\\_campaign=signature](https://inboxwhenready.org/?utm_campaign=signature)

[signature&utm\\_medium=email&utm\\_source=signature](#)  
> to protect my focus.

Maren Friesen <maren.l.friesen@gmail.com>

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## WesleyanU EvolutionPlasticity

Postdoctoral Position Available in Plant Evolutionary Ecology, Sultan Lab

Transgenerational plasticity

The Sultan lab at Wesleyan University is seeking a postdoctoral research associate with greenhouse experience who is scientifically creative, a capable statistician, and interested in current ideas regarding inclusive inheritance and plasticity, for a grant-funded study of inherited environmental effects.

The position can begin any time between December 2020 and early 2021, and will continue until October 15 2022 (up to 22 months full-time salary).

Familiarity with molecular approaches is a plus but is not essential.

The project will continue the lab's work on transgenerational effects of parental light vs shade conditions in the generalist annual *Polygonum persicaria*.

The goal is to examine how genotype, parent environment, and current environment interactively influence phenotypic outcomes and hence adaptive variation in a natural system.

Using inbred genotypes raised in factorial combinations of previous and current environments, we will collect data across the life cycle on phenotypic trait expression, transcriptome changes, and site-specific methylation changes, though a combination of greenhouse growth experiments and molecular work (which will be carried out by graduate students and another postdoc in the lab). Depending on the post-doc's interests and toolbox,

there is plenty of opportunity to add elements to the project, such as an ecophysiology or field study, a modeling dimension, additional greenhouse or demethylation experiments, etc.

This work is part of a \$2 million consortium grant from the Templeton Foundation to investigate how environmentally influenced, real-time regulatory, developmental and behavioral processes in organisms may lead to adaptation and trait innovation (<https://agencyinlivingsystems.com/>). The overall project includes 4 research labs including Armin Moczek (Indiana Univ), Jukka Jernvall (Helsinki) and Deborah Gordon (Stanford), with each lab investigating a different level of biological organization.

A philosophy of biology group (led by Denis Walsh at Univ of Toronto) is working on theoretical implications. The grant includes collaborative travel among team PI's and postdocs as well as international workshops. For a young scientist who is keen to explore new ideas in evolutionary biology, this should be an exciting opportunity.

Wesleyan is a small, selective Liberal Arts university with a diverse student and faculty community, outstanding arts and culture (especially music and the performing arts), and a tradition of excellence in both research and teaching. The Sultan lab is a supportive, high-energy group that currently includes 3 grad students and 4 undergrads.

The campus is located in the small city of Middletown on the Connecticut River in central CT, close to many hiking and kayaking options. It is 30 minutes from Yale and University of Connecticut, and 2 hours' drive to Boston or New York City.

To apply or for further information, please contact Prof. Sonia Sultan at [sesultan@wesleyan.edu](mailto:sesultan@wesleyan.edu). Kindly attach a cv that includes: a short description of PhD project; list of publications or manuscripts in progress; research skills/experience; and contact information for PhD advisor and any previous postdoctoral mentors. For position listing see <http://careers.wesleyan.edu/postings/7198> "Sultan, Sonia" <[sesultan@wesleyan.edu](mailto:sesultan@wesleyan.edu)>

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## Workshops Courses

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### Berlin 16SMetabarcoding Mar9-13

Dear all,

we have the last 5 spots available on the course “16 S/ITS Metabarcoding of microbial communities” <https://www.physalia-courses.org/courses-workshops/-course30/> When: 9-13 March 2020

Where: Free University (FU) Berlin (Germany)

Instructors:

Dr. Anna Sandionigi (University of Milan Bicocca, Italy)

Dr. Xavier Harrison (University of Exeter, UK)

Dr. Bruno Fosso (Institute of Biomembrane, Bioenergetics and Molecular Biotechnologies, CNR, Italy)

This course will provide a thorough introduction to the application of metabarcoding techniques in microbial

ecology. The topics covered by the course range from bioinformatic processing of next-generation sequencing data to the most important approaches in multivariate statistics. Using a combination of theoretical lectures and hands-on exercises, the participants will learn the most important computational steps of a metabarcoding study from the processing of raw sequencing reads down to the final statistical evaluations.

Learning Outcomes:

- 1) Understanding the concept, potential and limitation of microbial metabarcoding techniques.
- 2) Learning how to process raw sequencing reads to obtain meaningful information.
- 3) Obtaining experience on how to statistically evaluate and visualize your data.
- 4) Being able to make informed decisions on best practices for your own data.

For more information about the program, please visit our website: <https://www.physalia-courses.org/courses-workshops/course30/> Here is the full list of our courses and Workshops: <https://www.physalia-courses.org/-courses-workshops> Should you have any questions,



please feel free to contact us: [info@physalia-courses.org](mailto:info@physalia-courses.org) <[info@physalia-courses.org](mailto:info@physalia-courses.org)>

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
[info@physalia-courses.org](mailto: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](mailto:info@physalia-courses.org)”  
 <[info@physalia-courses.org](mailto:info@physalia-courses.org)>

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## Berlin DatavizInRggplot Mar2-6 deadline

Dear all,

the registration deadline is soon approaching (6th February) for our 5-day course on “Data visualization IN R with ggplot2” which will be held at the Free University Berlin (Germany) in March (2-6) : <https://www.physalia-courses.org/courses-workshops/course56/> This workshop is aimed at researchers and technical workers with a background in any data-related field. In general, no programming experience is needed. The course teaches all relevant steps to load, transform and visualize the data. However, basic knowledge of R is beneficial.

After completing the workshop, students should be in a position to: - know and apply the principles of good data visualization such as the right choice of colors and chart types - load and transform data in R using ‘tidyverse’ - understand the layered structure of ‘ggplot2’ - visualize the data in multiple ways using ‘ggplot2’ - create publication quality and easy understandable figures - perform reproducible by using version control and project organization

Program: <https://www.physalia-courses.org/courses-workshops/course56/curriculum56/> Here is the full list of our courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops/> )

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
[info@physalia-courses.org](mailto: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](mailto:info@physalia-courses.org)”

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## Berlin GWAS Mar2-6

Dear all,

we still have a few places left on the course “Introduction to genome-wide association studies (GWAS)” at the Free University (FU) Berlin (Germany) from the 2nd to the 6th of March. <https://www.physalia-courses.org/-courses-workshops/course49> Instructors: 1) Dr. Filippo Biscarini (CNR, Italy); 2) Dr. Oscar González-Recio (INIA, Spain); 3) Dr. Christian Werner (University of Edinburgh, UK)

### OVERVIEW

This course will introduce students, researchers and professionals to the steps needed to build an analysis pipeline for Genome-Wide Association Studies (GWAS). The course will describe all the necessary steps involved in a typical GWAS study, which will then be used to build a reusable and reproducible bioinformatics pipeline.

### TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at students, researchers and professionals interested in learning the different steps involved in a GWAS study using them to build a structured pipeline for semi-automated and reproducible GWAS analyses. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of GWAS and bioinformatics pipeline building, progressively describing all steps and putting there seamlessly together in a general workflow. Attendees should have a background in biology, specifically genetics; previous exposure to GWAS experiments would also be beneficial. There will be a mix of lectures and hands-on practical exercises using R, Linux command line and custom software. Some basic understanding of R programming and Unix will be advantageous. Attendees should also have some basic familiarity with genomic data such as those arising from NGS experiments.

Program: ( <https://www.physalia-courses.org/courses-workshops/course49/curriculum49/> )

Full list of our courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops/> )

Should you have any questions, please feel free to contact

us: info@physalia-courses.org

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR  
 info@physalia-courses.org <http://www.physalia-courses.org/> Twitter: @physacourses mobile: +49 17645230846 <https://groups.google.com/forum/#!forum/physalia-courses> info@physalia-courses.org

## Berlin NanoporeGenomeAssembly Feb10-14 LastCall

Dear all,

last places left on our course “GENOME ASSEMBLY USING OXFORD NANOPORE SEQUENCING”

Where: Free University Berlin (Germany) When: 10 - 14 February 2020

Course website: <https://www.physalia-courses.org/courses-workshops/course59/> Registration deadline: 18th January 2020

Instructors: Dr. Robert Vaser and Josip Maric (University of Zagreb, Croatia - (<http://complex.zesoi.fer.hr/index.php/en/>)). Here you can find our interview with our instructors: (<https://www.physalia-courses.org/news/n16/>)

This course will introduce the audience with a spectre of methods which are present in a usual assembly workflow, starting from raw data and finishing with a fully assembled genome. We will see how to obtain nucleotide sequences from raw signals, dive deeper into the most used assembly paradigm for long fragments, try out and compare several state-of-the-art assemblers, and at last, assess the quality of the obtained assembly with and without a reference genome. Structured over five days, this course consists of both theoretical and practical aspects which are intertwined through each day. The presented theoretical foundation will be applied on small bacterial datasets and visualized in order to better grasp the algorithms at hand.

Best regards, Carlo

Carlo Pecoraro, Ph.D

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courses “info@physalia-courses.org” <info@physalia-courses.org>

## Berlin ProteomicsUsingR Feb17-19

Course: Proteomics Using R/Bioconductor

Where: Free University (FU) Berlin (Germany)

When: 17th-19th February 2020

Instructor: Dr. Laurent Gatto (de Duve Institute, UCLouvain, Belgium)

Course website: (<https://www.physalia-courses.org/courses-workshops/course58/>)

Registration deadline: 18th January 2020

This course will introduce participants to the analysis and exploration of mass spectrometry (MS) based proteomics data using R and Bioconductor. The course will cover all levels of MS data, from raw data to identification and quantitation data, up to the statistical interpretation of a typical shotgun MS experiment and will focus on hands-on tutorials. At the end of this course, the participants will be able to manipulate MS data in R and use existing packages for their exploratory and statistical proteomics data analysis.

Program Monday - Classes from 9:30 to 17:30

During the first day, we will focus on raw MS data, including how mass spectrometry works, how raw MS data looks like, MS data formats, and how to extract, manipulate and visualise raw data.

Tuesday- Classes from 9:30 to 17:30

The second day will focus in identification data, how to combine them with raw data, quantitation of MS data, and introduce data structure of quantitative proteomics data

Wednesday- Classes from 9:30 to 17:30

The last day will focus on quantitative proteomics, including data structures, data processing, visualisation statistical analysis to identify differentially expression proteins between two groups.

For the full list of our courses and Workshops, please see: (<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>

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## Berlin RNAseqWithBioconductor Jun15-19

Dear all,

Registrations are now open for the 2nd edition of the course "Analysis of RNA sequencing data with R/Bioconductor": ( <https://www.physalia-courses.org/courses-workshops/course19/> )

Where: Freie Universität Berlin - Altensteinstraße 40, 14195 Berlin, Germany

When: 15-19 June 2020

Instructor: Dr. Ludwig Geistlinger (City University of New York School of Public Health, USA)

This course will provide biologists and bioinformaticians with practical statistical analysis skills to perform rigorous analysis of RNAseq data with R and Bioconductor. The course assumes basic familiarity with genomics, but does not assume prior statistical training. It covers the statistical concepts necessary to design experiments and analyze high-throughput data generated by next-generation sequencing, including: exploratory data analysis, principal components analysis, clustering, differential expression, and gene set analysis.

Program: ( <https://www.physalia-courses.org/courses-workshops/course19/curriculum-19/> )

Here is the full list of our courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops/> )

Best regards,

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>

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## BGI-Qingdao China ConservationGenetics Jun9-19

To the Conservation Genetics Community:

We are pleased to announce that ConGen GLOBAL is offering a the next edition of the Recent Advances in Conservation Genetics Course (ConGen2020), which will be held in at the BGI Genomics Research Laboratories in Qingdao, China, June 9-19, 2020.

The venue is located on the outskirts of the beautiful city of Qingdao, in China's eastern Shandong province, a port city of skyscrapers, parks and beaches bordering the Yellow Sea. QĀĀĀ (QĀĀĀ) means "Green Island". The winding cobbled streets, historic German architecture and red-capped hillside villas are captivating and there's so much to enjoy in the city's diverse food scene, headlined by the ubiquitous home town beer, Tsingtao, first brewed in 1903. The nearby sea keeps the town cool during the summer, and slightly warmer in winter. We chose this location for ConGen2020, as it combines the fresh sea air, a mix of European and Chinese architecture, and dashing modern face looking into the future. QĀĀĀ (QĀĀĀ) is also adjacent to some of the most scenic natural sites in China.

Qingdao is now home to the new BGI Genomics Research Laboratories, who will serve as the local host and a generous sponsor for ConGen 2020. BGI-Qingdao is the major center of theoretical and technical research for genomics in northern China. BGI was the first major collaborator and sponsor of the Genome 10K project. Together with the collaborators, BGI-Qingdao contributed to a number of conservation genomics projects including genomes of oyster, proteus, bamboo shark, and flatfish.

The course will host 25-30 participants dedicated to the conservation of animals and plants and about 20-25 distinguished faculty from around the world. The course is directed by its founder, Dr. Stephen J. O'ÁBrien, and taught by renowned scientists conversant in the methods, interpretation, and applications of genomic-based analyses for conservation of endangered species. The 20-25 esteemed experts listed below will share their personal research expertise and experiences in this important and rapidly developing field. The ConGen2020 faculty represent an amazing group of people who come from around the world and will be teaching, sharing their current research and conservation stories, and interacting with students during the course.

Participants will learn how to handle bioinformatics pipelines and algorithms for analyzing genomic and genetic data through lectures and hands-on computer tutorials. Some of the topics to be covered include:

?C Study design for conservation genomic projects ?C Overview of genome sequencing and reduced representation methods ?C Genome assembly and annotation ?C Read mapping ?C Variant discovery ?C Analysis of genomic diversity and inbreeding ?C Identification of deleterious variants ?C Admixture analysis ?C Estimation of historical effective population size ?C Application of genomic data to aid conservation of ex situ and in situ populations,

Each evening will feature a keynote-style lecture by guest faculty on their seminal research advances and interpretations in conservation biology and genomics. A full day wildlife-based field trip will be planned by local hosts from BGI-Qingdao.

Please fill out the registration form on the <https://conservationgenetics.org/congen2020/registration/> website to be considered as one of the participants for the course. We encourage graduate students, postdoctoral scholars, early-career researchers and established research scientists to apply. Participants should have previous coursework and/or experience in evolutionary biology, genetics, genomics, and/or population genetics and be familiar working in the command-line environment. The ConGen2020 committee will review the applications and announce acceptances by March 1. Admittance to the course is competitive so please be sure to submit your application in a timely manner.

The cost of participation in ConGen2020 is \$2,300, which includes tuition, lodging, meals, and transportation from and to Qingdao Liuting International Airport (TAO) to and from the course venue on the first day and last day of the course.

Time: June 9-19, 2020

Address: BGI-Qingdao, BGI-Shenzhen, Q&A@ngd&A, Shandong Province, 266555, China

Contact: [congen2020@conservationgenetics.org](mailto:congen2020@conservationgenetics.org) webpage: <http://conservationgenetics.org> Deadline Applications Close: February 14, 2020

P.S. Application for the ConGen2020 acceptance is a competitive process: the committee will evaluate your application and will mail you an acceptance letter if you are qualified. You do not need to pay the registration fee before receiving the acceptance letter. You will have at least until April 15th to pay your registration deposit, or forfeit your

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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>

## Cal Academy Genomics In Natural History Collections Mar 12-14

Beth Shapiro (Paleogenomics Lab, UC Santa Cruz), Brian Simison (Center for Comparative Genomics, California Academy of Sciences), and I (Paleogenomics Lab, UC Santa Cruz) are organizing a workshop on genomic techniques and challenges in collections, sponsored by the Institute for Museum and Library Services. This workshop is specifically aimed at researchers and curators with little or no experience in genetic/genomic work, to enable them to utilize emerging DNA sequencing technologies and facilitate genomic research in natural history collections. We will hold the workshop at the California Academy of Sciences in San Francisco from 12-14 March, 2020.

We have a fantastic line-up of speakers, hands-on demonstrations, and panel discussions, including a keynote talk by genomicist Dr. Ed Green, who was the first to sequence the complete Neanderthal genome. Admission to the Cal Academy public exhibits and NightLife event (21+) on Thursday 12th is included in the workshop registration.

Please follow the link below to see the full schedule and to register. Feel free to contact me directly if you have any questions.

<https://www.calacademy.org/imls-museum-genomics-workshop-2020> – Kim Ballare, PhD Post-Doctoral Scholar, Paleogenomics Lab University of California, Santa Cruz lab website: <https://ppl.soe.ucsc.edu/> e-mail: [kballare@ucsc.edu](mailto:kballare@ucsc.edu)

[kim.ballare@gmail.com](mailto:kim.ballare@gmail.com)

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## **cE3c-Portugal AdvancedR Ma30-Apr3 deadlineFeb20**

Course Advanced R for Ecology and Evolutionary Biology

Taught by Ines Fragata and Vitor Sousa | March 30-April 3, 2020 @ Lisbon, Portugal

Objectives: Provide students with statistical knowledge and tools to manipulate, analyze and visualize biological data with R. Introduction to modeling, simulations and Bayesian statistics.

Topics: - Refresher into R - Exploratory analysis for ecology and evolution (Principal Component Analysis) - Linear regression and ANOVA - Hypothesis testing using bootstrap and permutations - Introduction to analysis of population genetics in R - Modeling and simulation of dynamics systems - Bayesian statistics and advanced inference algorithms (Markov chain Monte Carlo) - Students case studies

Course INSTRUCTORS Ines Fragata (irfragata@gmail.com) (<http://ce3c.ciencias.ulisboa.pt/member/inesfragata>) Researcher at cE3c

and

Vitor Sousa (vmsousa@fc.ul.pt) (<http://ce3c.ciencias.ulisboa.pt/member/vitorsousa>) Researcher at cE3c Coordinator of the Evolutionary Genetics Group

Intended audience: This five days intensive course will be open to a maximum of 20 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics.

Minimum formation: Knowledge of R programming syntax and Rstudio. Preference will be given to participants that attend the introductory course in R or that have previous knowledge in R.

The course is free for a maximum of 10 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL, UP) and Biology and Ecology of Global Changes (BEAG UL, UA). For information of fees for other participants see the programme details.

Deadline for applications: February 20, 2020 Candidates should send a short CV and motivation letter

to Vitor Sousa (vmsousa@fc.ul.pt) and Ines Fragata (irfragata@gmail.com).

For additional details about the course and others go to: <https://ce3c.ciencias.ulisboa.pt/training/> Margarida Matos <mmmatos@fc.ul.pt>

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## **CIBIO-Porto Archaeogenomics Domestic Animals May11-15**

\*The Archaeogenomics of Domestic Animals\*

It is now generally agreed that diachronic genetic studies are required in order to infer the origins and evolutionary trajectories of domestic animals. The objective of this course is to provide an overview of the most recent Archaeogenomics findings on the origin and evolution of domestic animals. It will cover some of the recommended bioinformatics tools and methods for the study of ancient DNA genomics data. There will be hands-on sessions, including bioinformatics on how to filter, infer damage patterns and authenticate next-generation-sequencing data obtained from archaeological specimens, as well as on population genomics.

IMPORTANT DATES \*Deadline for applications: March 13, 2020\*

Notification of acceptance: March 18, 2020

Course dates: May 11-15, 2020

Full details, including the course programme and instructors, application form, selection criteria and requirements, can be found here: <https://cibio.up.pt/workshops-courses/details/advanced-course-archaeogenomics-of-domestic-animals> This course is aimed at Ph.D. students, postdocs and other researchers in the fields of evolutionary biology, zooarchaeology and archaeology with a specific interest in Archaeogenomics.

catarinaginja@gmail.com

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## Crete FiniteElementAnalysis Jun8-12

Dear evoldir members,

Transmitting Science is offering the course 'FINITE ELEMENT ANALYSIS APPLIED TO LIFE SCIENCES'.

Instructors: Dr. Josep Fortuny (Institut Catala de Paleontologia M. C., Spain) and Dr. Jordi Marce-Nogue (Universitat Rovira i Virgili, Spain) Dates: June 8th-12th, 2020 Location: Crete, Greece Early-bird deadline: April 30th, 2020

**COURSE OVERVIEW:** Finite Element Analysis (FEA) is a great tool for biologists, palaeontologists, doctors, veterinarians, and other life sciences specialities in which researchers face questions about biomechanics of living and extinct organisms. Elements like bone, arthropod exoskeleton, mollusc shells, or the stems and leaves of plants can be analysed using this technique. FEA is a non-invasive modelling technique, based on the principle of dividing a system into a finite number of discrete elements where the equations are applied. Although static and dynamic analysis can be solved using FEA, in this course only static analysis will be covered.

In this course, there will be an introduction to the Finite Element in order to model biological structures and understand how they work. We will cover all the steps involved in FEA (for static analysis) except the creation or reconstruction of the model. After the theoretical introduction, we will build and analyse 2D and 3D finite element models of skeletal elements and deepen on the methods and software's required to perform FEA. Key questions as mesh size, boundary conditions, applied forces, scaling and numerical singularities will be thoroughly addressed.

**PROGRAM:** Monday

An introduction to the use of Finite Element Analysis (FEA): - Mathematical model, features and practical procedure.

Basic continuum mechanics: - Stress, displacements, strain, constitutive equations. - Failure criteria on elastic materials.

Tuesday

Theoretical approach to Meshing: - Types of mesh. - Mesh generation. - How to evaluate a mesh (quality and reliability). - Recommendations for a good practice.

Material Properties: - Biomechanical properties of the bones to be used in FEA. - Considerations for non-linear materials to understand the modelling of soft tissues. - Boundary conditions and Forces in biological systems.

Wednesday

2D Plane models reconstruction: - Theoretical tools for the creation of 2D plane FEA models of biological structures. - A practical guided example in an Artiodactyla jaw.

Thursday

3D models: - Theoretical tools for the creation of 3D FEA models of biological structures.

CASE STUDY: - Alligator jaw: Biological Implications. Interpretation of the results.

Friday

Working with real examples. Creation of a complete FEA model.

For more information and registration: <http://bit.ly/FEA-course> Contact: [courses.crete@transmittingscience.org](mailto:courses.crete@transmittingscience.org)

All the best, Haris Saslis, PhD Course Coordinator Transmitting Science [www.transmittingscience.org](http://www.transmittingscience.org) Haris Saslis <[haris.saslis@gmail.com](mailto:haris.saslis@gmail.com)>

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## FridayHarborLabs EvolutionaryQuantitativeGenetics Jun7-10

Evolutionary Quantitative Genetics Workshop Friday Harbor Laboratories, University of Washington, 7-13 June 2020

Credits: none Instructor(s): Dr. Stevan J. Arnold, Dr. Joe Felsenstein Dates: Arrive Sunday, June 7th; depart Saturday, June 13th Maximum number of participants: 30 Dates of instruction: Monday, June 8th - Friday, June 12th Application deadline: March 15, 2020

The application form will be found here: <https://tinyurl.com/EQG2020Application> The blog web pages for the workshop will be found at <https://blogs.uw.edu/fhleqq/> They currently include a 2019 workshop schedule which has links to the materials for that year's workshop. The web page for the workshop at Friday Harbor Laboratories will be found at <https://tinyurl.com/EQG2020> Instructors: Dr. Stevan J. Arnold, Department of

Integrative Biology, Oregon State University Dr. Joe Felsenstein, Dept. of Genome Sciences and Dept. of Biology, University of Washington

This workshop has been given yearly since 2011. Since 2017 it has been given at the Friday Harbor Laboratories of the University of Washington, located at Friday Harbor on beautiful San Juan Island.

The workshop will review the basics of theory in the field of evolutionary quantitative genetics and its connections to evolution observed at various time scales. One aim of the workshop is to build a bridge between the traditionally separate disciplines of quantitative genetics and comparative methods.

Quantitative genetic theory for natural populations was developed considerably in the period from 1970 to 1990 and up to the present, and it has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements.

Phylogenetic approaches to comparative biology were developed in the 1980s and 1990s, including inferring how traits covary in evolution and how optimum values of traits vary between species.

Textbooks have not kept pace with these developments, and currently few universities offer courses on these subjects aimed at evolutionary biologists.

Evolutionary biologists need to understand this field because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics. This workshop aims to fill this need by reviewing basic aspects of theory and illustrating how that theory can be tested with data, both from single species and from multiple-species phylogenies. Participants will use R, an open-source statistical programming language, to build and test evolutionary models.

The workshop involves lectures and in-class computer exercises. You can consult the 2019 workshop website for examples, using the links found at the 2019 schedule mentioned above.

The intended participants for this workshop are graduate students, postdoctoral fellows, and junior faculty members in evolutionary biology. The workshop can accommodate up to 30 participants. Guest instructors are:

\* Patrick Carter, Evolutionary Physiology, Washington State University, Pullman \* Adam Jones, Biological

Sciences, University of Idaho \* Michelle Lawing, Ecology and Conservation Biology, Texas A&M University \* Brian O'Meara, Ecology & Evolutionary Biology, Univ. of Tennessee, Knoxville \* Samantha Price, Biological Sciences, Clemson University \* Josef Uyeda, Biological Sciences, Virginia Tech,

Cost: \$1000, to be paid to Friday Harbor Laboratories. This fee will cover housing and meals at FHL and all other workshop expenses except travel. Participants who have been admitted to attend will make their payment prior to arrival at FHL. Details of payment by credit card or check will be provided once the applicant has been admitted to attend.

We have also applied to several scientific societies for additional support which would enable a 20% refund of the workshop fee to participants who are members of those societies, if the societies agree to provide this support. We will know whether this will be available by the time that we notify people of acceptance to the Workshop, and details will also appear on the Workshop web pages by then.

Joe

Joe Felsenstein joe@gs.washington.edu Department of Genome Sciences and Department of Biology, University of Washington, Box 355065, Seattle, WA 98195-5065 USA

Joe Felsenstein <joe@gs.washington.edu>

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## Glasgow 2 Python Jun29-Jul3 Migrate Mar16-20

Two Courses:

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Advanced Python for biologists (APYB04) FREE ACCOMMODATION AVAILABLE

<https://www.prinformatix.com/course/advanced-python-biologists-apyb04/> This course will be delivered by Dr Martin Jones from the 29th June - 3rd July in Glasgow CityCentre.

Course overview:

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at people who already have a basic knowledge of Python and are interested in using

the language to tackle larger problems. In it, we will look in detail at the parts of the language which are particularly useful in scientific programming, and at the tools Python offers for making development faster and easier. The course will use examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) take advantage of the advanced language features in their own programs and (2) use appropriate tools when developing software programs.

Other relevant courses, please feel free to share.

1) May 4th ' May 8th

PYTHON FOR DATA SCIENCE, MACHINE LEARNING, AND SCIENTIFIC COMPUTING (PDMS02)

FREE ACCOMMODATION AVAILABLE

Glasgow, Scotland, Dr. Mark Andrews

<https://www.prinformatics.com/course/python-for-data-science-machine-learning-and-scientific-computing-pdms02/> 2) March 16th ' 20th

POPULATION GENETICS INFERENCE WITH 'MIGRATE' (PGMG01)

Glasgow, Scotland, Prof. Peter Beerli

<https://www.prstatistics.com/course/population-genetics-inference-with-migrate-pgm01/> 3) January 20th ' 24th

R4ALL ' INTRODUCTION TO R (R4ALL01) Introductory course to R, RStudio and statistics for Biologists

FREE ACCOMMODATION AVAILABLE

Glasgow, Scotland, Dr Andrew Beckerman, Dr. Dylan Childs

<https://www.prstatistics.com/course/r-4-all-andrew-beckerman-dylan-childs-r4all01/> 4) March 23rd ' 27th

INTRODUCTION TO BAYESIAN HIERARCHICAL MODELLING USING R (IBHM04)

FREE ACCOMMODATION AVAILABLE

Glasgow, Scotland, Dr Andrew Parnell

<https://www.psstatistics.com/course/introduction-to-bayesian-hierarchical-modelling-using-r-ibhm04/> 5) May 25th ' 29th

GENERALISED LINEAR (MIXED) (GLMM), NON-LINEAR (NLGLM) AND GENERAL ADDITIVE MODELS (MIXED) (GAMM) (GNAM01)

FREE ACCOMMODATION AVAILABLE

Glasgow, Scotland, Dr Mark Andrews

<https://www.psstatistics.com/course/generalised-linear-glm-nonlinear-nlglm-and-general-additive-models-gnam02/> 6) July 20th ' 24th

APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS (ABME06)

Glasgow, Scotland, Dr Matt Denwood

<https://www.prstatistics.com/course/applied-bayesian-modelling-for-ecologists-and-epidemiologists-abme06/> 7) February 3rd ' 7th

INTRODUCTION TO SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R (ISPE02)

FREE ACCOMMODATION AVAILABLE

Glasgow, Scotland, Dr. Jakub Nowosad

<https://www.prstatistics.com/course/introduction-to-spatial-analysis-of-ecological-data-using-r-ispe02/> 8) February 24th ' 28th

MOVEMENT ECOLOGY (MOVE03)

Margam Discovery Centre, Wales, Dr. Luca Borger, Dr Jonathan Potts

<https://www.prstatistics.com/course/movement-ecology-move03/> Please email any enquiries to [oliverhooker@prinformatics.com](mailto:oliverhooker@prinformatics.com)

—  
Oliver Hooker PhD.

2019 publications; A way forward with eco evo devo: an extended theory of resource polymorphism with post-glacial fishes as model systems. *Biological Reviews* (2019).

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6 Hope Park Crescent Edinburgh EH8 9NA

44 (0) 7966500340

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Population genetics inference with 'Migrate' (PGMG01)  
FREE ACCOMMODATION AVAILABLE

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



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## Guarda Switzerland Evolution Jun20-27

Guarda summer school in evolutionary biology 2020

It is my pleasure to announce the 2020 Guarda summer school in Evolutionary Biology for master and PhD students. The main aim of the course is to develop the skills to produce an independent research project in evolutionary biology.

The summer school takes place 20. 'V 27. June (Saturday to Saturday) in the Swiss mountain village Guarda. Faculty includes Hopi Hokstra (Harvard University, USA), John Krebs (Oxford University, UK), Sebastian Bonhoeffer (ETH-Zurich, Switzerland) and Dieter Ebert (Basel University, Switzerland; organizer).

The course is intended for master students and early PhD students with a keen interest in evolutionary biology.

The web page with all details can be found: <http://www.evolution.unibas.ch/teaching/guarda/index.htm>  
Application is open now. Deadline is 8. February 2020

Please communicate this information to interested students.

With best wishes,

dieter ebert

Dieter Ebert University of Basel, Department of Environmental Sciences, Zoology Vesalgasse 1, CH-4051 Basel, Switzerland <http://evolution.unibas.ch/> Email: dieter.ebert@unibas.ch Tel. +41-(0)61-207 03 60

Dieter Ebert <dieter.ebert@unibas.ch>

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## HarvardU SLiMEvolutionaryModeling May18-22

Hi all.

First of all, as background: SLiM is a software package for creating evolutionary models/simulations that are

individual-based and genetically explicit. It is scriptable, flexible, fast, and includes an interactive graphical modeling environment. You can read more about it on its home page (<https://messerlab.org/slim/>).

May 18-22, 2020, a five-day SLiM workshop will be offered at Harvard University (Cambridge, MA, USA). It will be hosted by Daren Card and Timothy Sackton, of Harvard. It will be free, and open to participants outside of the university. HOWEVER, registration is required, a limited number of seats are available, and a set portion of seats will be given to registrants affiliated with Harvard. To apply, please send an email to ALL OF Daren, Timothy, and myself (dcard@fas.harvard.edu, tsackton@g.harvard.edu, bhaller@mac.com) with the info below. Priority for Harvard applicants will end on 15 February; after that date it will be first-come-first-served for all remaining seats so that we can notify everyone of their acceptance in time to make travel arrangements. Early application is advised; these workshops have been filling to capacity.

For this workshop, your application email should include: (1) your name, (2) your university or institutional affiliation, (3) a link to a research website or similar academic page, if you have one, (4) a 1-2 sentence description of your level of experience with SLiM and any other forward genetic simulation software, if any, (5) a 1-2 sentence summary of why you want to attend the workshop (i.e., the connection to your research), and (6) 1-2 sentences about any specific topics within SLiM that you hope to learn about in the workshop. Note that you will be responsible for your own lodging and your own transportation. Please do not apply to the workshop unless you are sufficiently serious that you will actually attend, if accepted.

The plan is to cover all the major topics in the SLiM manual, starting with lots of introductory material to get beginners up to speed with SLiM and its associated scripting language Eidos, and ending up at advanced topics like non-Wright-Fisher models, tree-sequence recording, continuous-space models, and nucleotide-based models. We won't cover everything in the manual "that would be overwhelming!" but we'll try to cover all the big topics. There will also be time for attendees to work on their own models with help from me, and we may also have time to explore some optional side topics that are of particular interest to those attending each workshop. The workshop will be taught principally using SLiMgui on macOS. Every attendee will need their own Mac laptop. Loaner Mac laptops are unlikely to be available for this workshop; running macOS inside VirtualBox on another operating system is also possible, but please make sure that this works for you before registering. (A Mac is required to run SLiMgui, which is necessary for

teaching purposes.)

I'm hoping to continue doing workshops in future; if you would like to invite me to give a workshop at your institution, please send me an email (off-list).

Cheers,

Benjamin C. Haller Messer Lab Cornell University  
bhaller@mac.com

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### Madrid StatisticalPhylogenetics Mar10-20

MADPHYLO: Madrid Workshop in Statistical Phylogenetics

Where: Real Jardin Botanico (CSIC), Madrid, Spain

When: 10-20 March 2020

[www.madphylo.com](http://www.madphylo.com) Course overview:

We are proud to announce the third edition of MADPHYLO, Madrid Workshop in Statistical Phylogenetics.

Darwin founded the field of evolutionary biology on the concept that all organisms are related to one another through an unknown evolutionary tree. Phylogenetic or evolutionary inference has become an essential tool in many disciplines across the life sciences, from molecular epidemiology to paleontology. In this workshop, the participants will learn the theoretical and technical basis of stochastic modeling in evolutionary biology and phylogenetics. The workshop will also provide full training in the open software RevBayes, an R-like interactive environment based on graphical model concepts for the modeling of complex evolutionary problems. At the end of the workshop, the student will have an understanding of the assumptions behind state-of-the-art methods used in modern phylogenetic analysis, as well as being able to build up new models from existing functions in RevBayes.

Instructors:

The lecturers are prominent analytical systematists and evolutionary biologists, who are behind the development of many of the methodological and computing tools routinely used in modern phylogenetic inference and evolutionary biology.

Workshop details:

The course will be taught from March 10 to March 20 2020. Lectures and practicals will be tightly linked,

meaning that you will learn the theory and also how to apply the theory on the same day. Students are encouraged to bring their own laptops. The tuition for the course has been lowered this year to 400 Euros. It includes coffee breaks and a light lunch. However, this tuition does not include room and board during the course. You will be required to find a place to stay if you are from outside of Madrid.

More details and how to register can be found on the website: <https://www.madphylo.com> Email isanmartin@rjb.csic.es or johnh@berkeley.edu for any questions.

John Huelsenbeck University of California, Berkeley Department of Integrative Biology 3060 VLSB # 3140 Berkeley, CA 94720-3140

E-mail: johnh@berkeley.edu Phone: (510) 502-5887

John Huelsenbeck <johnh@berkeley.edu>

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### MountainLakeBiologicalStation NaturalHistory

[Summer Courses at MLBS] < <https://mlbs.us14.list-manage.com/track/-click?udd2397558126f5ceb0c7824&id30f7b4d2&eKa1f3f3e0> > 2020 Summer Courses at Mountain Lake Biological Station Field-based courses are UVA Summer Session classes taught by nationally-recruited faculty. Courses are offered at undergraduate and graduate levels.

Field Courses

Natural History of the Appalachians: Summer Session I: May 25-June 12 Field Herpetology: Summer Session I: May 25-June 12 Field Biology of Fishes: Summer Session II: June 15-July 3 Stream Ecology: Summer Session III: July 13-31

Rolling enrollment. Financial aid is available. Apply by March 15. MLBS courses are field-intensive, research-based experiences. Courses earn 3 UVA Biology lab credits. Non-college students are welcome to enroll.

Learn More and Apply < <https://mlbs.us14.list-manage.com/track/-click?udd2397558126f5ceb0c7824&id5fd1b559&eKa1f3f3e0> >

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 click?udd2397558126f5ceb0c7824&id}6d41ea10&eKa1f3f3e0  
 >

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 Charlottesville, VA 22904-4327 USA +1-434-243-4989 o | +1-434-906-3122 c enagy@virginia.edu  
 bio.as.virginia.edu/people/esn8n | mlbs.org

“Nagy, Eric S (esn8n)” <esn8n@virginia.edu>

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## Ploen Evolving Microbial Communities Apr27-30

This small workshop (~50 participants) will take place at the Max Planck Institute for Evolutionary Biology, in Plön, Germany, from April 27th to April 30, 2020.

The realisation that evolution can be fast enough to affect microbial species interactions and abundance has changed the field of community dynamics. Scientists have started integrating methods from population biology and evolutionary biology to understand how microbial communities may change under different conditions and spatial scales. Although progress has been made, it is yet quite challenging to understand microbial communities in their natural complexity. With our workshop “Evolving Microbial Communities” we aim to discuss the recent advances in the field and new concepts for understanding and predicting how and why communities are changing over time. We aim to invite top researchers that investigate the area from different fields (experiment, theory) and promote dialogue among them. We would be very excited if you could join us as a leader in this conversation. We would ask you to prepare a 30 min talk plus 10 min discussion.

Here is a link to register to our workshop. <https://workshops.evolbio.mpg.de/event/26/registrations/25/>

We are looking forward to welcoming you in Plön, located within a beautiful lake region not far from the Baltic Sea. Please send your abstract no later than March 6th, 2020.

If you have further questions please contact Dr Andy Farr (afarr@evolbio.mpg.de) and Dr Loukas Theodosiou (theodosiou@evolbio.mpg.de).

Sincerely, Andy Farr and Loukas Theodosiou

Loukas Theodosiou Department Microbial Population Biology Max-Planck-Institut für Evolutionsbiologie August-Thienemann-Straße 2, 24306 Plön, Germany

Loukas Theodosiou <theodosiou@evolbio.mpg.de>

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## Portal Arizona Bees Aug16-26

In Partnership with the American Museum of Natural History, Cornell University, and the Southwestern Research Station, we are proud to announce the 22nd installment of The Bee Course. The Bee Course is a ten-day workshop held at the Southwestern Research Station in Portal, Arizona from August 16th through the 26th, 2020. The course is designed to provide biologists interested in pollinators with the tools and knowledge necessary to collect, process, and to begin to identify bee specimens. We encourage all interested parties to apply. For more information, including instructions on how to apply, a list of this year’s instructors, and course testimonials, please visit the course website at [www.thebeecourse.org](http://www.thebeecourse.org). Bryan N. Danforth, Professor and Chair Department of Entomology 3124 Comstock Hall Cornell University Ithaca, NY 14853-2601 phone: 607-255-3563/FAX: 607-255-0939 email: bnd1@cornell.edu Lab website: <http://www.danforthlab.entomology.cornell.edu/> The Solitary Bees (now available): <https://press.princeton.edu/titles/13525.html> The Bee Course (2020): <https://www.thebeecourse.org/> bnd1@cornell.edu

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## Procida EMBO Population Genomics Apr1-8

Deadline for registration is approaching for the upcoming EMBO Practical Course “Population Genomics: background, tools and programming”.

IMPORTANT DATES for this Course:

Deadline for applications: 28/01/2020

Latest notification of acceptance: 11/02/2020

Course dates: 01-08/04/2020

Travel and childcare grants available!

Full details, including the course programme, invited speakers and the application form, at: <http://meetings.embo.org/event/20-populationgenomics> This EMBO Practical Course will cover coalescent theory, the effect of demography in space and time, genetic clustering, the detection and quantification of admixture and selection. Lectures on these topics will be complemented by hands-on computer practicals introducing a wide range of software packages, both in R and Python. This course is aimed at evolutionary biologists who already have basic bioinformatics skills. A main criterion for selection will be how much a candidate can benefit from the course. This implies that Ph.D. students and Postdoc researchers will likely be favoured; however, applications from candidates at all levels will be considered.

Chiara Batini, University of Leicester, UK  
Vincenza Colonna, Consiglio Nazionale delle Ricerche, It  
Andrea Manica, University of Cambridge, UK

“Batini, Chiara (Dr.)” <cb334@leicester.ac.uk>

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## Quebec City RADseq Seascape Genomics Oct5-16

Dear all,

Physalia-courses in collaboration with the University Laval will run two courses in Quebec City (Canada) in October 2020.

1) RADseq data analysis When: 5-9 October 2020

Where: Laval University

Instructors: Dr. Julian Catchen (University of Illinois, Urbana-Champaign, USA) and Eric Normandeau (Laval University, Canada)

Course website: <https://www.physalia-courses.org/courses-workshops/course16/> 2) Seascape Genomics  
When: 12-16 October 2020

Where: Laval University

Instructors: Dr. Laura Benestan (University of Montpellier, France) and Oliver Selmoni (EPFL, Lousanne, Switzerland)

Course website: ( <https://www.physalia-courses.org/courses-workshops/course70/> )

All the best, 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

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## Raleigh NC Evolutionary Medicine May17-22

The Triangle Center for Evolutionary Medicine (TriCEM) is now accepting applications for the 2020 Evolutionary Medicine Summer Institute (EMSI), held May 17-22 at NC State in Raleigh, NC. The goal of EMSI is to introduce core evolutionary concepts to a wide range of topics in human health and disease, including public health, and to train physicians and medical scientists in computational methods used in evolutionary and ecological research.

EMSI brings together internationally recognized experts in evolutionary biology with students and health practitioners who want to apply these perspectives to cancer, infectious disease, evolution of microbial resistance, neurology, autoimmune disease, the microbiome, and more. Lectures on key concepts are complimented with hands-on computational exercises. Our goal is to give participants the background on evolutionary principles and the tools to apply evolutionary biology to questions of medical and veterinary importance.

For more information (including last year’s schedule) and to apply, please visit the EMSI website at <https://->

[sites.duke.edu/emsi/](http://sites.duke.edu/emsi/). Application deadline is March 20, 2020.

If you have any questions, please feel free to reach out to Meredith Spence Beaulieu ([meredith.spence.beaulieu@duke.edu](mailto:meredith.spence.beaulieu@duke.edu)) or Courtni France ([cnf12@duke.edu](mailto:cnf12@duke.edu)).

– Meredith R. Spence Beaulieu, PhD, BCE-Intern  
Pronouns: she/her/hers Assistant Director, Triangle Center for Evolutionary Medicine (TriCEM) 103A Biological Sciences, Duke University [meredith.spence.beaulieu@duke.edu](mailto:meredith.spence.beaulieu@duke.edu) (919) 684-9681

“Meredith Spence Beaulieu, Ph.D.”  
<[meredith.spence.beaulieu@duke.edu](mailto:meredith.spence.beaulieu@duke.edu)>

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## Toulouse ScienceMediaTrainingSchool Apr14-16

EuroScitizen COST Action is organizing a Science-Media Training School directed at young journalists and young scientists. By joining these two groups we aim to improve the quality of the communication and understanding between scientists and media, thus to contribute to the increase of the quality of science communication.

Our goal is to create a new wave of effective communication between scientists and journalists to demonstrate that by working together, those groups have power to create meaningful, understandable and open science messages for the public. We hope to provide a foundation for developing efficient links between the scientific and media communities counteracting the increase in fake news, the plummeting quality of journalistic outputs, in this complex, constantly changing landscape of scientific evidence. In fact we believe that this will empower the society and raise science awareness among people because knowledge has the power to improve our surroundings and quality of life. This Training School will offer you an extensive practice, conducted by a diverse and experienced trainers with scientific and media background. The Training School has three main objectives:

1. Information sharing - to spread awareness across trainees who are interested in disseminating reliable scientific information in media, by providing them with skills and tools to communicate science effectively;
2. Discussion - to exchange perspectives on topics from

two different angles and two, not so different, attitudes represented by journalists and scientists, promoting the communication between these two groups; 3. Community building - to help scientists and journalists find best ways of engaging in science communication together, bringing to it the best of the two worlds.

The event will take place from 8AM of 14th of April to 17PM of the 16th April 2020.

We welcome both young journalists and young scientists to our training school. For more details and information on how to apply - please visit: <http://www.euroscitizen.eu/2020/01/20/euroscitizen-science-media-training-school-toulouse-14-16th-april-2020/>  
Szymon Drobnik & Rita Ponce EuroScitizen COST Action Media Working Group

Szymek Drobnik <[geralttee@gmail.com](mailto:geralttee@gmail.com)>

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## Trieste Italy PlasmidsEvolution Mar2-6

Just one week left to apply to “Plasmids as vehicles of AMR spread”!

<http://indico.ictp.it/event/9022/> The workshop runs from March 2nd to March 6th 2020 at ICTP in Trieste Italy.

It will be preceded by a school on Bacterial evolution, population genetics and epidemiology.

Deadline for applications January 15th, 2020.

The speakers include:

Bruce Levin (Emory U.)

Sebastian Bonhoeffer (ETH Zurich)

James McInerney (Nottingham U.)

Fernando de la Cruz (Cantabria U.)

Richard Neher (U. Basel - Biozentrum)

Please spread this email to your network.

“Ledda, Alice” <[a.ledda@imperial.ac.uk](mailto:a.ledda@imperial.ac.uk)>

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## Turku Finland

### Mathematical Evolution Aug23-30

#### THE HELSINKI SUMMER SCHOOL ON MATHEMATICAL ECOLOGY AND EVOLUTION 2020

Dear Colleagues,

We are glad to invite applications to the 2020 edition of The Helsinki Summer School on Mathematical Ecology and Evolution, an EMS-ESMTB School in Applied Mathematics to be held between 23 and 30 August 2020 in Turku, Finland.

The core program consists of five series of lectures:

- Josef Hofbauer (University of Vienna): Dynamical systems in mathematical ecology
- Julia Gog (University of Cambridge): The mathematics of infectious diseases
- Pieter Trapman (Stockholm University): Stochastic models of epidemics
- Jarno Vanhatalo (University of Helsinki): Linking ecological models to data through Bayesian statistics
- Christian Hilbe (Max Planck Institute for Evolutionary Biology): Dynamics of social behaviour

All young researchers working in mathematical ecology can apply from all countries, especially from Europe and the Mediterranean. The school is aimed at graduate students of mathematics, but we also welcome students of biology with sufficient background in mathematics, as well as advanced undergraduates and postdocs.

For more information and details of the application procedure, please visit the school's webpage

<https://wiki.helsinki.fi/display/BioMath/-The+Helsinki+Summer+School+on+Mathematical+Ecology+and+Evolution+2020>

With best regards, Eva Kisdi (eva.kisdi@helsinki.fi)

“Kisdi, Eva” <eva.kisdi@helsinki.fi>

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## UFreiburg Phylogenomics

### Feb29-Mar1

Freiburg.Phylogenomics.Feb29-Mar1

Course: The battle of species tree estimation - a coalescent-based approach or concatenation?

Where: University of Freiburg (Germany)

When: 28th February - 1st March 2020

Instructor: Siavash Mirarab (University of California, US), Sabrina Simon (Wageningen University, NL), Manuela Sann (Albert Ludwig University of Freiburg) and Karen Meusemann (Albert Ludwig University of Freiburg)

Registration deadline: February 1st, 2020 at [systematik@dzg-ev.de](mailto:systematik@dzg-ev.de)

The group “Systematics, Biogeography and Diversity” of the German Zoological Society (DZG) will host a workshop named “The battle of species tree estimation - a coalescent-based approach or concatenation?” from February 28th to March 1st 2020 at the University of Freiburg. The workshop pays particular attention to the practical application and comprises some short lectures. Time is reserved for practical exercises and genomic data analyses of your own or provided datasets covering zoological research questions. As guest speaker and teacher Siavash Mirarab (University of California, US), the international expert and developer of the ASTRAL algorithm, confirmed his attendance. The number of participants is limited to 25 to ensure effective support during the workshop. The places will be allocated according to the “first come, first served” principle. No participation fee will be charged. Board and accommodation are at your own expenses.

Workshop information: Nowadays, systematic studies are characterized by the analysis of large molecular data sets (phylogenomics). With the generation and increasing availability of large sequence data by e.g. genome or transcriptome sequencing efforts, phylogenetic systematics faces the challenge of adapting traditional analysis methods. The traditional phylogenomic approach is the analysis of multi-gene matrices, in which different loci are combined into a single supermatrix (concatenation). In recent years, this approach has been increasingly controversial discussed because it does not take into account biological processes such as gene duplication and loss, horizontal gene transfer and incomplete lineage sorting (ILS). In this context, the multispecies coalescent (MSC) model has proven to be a highly effective method for evaluating phylogenies, since it involves ancestral polymorphisms and conflicts between species and gene trees. However, since the coalescence method is also based on the assumption that the examined locus always has a history, but this is not always the case due to far-reaching splitting events and / or high recombination rates, this method is again critically discussed. As a result, a critical evaluation of both phylogenetic reconstruction methods and their resulting phylogenetic relationships is more important than ever. During the 2½ day work-

shop, a theoretical and practical introduction to both reconstruction methods will be given, whereby the participants should work on their own or provided reduced genomic data sets. The different approaches and the methods used for phylogenetic reconstruction are then discussed, compared and critically examined. For the multispecies coalescent (MSC) method, ASTRAL (Accurate Species TRee Algorithm) has been established in recent years as the preferred and proven method for estimating a species tree under the MSC model. Siavash Mirarab (University of California, US), Sabrina Simon (Wageningen University, NL), Manuela Sann (Albert Ludwig University of Freiburg) and Karen Meusemann (Albert Ludwig University) provide an introduction to the multispecies coalescent (MSC) method (ASTRAL-Pro, ASTRAL-MP), the analysis of multi-gene matrices, and methods for evaluating resulting family trees, e.g. quartet scores.

The following requirements are necessary for participation: Participants must bring their own laptop for the analyses (preferred operating system is Linux or Mac OS). Alternatively, we ask the participants to install a virtual machine with Ubuntu 18.04 (e.g. VMWare or Virtual Box) ahead the course. It is explicitly requested that the participants bring their own genomic data sets (reduced to approx. 10 genes and 10-20 species). However, we will also provide sample datasets. The workshop will be held in English.

Please register for the workshop by February 1st, 2020 at [systematik@dzg-ev.de](mailto:systematik@dzg-ev.de)

We look forward to seeing you at the workshop, Sabrina Simon [info@sabrina-simon.com](mailto:info@sabrina-simon.com) Manuela Sann [manuela.sann@biologie.uni-freiburg.de](mailto:manuela.sann@biologie.uni-freiburg.de)

Dr. Sabrina Simon | Assistant Professor Biosystematics | Wageningen University & Research phone: +31317-483175<tel:+31317-483175>

Wageningen Campus | Radix Building 107 | Room W2.Ca.103 Droevendaalsesteeg 1 | 6708 PB Wageningen The Netherlands

Sabrina Simon <[sabrina.simon@wur.nl](mailto:sabrina.simon@wur.nl)> Sabrina Simon <[sabrina.simon@wur.nl](mailto:sabrina.simon@wur.nl)>

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**UIceland Reykjavik**  
**SLiMEvolutionaryModeling**  
**Mar6-10**

Hi all. I'm posting this workshop a second time, since

there are still a couple of spaces free. THIS IS THE ONLY WORKSHOP I AM LIKELY TO RUN IN EUROPE UNTIL MID-2021.

March 6-10, 2020, a five-day SLiM workshop will be offered at the University of Iceland (Reykjavík, Iceland). It will be hosted by SnÁbjörn Pálsson and Arnar Pálsson, of the University of Iceland (Háskóli Íslands). It will be free, and open to participants outside of the university. HOWEVER, registration is required, and a limited number of seats are available. To apply, please send an email to BOTH SnÁbjörn and myself ([snaebj@hi.is](mailto:snaebj@hi.is), [bhaller@mac.com](mailto:bhaller@mac.com)) with the info below. Admission is now first-come-first-served so that we can notify everyone of their acceptance in time to make travel arrangements.

As background: SLiM is a software package for creating evolutionary models/simulations that are individual-based and genetically explicit. It is scriptable, flexible, fast, and includes an interactive graphical modeling environment. You can read more about it on its home page (<https://messerlab.org/slim/>).

The dates for it have been chosen to dovetail with the Oikos conference in Reykjavík, which is March 3-5 (<https://www.oikos2020.org>); we hope that this will make the workshop more convenient for many to attend, but the two events are not affiliated (in other words, attendance at Oikos is not required to attend the workshop).

For this workshop, your application email should include: (1) your name, (2) your university or institutional affiliation, (3) a link to a research website or similar academic page, if you have one, (4) a 1-2 sentence description of your level of experience with SLiM and any other forward genetic simulation software, if any, (5) a 1-2 sentence summary of why you want to attend the workshop (i.e., the connection to your research), and (6) 1-2 sentences about any specific topics within SLiM that you hope to learn about in the workshop. Note that you will be responsible for your own lodging and your own transportation. Please do not apply to the workshop unless you are sufficiently serious that you will actually attend, if accepted.

The plan is to cover all the major topics in the SLiM manual, starting with lots of introductory material to get beginners up to speed with SLiM and its associated scripting language Eidos, and ending up at advanced topics like non-Wright-Fisher models, tree-sequence recording, continuous-space models, and nucleotide-based models. We won't cover everything in the manual - that would be overwhelming! - but we'll try to cover all the big topics. There will also be time for attendees to work on their own models with help from me, and we may also

have time to explore some optional side topics that are of particular interest to those attending each workshop. The workshop will be taught principally using SLiMgui on macOS. Every attendee will need their own Mac laptop, but running macOS inside VirtualBox on another operating system is also possible. (A Mac is required to run SLiMgui, which is necessary for teaching purposes.)

I'm hoping to continue doing workshops in future; if you would like to invite me to give a workshop at your institution, please send me an email (off-list).

Cheers,

Benjamin C. Haller Messer Lab Cornell University

Ben Haller <bhaller@mac.com>

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### UKansas GraduateAdmissionsWorkshop Apr18

The natural sciences departments at the University of Kansas are excited to offer a one-day Graduate Admissions Workshop on April 18th, 2020. Sessions will include CV and personal statement writing, navigating the admissions process and more. Admission is free, reasonable travel will be covered and preference will be given to people from backgrounds underrepresented in the sciences. Participating departments include Chemistry, EEB, Molecular Biosciences and Physics & Astronomy. Application deadline is March 15th. Information at: <http://dnsku.weebly.com>. Email kudns@ku.edu with questions.

“unckless@ku.edu” <unckless@ku.edu>

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### UMichigan Diversity May4-7

NextProf Science workshop

We wish to invite interested evolutionary biologists, ecologists, and organismal biologists to the NextProf Science workshop at the University of Michigan.

NextProf ScienceFuture Faculty Workshop

The University of Michigan will offer a NextProf Science workshop, May 4-May 7, 2020. The workshop is

aimed at encouraging talented scientists and mathematicians with a demonstrated commitment to diversity to consider academia as a career.

Participants will develop strategies to prepare them to pursue academic careers. The workshop is targeted at scholars ready to take the next stepâ euro “post-doctoral fellows and very advanced doctoral students. Underrepresented minorities and women are especially encouraged to apply. Travel, lodging, and meals will be provided for those selected to participate.

Deadline for submission of the application and reference letter is January 19, 2020.

Learn more at: <https://sites.lsa.umich.edu/nextprof-science> U-M EEB NextProf Organizing Committee (Tom Duda & Meg Duffy)

”tfduda@umich.edu“ <tfduda@umich.edu>

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### UMichigan NextProf:DiversifyingAcademia

NextProf Science workshopextended application deadline (1/26/20)

We wish to invite interested evolutionary biologists, ecologists, and organismal biologists to the NextProf Science workshop at the University of Michigan.

NextProf ScienceFuture Faculty Workshop

The University of Michigan will offer a NextProf Science workshop, May 4-May 7, 2020. The workshop is aimed at encouraging talented scientists and mathematicians with a demonstrated commitment to diversity to consider academia as a career.

Participants will develop strategies to prepare them to pursue academic careers. The workshop is targeted at scholars ready to take the next stepâ euro “post-doctoral fellows and very advanced doctoral students. Underrepresented minorities and women are especially encouraged to apply. Travel, lodging, and meals will be provided for those selected to participate.

Extended deadline for submission of the application and reference letter is January 26, 2020.

Learn more at: <https://sites.lsa.umich.edu/nextprof-science> U-M EEB NextProf Organizing Committee (Tom Duda, Meg Duffy, and Andre Green)

”tfduda@umich.edu“ <tfduda@umich.edu>



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## Uruguay ViralBioinformatics Jun7-12

Viral Genomics and Bioinformatics course (Montevideo, Uruguay) 07 - 12 June 2020

Application deadline: 5th March 2020 <https://coursesandconferences.wellcomegenomecampus.org/our-events/viral-bioinformatics-genomics-uruguay-2020/> In collaboration with the Institute of Hygiene, Montevideo, Uruguay and the MRC-University of Glasgow Centre for Virus Research, we are pleased to announce the 2020 overseas course in Viral Bioinformatics and Genomics.

The Viral Genomics and Bioinformatics course will provide participants with a working knowledge of viral genome sequence analysis and interpretation of genomics data generated from high-throughput sequencing. Topics will include the use of the command line to perform analysis of viral NGS data, quality control of sequences, reference and de-novo assemblies, pathogen detection from metagenomics data and building phylogenetic trees. Participants, along with gaining bioinformatics knowledge, will have an opportunity to establish links and networks and develop future collaborative projects.

The course is free to attend and open to applicants based in Latin America and the Caribbean who are engaged in relevant research/clinical activities. The programme is aimed at researchers at various levels including Senior Research Assistants, PhD students, Postdoctoral Researchers, Laboratory Scientists and Clinical Scientists/Healthcare Professionals. A limited number of bursaries is available to assist with travel and accommodation expenses. The course will be taught in English.

Richard Orton <Richard.Orton@glasgow.ac.uk>

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## Vienna MIC-Phy May25-27

Meeting: Mathematical, inferential and computational phylogenomics (MIC-Phy)

Date: 25-27 May 2020

Location: Vetmeduni Vienna, Austria

Scope: Phylogenomics aims at reconstructing the evolu-

tionary histories of organisms considering whole genomes or large fractions of genomes. The abundance of genomic data for an enormous variety of organisms has enabled phylogenomic inference of many groups, and this has motivated the development of a myriad of models and methods. The MIC-Phy meeting intends to stimulate a larger debate focus on the main advances and challenges of the current phylogenetic models, methods and algorithms that are permitting to make sense of phylogenomic data.

Cost: The meeting is sponsored by WWTF and there is no registration fee.

Workshop: The meeting includes a workshop entitled \*New approaches and methods to phylogeny inference\* that will focus on the polymorphism-aware phylogeny estimation, including practical exercises based on the software IQ-TREE and RevBayes.

Keynote speakers: \* Ziheng Yang (University College of London, UK) \* Tracy Heath (Iowa State University of Science and Technology, USA)

Important dates: \* Deadline for workshop registration and abstract submission: March 31, 2020 \* Notification of oral presentation and/or workshop acceptance: April 15, 2020 \* Registration deadline: May 1, 2020

Registration: Please visit <https://www.vetmeduni.ac.at/de/micphy2020/home/> for more information on how to register, submit your abstract and participate in the workshop.

Local organizers: Carolin Kosiol and Rui Borges

Questions: micmeeting2020@gmail.com

Rui Borges <ruiborges23@gmail.com>

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## WashingtonDC EvolutionaryNeurobiology

We are now accepting submissions of Karger Workshop Proposals. The Karger Workshop is a one-day symposium on a specific topic in comparative or evolutionary neurobiology and is preceded by the JB Johnston Club for Evolutionary Neuroscience. We are particularly interested in proposals that use cross-disciplinary methods to explore new questions in evolutionary neuroscience. Proposals are due \*FEBRUARY 1st, 2020. \*

The 2020 Karger Workshop will be held at the Crystal City Marriott < <https://www.marriott.com/hotels/>

[travel/wascc-crystal-city-marriott-at-reagan-national-airport/](https://www.wascc-crystal-city-marriott-at-reagan-national-airport/) >, in Washington DC on Thursday, October 22nd, 2020. The Karger Workshop will precede the regular annual meeting of the JBJC, which will be held on Friday, October 23rd. These meetings are held in conjunction with the annual SFN meetings. Please contact Muhammad Spocter (spocter@gmail.com) or Christine Charvet (charvetcj@gmail.com) if you would like to discuss your proposal.

If you'd like to submit a proposal: please visit the following link: <https://www.jbjclub.org/karger-workshop.html> charvetcj@gmail.com

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## WoodsHole MolecularEvolution May31-Jun10

The 2020 Workshop on Molecular Evolution at the Marine Biological Laboratory in Woods Hole, Massachusetts, USA, will be held \*\*\* MAY 31 to JUNE 10 \*\*\* (note that this is earlier than past years).

Deadline for applications is \*\*\* FEBRUARY 12, 2020 \*\*\* : see <https://ws2.mbl.edu/studentapp/studentapp.asp?courseid=mole> Founded in 1988, the Workshop on Molecular Evolution is the longest-running workshop of its kind. The Workshop is the premier program for integrating the methods, theory, and applications of molecular phylogenetics, statistical genetics, molecular evolution, and related disciplines. Students work closely with internationally-recognized scientists, receiving: (i) high-level instruction in the principles of molecular evolution, phylogenetic inference, and evolutionary genomics; (ii) advanced training in statistical methods best suited to modern datasets; and (iii)

hands-on experience with the latest software tools (often from the authors of the programs they are using). The material is delivered via lectures, discussions, and bioinformatic exercises motivated by contemporary topics in molecular evolution. A hallmark of this workshop is the direct interaction between students and field-leading scientists. The workshop serves graduate students, post-docs, and established faculty from around the world seeking to apply the principles of molecular evolution to questions of both basic and applied biological sciences. A priority of this workshop is to foster an environment where students can learn from each other as well from the course faculty.

As the course progresses, participants learn how to use the following software to address questions concerning the origins, maintenance, and function of molecular variation: ASTRAL, BEST, FASTA, FigTree, IQTree, MIGRATE, MAFFT, MP-EST, RaxML, RevBayes, PAML, PAUP\*, SVD Quartets, and SNaQ. Students will have the opportunity to work with software on their own laptops as well as receive training on how to use the same programs on a computer cluster.

In 2020 the course instructors include Peter Beerli, Joe Bielawski, Jeremy Brown, Minh Bui, Belinda Chang, Scott Edwards, Deise Goncalves, Kelley Harris, Tracy Heath, John Huelsenbeck, Lacey Knowles, Laura Kubatko, Aki Laruson, Paul Lewis, Emily Jane McTavish, Claudia Solis-Lemus, Ed Susko, David Swofford, Katie Taylor, George Tiley, and Anne Yoder.

More information on the Workshop is available on the dedicated course website: <https://molevolworkshop.github.io> For further information, please contact the Workshop Co-Directors:

Paul Lewis (paul.lewis@uconn.edu) and/or Peter Beerli (pbeerli@fsu.edu)

paul.lewis@uconn.edu

Instructions: To be added to the EvoDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvoDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvoDir direct them to the email [evodir@evol.biology.McMaster.CA](mailto:evodir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be send to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA) and processed later. In either case, please do not expect an instant response.

## Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L<sup>A</sup>T<sub>E</sub>X do not try to embed L<sup>A</sup>T<sub>E</sub>X or T<sub>E</sub>X in your message (or other formats) since my program will strip these from the message.