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# E v o l D i r

May 1, 2018

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

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## Foreword

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

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

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



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### AGA Hawaii Origins Jul22-25 CallForAbstracts

The 2018 American Genetic Association Symposium, “\*Origins of Adaptive Radiation\*” is being held \*July 22-25 in Waimea, Hawaii.\* The meeting will explore processes at the early stages of adaptive diversification. Invited speakers cover diverse systems, including African cichlids, sticklebacks, Anolis lizards, Galapagos finches and snails, Heliconius butterflies, Aquilegia plants, Hawaiian honeycreepers, spiders, insects, and trees. Concepts explored cover admixture, hybridization, fragmentation, plasticity, and priority. The goal is to look for commonalities, while also providing the opportunity to explore the many local Hawaiian radiations.

- We encourage all those that are interested to submit abstracts for posters - Oral presentations are limited. However, \*a small number of abstracts will be selected for oral presentations and associated travel compensation.

For this, we are particularly encouraging junior scientists to apply. We have extended the deadline to be

considered for an oral presentation: abstracts must be submitted by April 6th 2018.\*

Register at\* <https://www.theaga.org> \*

If you have any logistical questions, please contact Anjanette Baker . For any questions regarding the content of the symposium, please contact Rosemary Gillespie

Best wishes,

Rosemary Gillespie, AGA President

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

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### AGA Hawaii Origins Jul22-25 DeadlineMay1

Early Bird Registration and poster abstract submission end May 1st - register today!

The 2018 American Genetic Association Symposium, “Origins of Adaptive Radiation” will be held July 22-25 in Waimea, Hawaii. The meeting will explore processes at the early stages of adaptive diversification.

Invited speakers will explore concepts of admixture, hy-

bridization, fragmentation, plasticity, and priority using diverse systems. The goal is to look for commonalities, while also exploring the many local Hawaiian radiations.

We are accepting poster abstracts until May 1st.

Register at <https://www.theaga.org> - \$200 Early Bird fee includes opening reception, closing luau, lunches and coffee breaks, and a 3-YEAR AGA membership plus Journal of Heredity subscription.

If you have any logistical questions, please contact Anjanette Baker. For any questions regarding the content of the symposium, please contact Rosemary Gillespie.

Best wishes,

Rosemary Gillespie, AGA President [gillespie@berkeley.edu](mailto:gillespie@berkeley.edu)

Anjanette Baker, AGA Manager [theaga@theaga.org](mailto:theaga@theaga.org)

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

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## Bangalore ConservationScience Sep27-30

Please circulate the following conference announcement:

Dear all,

The Student Conference on Conservation Science (SCCS) 'V Bengaluru brings together young researchers in the science and practice of biodiversity conservation. The conference facilitates interaction, encourages exchange of research ideas and methods, sharing of knowledge and experience related to conserving wildlife and helps build contacts and capacity. As a sister conference to SCCS-Cambridge, SCCS-Bengaluru focuses on attracting student participants, primarily from countries in South and South-east Asia and Africa.

Early Bird registrations and Abstract submissions are now open on our website < <https://sccs-bng.org/> > (<https://sccs-bng.org/>)! Abstract submissions are open for those who want to present either a talk or a poster. Students need to register and pay the conference fee before being able to submit an abstract. Student travel bursaries are available for a limited number of candidates.

Dates:

\* The 2018 conference will be held at the JN Tata Auditorium, Indian Institute of Science, Bengaluru (INDIA), from 27th - 30th September 2018.

\* Abstract Submission Deadline : 25 April 2018

\* Early-bird Registration Deadline : 10 June 2018

\* Our 2018 plenaries are announced: <http://bit.ly/2HiYsfU> SCCS-Bengaluru is a four-day conference, where you can look forward to a host of long and short workshops (which are research focused and equip students with skills required for conservation), plenary talks < <http://bit.ly/2HiYsfU> > by invited speakers, close to 15+ student talks and about 80 student poster presentations.

We will also have sessions on 'Who's Who in Conservation' and 'Birds of a Feather' for students to learn about the work done by a diversity of academic institutions and conservation organisations, to discover work and research opportunities they offer, and to network with students and scientists working on similar issues. Based on feedback from previous years we are working towards a slightly new format for this year's conference, so do keep a lookout for our announcements via email, our website < <https://sccs-bng.org/> >, Facebook < <https://www.facebook.com/sccsbengaluru/> > and Twitter < <https://twitter.com/sccsbng> >.

For further information don't hesitate to contact us at [sccs@sccs-bng.org](mailto:sccs@sccs-bng.org)

\*Warm regards,\*

\*Shreekant Deodhar\*

\*Conference Administrator\*

\*On behalf of the Organizing Committee of SCCS-Bengaluru 2018\*

\*(Abinand Reddy, Arshiya Bose, Krishnapriya Tamma, Raman Sukumar, Ravi Chellam, Shomen Mukherjee, Tarsh Thekaekara, Uma Ramakrishnan, Vani Sreekanta)\*

SCCS - Bangalore <[sccs@sccs-bng.org](mailto:sccs@sccs-bng.org)>

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## Curacao InvertGenomics Oct19-21

Travel Support Award to attend 3rd Bi-annual Global Invertebrate Genomics Alliance Conference and Workshop (GIGAIII)

We would like to announce a funding opportunity to support graduate and postdoctoral student attendance to the 3rd bi-annual Global Invertebrate Genomics Alliance Conference and Workshop (GIGAIII) to be held in Curaçao this Fall, October 19-21st, 2018. The fund-

ing is available through a recent NSF conference grant awarded to GIGA researchers at Florida International University. The overarching goal of GIGA is to form a collaborative network of diverse scientists that wish to advance the state of invertebrate (non-insect/non-nematode) genomic research for the international scientific community. The 3-day conference will include a series of training and breakout sessions in addition to more formal presentations and posters. GIGAIII will provide opportunities for training at multiple career levels and the purpose of this travel support is to encourage advanced graduate student and postdoctoral attendance to actively engage with experts in their field. More information on GIGAIII can be found on the conference website (<https://gigaiii.weebly.com/>). A limited number of fellowships are being made available to advanced-standing graduate students and postdoctoral researchers and will facilitate international travel to Curaçao and lodging at the conference hotel (Hilton Hotel Curaçao). Applicants must be registered for the conference and currently enrolled/ employed at a US-based institution to be eligible for this funding. Applications by members of underrepresented groups are especially encouraged. To apply, applicants must submit \*1)\* a curriculum vitae \*2)\* a 2-page statement that includes a) how attendance at this conference will advance their future career goals and b) an explanation for the financial need. Applicants must also include \*3)\* a budget with a cost breakdown for the proposed travel, including total costs and any possibility of co-funding. \*If applicants are willing to share hotel lodging (max. 2 person/room), this should be indicated in the budget justification and will increase the number of awards we can provide. \*Successful applicants will receive support towards airfare expenses and/or lodging at the Hilton Curaçao < <https://secure3.hilton.com/en.US/hi/reservation/-book.htm?execution=e2s1> > during GIGAIII. Applications must be submitted to hbracken@fiu.edu as a \*single PDF\* by June 1, 2018.

Contact information about award:

Heather Bracken-Grissom, PhD

Dept. of Biological Sciences Florida International University-Biscayne Bay Campus

North Miami, Florida 33181, USA

Email: hbracken@fiu.edu

CRUSTOMICS LAB: [\\*http://www.brackengrissomlab.com/](http://www.brackengrissomlab.com/) – Heather Bracken-Grissom, PhD Assistant Professor Dept. of Biological Sciences Florida International University-Biscayne Bay Campus 3000 NE 151 Street, MSB-353 North Miami, Florida 33181, USA 305 919-4190 (Phone) 305 919-4030

(Fax)

\*CRUSTOMICS: Crustacean Genomics and Systematics Lab\* [\\*http://www.brackengrissomlab.com/](http://www.brackengrissomlab.com/)  
heather.brackengrissom@fiu.edu  
<Valerie.Hall@fiu.edu> [www.fiu.edu/~marine](http://www.fiu.edu/~marine) Heather Bracken-Grissom <heather.bracken@gmail.com>

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## Izmir Turkey EcolEvolution Jul18-20

Dear Colleagues,

We would like to remind you to the Ecology and Evolutionary Biology Symposium in Turkey (EEBST), which will take place this year on 18-20 July 2018 at Dokuz Eylul University, in Izmir, Turkey.

More information and registration information can be found at the symposium web site:

<http://eebst.org/> Abstracts submission deadline is 1 May 2018

EEBST'18 will be the fifth in a series of symposia organized yearly by the Ecology and Evolutionary Biology Society of Turkey. The language of the symposium is English, and is well attended by diverse international faculty and students from Europe, Middle East, West Asia, and North America. The symposia also aims to stimulate international collaborations.

Hope to see you in İzmir

On behalf of the EEBST'18 Organizing Committee

Efe Sezgin <efeszgn0@gmail.com>

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## Lisbon MicrobialEvolution Oct22-24 CallAbstracts

Dear all,

We are very happy to announce the IGC Symposium 2018: Microbial Eco-Evolutionary Dynamics. This symposium will take place from 22nd to 24th of October 2018 at the Instituto Gulbenkian de Ciencia, Oeiras, Portugal.

More information is available at: <https://microbial.eco-evo.science> Flyer at: <https://goo.gl/moVptx> The focus

of the symposium will be on the interplay between ecology and evolution in order to understand how ecology shapes the adaptive process and diversity of microbial populations and how adaptation and diversification feed-back into ecology. This meeting aims to be a venue for researchers at different career levels (Ph.D. students, post-docs, and well-established researchers) to discuss current concepts and build a diverse community in Ecology and Evolution.

We are pleased to announce that the keynote speakers are: Paul Rainey (MPI Plon, U. Massey) Sara Mitri (U. Lausanne) Nicole Mideo (U. Toronto) Andrew Hendry (U. McGill) Isabel Gordo (IGC) Sinead Collins (U. Edinburgh) Sarah Cobey (U. Chicago) Luis Miguel Chevin (CEFE Montpellier) Tim Barraclough (Imperial College London)

Abstract submission is now open. All participants are encouraged to present either via poster or oral presentation.

Important dates for the symposium: Abstract submission deadline: 15th of June 2018 Early bird registrations: 15th of July 2018 Regular registrations: 1st August 2018 Instituto Gulbenkian de Ciencia is a multidisciplinary biomedical research institute. IGC is a 10-minute walk from the beach and 20 minutes away from Lisbon, Cascais, and Sintra historic city centers (by train/car). Lisbon, in particular, is a beautiful hilly city, full of history and with a diverse cultural and gastronomic heritage.

Kind regards, The Organizing Committee Ana-Hermina Ghenu Hugo Barreto Tanja Dapa Ines Fragata Ricardo Ramiro

Ricardo Ramiro <ramiroricardo@gmail.com>

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## Minneapolis Behavioral Evolution Aug

International Society for Behavioral Ecology Biennial Meeting

Deadline for talk abstracts and Early-bird registration extended until April 10th!

Over the past few days, the ISBE 2018 Local Organizers have received numerous reports that the ISBE Membership site (operated by Oxford University Press) is experiencing technical difficulties that may have prevented some would-be attendees from joining ISBE or renewing their memberships prior to registering. In

light of this issue, we are suspending the membership requirement for registration and extending both early-bird registration and the deadline to submit an abstract for a talk to April 10. \*Abstracts submitted after April 10 will be assigned to poster presentations.\* Be sure to mark your calendars with the following important dates:

April 10, 2018 \*Talk\* Abstract Submission Closes Discounted Early-Bird Registration Closes July 20, 2018 \*Poster\* Abstract Submission Closes Online Registration Closes Special Meeting Rates at Conference Hotels End August 11, 2018 ISBE 2018 Begins!

Please visit the ISBE 2018 conference website for updates and additional information: <http://z.umn.edu/-ISBE2018>. Follow ISBE 2018 on facebook and twitter, and please share this email with anyone you believe may be interested in attending. We look forward to seeing you in the Twin Cities in August 2018!

Emilie Snell-Rood <emilies@umn.edu>

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## Montpellier EvolutionGenetResources Sep10-14

Dear colleagues,

We are pleased to announce that the Call for abstracts is now opened for the Third Jack R. Harlan International Symposium Dedicated to the Origins of Agriculture and the Domestication, Evolution, and Utilization of Genetic Resources, Montpellier (France), 10-14th September 2018.

Abstracts can be sent until the 15th of Mai.

Please refer to our website for all practical and scientific details : [www.harlan3symposium.org/call\\_for\\_abstracts](http://www.harlan3symposium.org/call_for_abstracts)  
Sincerely,

The organization team.

“yves.vigouroux@ird.fr” <yves.vigouroux@ird.fr>

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## Moscow Phylogenetic Biobanking Aug25-28

V Moscow International Conference “Molecular Phylogenetics and Biodiversity Biobanking Molphy-5”

Moscow State University, 25-28 August 2018, Russia

Dear colleagues,

you are welcome to take part in the MolPhy conference 2018. The “MOLECULAR PHYLOGENETICS” conference series is organized to provide a platform for the exchange of ideas and experiences in contemporary phylogenetics, evolutionary genomics, and bioinformatics of molecular evolution. This round the program also places emphasis on genomics of biodiversity, and various aspects of establishing and sustaining banks of molecular data and tissue samples for biodiversity research. This interface is rapidly developing, and is identified as an inter-faculty initiative of Moscow State University funded by the Russian Science Fund. Primary organizers are Moscow State University and the Russian Academy of Sciences, with support from other established academic and commercial organizations.

The major scope includes:

- Evolutionary genomics - Molecular phylogenetics and systematics - Genomics of biodiversity - Biobanking - Molecular dating and scenarios of coevolution - Evolution and development (evo-devo) - Models and algorithms for molecular evolution - Molecular ecology and biogeography - Applied phylogenetics

We welcome attendees internationally from academia, Research & Development, and service companies. Plenary speakers are invited by the Committee. The speakers of last rounds can be found in archive sections at [www.molphy.ru](http://www.molphy.ru). Important dates: June 28, 2018 registration deadline, abstract submission deadline July 10, 2018 abstract acceptance notification date July 18, 2018 normal registration fee payment deadline

The conference will take place in a multifunctional building at the Moscow State University campus on Sparrow Hills (Vorob'evy Gory) located about halfway between the center of Moscow at the Kremlin and the city's current outskirts. The campus has a much peculiar history, and is inimitable from the standpoint of architecture and its location as the roof of the city.

Further information is available on the conference web-

site at [www.molphy.ru](http://www.molphy.ru). You are welcome, and see you in Moscow!

Organizers of MolPhy-5 phone +7 (495) 939-3193, +7 (495) 924-9300 fax +7 (495) 939-3181 [molphy@molphy.ru](mailto:molphy@molphy.ru)

Leonid Rusin <[roussine@yandex.ru](mailto:roussine@yandex.ru)>

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## Muenster Evolution Meeting Oct4-6 Deadline May14

We are pleased to announce that the deadline for abstract submission for the Münster Evolution Meeting has been extended to 14th May 2018.

The first Münster Evolution Meeting (MEM) will take place on 4th - 6th October 2018 at the University of Münster, Germany. It will provide a forum to present and discuss evolutionary questions across all fields (Botany, Zoology, Microbiology, Medicine, Philosophy, ...) and levels (from molecules to societies).

A list of invited speakers and registration information can be found on our website: <https://www.uni-muenster.de/Evolution/MEM/main.shtml> Follow us on Twitter: @MEM2018WWU

Best regards, MEM Organizing Committee

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## Seattle Prokaryote Evolution Aug5-9

To anyone interested in horizontal gene transfer and its role in the evolution of Prokaryotes:

We invite you to attend and present at the Plasmid Biology 2018 conference this summer in Seattle! The meeting, supported by the International Society for Plasmid Biology < <http://www.plasmidbiologysociety.org/> > and other Mobile Genetic Elements, will take place August 5-9 on the beautiful University of Washington campus. Our Keynote speaker will be Dr. Dan Andersson from Uppsala University, who will talk about \$B!H(Bthe evolution of antibiotic resistance \$B!I(B. Please go to the meeting website < <https://uw.cloud-cme.com/-Ap2.aspx?EID=5866&P=5> > for more information on speakers and program, and for registration, abstract submission (oral or poster), and lodging reservations.



The deadline for early-bird registration and for abstracts to be considered for oral presentation is coming up soon, April 30: <https://uw.cloud-cme.com/Ap2.aspx?EID=5866&P=5> Traditionally the biannual Plasmid Biology conference brings together scientists from all over the world who are interested in the biology, evolution, ecology, epidemiology and biotechnological applications of plasmids and other mobile genetic elements, as well as their central role in horizontal transfer among Prokaryotes. This year, we have an intentional focus on evolution and antibiotic resistance, but have a continuing interest in DNA replication, plasmid stability, and DNA transfer. We have an amazing program with 31 invited speakers from 13 countries, and can't wait to add your oral or poster presentation to it. Submit your abstract now! We promise you will encounter an engaged and interactive community of scientists who are eager to hear your presentation. Please join us to talk about great science, renew old friendships, make new acquaintances, and establish collaborations.

Best regards,

Drs. Eva Top and Beth Traxler, and the organizing committee [Drs. Barbara Funnell (U. Toronto, Canada), Hideaki Nojiri (U. Tokyo, Japan), and Alvaro San Millan (U. Hospital, Madrid, Spain)]

Dr. Eva Top Professor Department of Biological Sciences University of Idaho E-mail: [evatop@uidaho.edu](mailto:evatop@uidaho.edu)

Dr. Beth Traxler Associate Professor Dept. of Microbiology University of Washington E-mail: [btraxler@uw.edu](mailto:btraxler@uw.edu)

Websites: Conference: <https://uw.cloud-cme.com/Ap2.aspx?EID=5866&P=5> Society: <http://www.plasmidbiologysociety.org/> Plasmid Biology Prize: <http://www.plasmidbiologysociety.org/plasmid-biology-prize/> "Top, Eva ([evatop@uidaho.edu](mailto:evatop@uidaho.edu))" <[evatop@uidaho.edu](mailto:evatop@uidaho.edu)>

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## Shenzhen AsiaEvo Apr18-20

Dear Colleagues:

The full program for the 1st Asian Evolution Conference now is available at: <http://asianevo.org/programme/-topics.html> We look forward to meet you at Shenzhen, China!

Regards

Qi Zhou, PhD Assistant Professor Life Sciences Institute Zhejiang University Lab: <http://www.qizhoulab.org/>

1st Asian Evolution Conf., April, 2018 <http://asianevo.org/>

Qi Zhou <[zhouqi1982@zju.edu.cn](mailto:zhouqi1982@zju.edu.cn)>

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## Sherbrooke Canada RECOMB-CG Oct9-12

RECOMB-CG 2018, SECOND CALL FOR PAPERS

16th RECOMB Satellite Conference on Comparative Genomics, RECOMB-CG 2018

Sherbrooke, Quebec, Canada - October 9-12, 2018

<https://recombcg2018.usherbrooke.ca>

SCOPE

The annual RECOMB Comparative Genomics Satellite Conference (RECOMB-CG) brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and the analysis of novel experimental results. The program will include keynote talks, contributed talks, and a poster session.

The 16th RECOMB-CG conference will be held at the Manoir des Sables, in beautiful Magog-Orford, near Sherbrooke, Québec, Canada on October 9-12 2018. With this Call for Papers we invite high-quality original full papers on topics related to the conference theme. The conference will also have a poster session. A detailed call for posters will be published later on the conference web page.

TOPICS

Papers are solicited on, but not limited to, the following topics: - genome evolution - population genomics - genome rearrangements - genome variation, diversity and dynamics - phylogenomics - comparative tools for genome assembly - comparison of functional networks - gene identification and/or annotation - cancer evolutionary genomics - comparative epigenomics - paleogenomics - epidemiology

IMPORTANT DATES

- Paper Submission Deadline: June 18, 2018 - Author Notification: July 20, 2018 - Final Version Due: August 3, 2018 - Conference: October 9-12, 2018

DETAILS ON SUBMITTING MANUSCRIPTS

Submitted papers must have not been published or be

currently under consideration for publication in any other journal or conference with formal proceedings. Each accepted paper has to be presented by one of the authors at the conference.

Accepted papers will be published in the conference proceedings, a volume in the Lecture Notes in Bioinformatics (LNBI) series. In addition, authors of selected papers will be invited, but not required, to submit a significantly extended version of their papers to Algorithms for Molecular Biology. Extended papers submitted will be handled by the Program Committee co-chairs. Authors who choose to publish their extended manuscripts will have to pay the journal's publication fees.

Authors are encouraged to submit their manuscripts in PDF format according to the LNBI series guidelines:

<http://www.springer.com/us/computer-science/lncs/-conference-proceedings-guidelines>

Submitted papers must be within 15 pages (in the LNBI format), with optionally a clearly marked appendix containing supplementary material made available to the reviewers.

All submissions must be made online, through the EasyChair submission system, at the following address:

<https://easychair.org/conferences/?conf=recombcg2018>

Authors need to register on that web site before submitting. A standard PDF file must be received by midnight on June 18, 2018 (any time zone) in order for a submission to be considered. Re-submission of already submitted papers will be possible until midnight June 18, 2018 (any time zone).

#### CONFIRMED KEYNOTE SPEAKERS

- Belinda Chang (Department of Ecology and Evolutionary Biology, University of Toronto, Canada) - Dannie Durand (Department of Biological Sciences, Carnegie Mellon University, USA) - Daniel Durocher (The Lunenfeld-Tanenbaum Research Institute, Mount Sinai Hospital, University of Toronto, Canada) - Christian Landry (Institute for Integrative Systems Biology, Laval University, Canada) - Gwenaël Piganeau (Banyuls Oceanographic Observatory and National Centre for Scientific Research, France) - Xavier Roucou (Department of Biochemistry, University of Sherbrooke, Canada)

#### PROGRAM COMMITTEE (PARTIAL)

Max Alekseyev (George Washington University) Lars Arvestad (Stockholm University) S everine B erard (U. Montpellier) Mathieu Blanchette (McGill University), co-chair Marilia Braga (Bielefeld University) Alessandra Carbone (CNRS, Universit e Pierre et Marie Curie) Cedric Chauve (Simon Fraser University) Leonid Chin-

delevitch (Simon Fraser University) Mikl os Cs  r os (University of Montreal) Daniel Doerr (Bielefeld University) Ingo Ebersberger (Goethe University Frankfurt) Nadia El-Mabrouk (University of Montr eal) Oliver Eulenstein (Iowa State University) Guillaume Fertin (University of Nantes) Pawel Gorecki (University of Warsaw) Michael Hallett (Concordia University) Katharina Jahn (ETH Zurich) Asif Javed (Genome Institute of Singapore) Manuel Lafond (University of Ottawa) Kevin Liu (Michigan State University) Joao Meidanis (UNICAMP) Istv an Mikl os (R enyi Institute, Hungarian Academy of Sciences)

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## UMichigan PlantEnvInteractions Sep27-28

This is a conference announcement that will be of interest to evolutionary biologists and evolutionary geneticists.

Dear all,

I am excited to announce that registration has opened for the University of Michigan's 2nd annual Green Life Sciences Symposium, to be held Sept 27th and 28th, 2018, at the University of Michigan in Ann Arbor, MI. This year's theme is “\*Plant-environment interactions across scales\*”.

We are currently soliciting talks and poster presentations. Below is more information about the symposium, along with a list of confirmed speakers and links to registration.

We hope you will be able to join us for the GLS symposium in the fall. Please pass along this opportunity to students and postdoctoral research associates, as well as any other potentially interested parties.

Best wishes, Gina Baucom

\*2nd Annual Green Life Sciences Symposium: Plant-Environment Interactions Across Scales\*

\*Link: <https://sites.lsa.umich.edu/green-life-sciences/-annual-symposium/> \*When: September 27 & 28, 2018 Where: D. Dan and Betty Kahn Auditorium,



Biomedical Science Research Building (BSRB), University of Michigan, Ann Arbor  
 Speakers: 2018 Symposia & Panelist List  
 Cost: FREE  
 Plants interact with both a variety of community members (other plants, the microbial community, pollinators, herbivores) and are exposed to a variety of abiotic environmental stressors (drought and changing climate, human-mediated agents of selection). These interactions are often examined at the phenotypic level by evolutionary ecologists whereas the mechanistic basis of such interactions are detailed by molecular geneticists; longer-term outcomes of such interactions are assessed by paleobiologists. It is rare however that plant-environment interactions are examined across scales within the same system, i.e. from genes, to molecular mechanism, phenotype, fitness, and deeper evolutionary patterns across time. The aim of this conference is to highlight the work of prominent evolutionary ecologists, molecular geneticists, ecophysiologists, and paleobiologists at the University of Michigan and beyond that examine similar plant-interaction phenomena but at very different scales of study. Our overall goal is to stimulate new collaborations and novel takes on overlapping phenomenon studied across scales.

**Format & Participation Opportunities:** Researchers will present their work during five sessions and have ample time for networking at coffee breaks. We are accepting a small number of outside presentations appropriate to any of our five main sub-themes via self-nomination. Early career researchers (undergraduate and graduate students, postdoctoral research scholars, assistant professors) are likewise encouraged to present a poster during the Thursday evening poster session which will be held at the Matthaei Botanical Gardens. If you wish to be considered for a talk, please submit an abstract, 250 words or less, in the field indicated in the registration form by May 1st, 2018. In the text, indicate if you would like to be considered for a poster presentation if we are unable to offer you a talk. Spaces for talks will be limited. A limited amount of funds are available to help offset the cost of travel or room and board for early-career researchers who are presenting either a talk or a poster; funding decisions will be made by the organizing committee before June. If you would like to be considered for travel funds, please email Gina Baucom with this information by May 1, 2018. Registration for this conference is free, and a dinner will be held Thursday night (Sept 27, 2018) for conference speakers and poster presenters. (Link to register: <https://sites.lsa.umich.edu/green-life-sciences/annual-symposium/> ) Below are the five symposia that will be held Sept 27th & 28th, 2018, with a list of confirmed speakers: Living together: Plant-microbe symbioses Carolyn Malmstrom, Plant Biology, Michigan State University Jessie Ueling, Population Genomics, University of California at Berkeley Katy Heath,

Department of Plant Biology, University of Illinois  
 Jill Myers, Ecology and Evolutionary Biology Department, University of Michigan  
 Interactions affecting plant reproduction Sharon Kessler, Purdue Department of Botany and Plant Pathology  
 Jannice Friedman, Department of Biology, Syracuse University  
 Cora MacAlister, Molecular, Cellular, and Developmental Biology Department, University of Michigan  
 Shape control Aman Husbands, Department of Molecular Genetics, Ohio State University  
 Siobhan Braybrook, Molecular, Cellular, and Developmental Biology Department, UCLA  
 Erik Nielsen lab, Molecular, Cellular, and Developmental Biology Department, University of Michigan  
 Stressful interactions: Plant adaptation to abiotic & biotic stressors  
 Jill Anderson, Departments of Ecology

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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>

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## UPorto Portugal HostParasiteInteractions Dec5-7

Dear All,

It's a pleasure to invite you to participate in Trends in Biodiversity and Evolution (TiBE) conferences, an annual meeting organized by the Center in Biodiversity and Genetic Resources (CIBIO-InBIO, Portugal).

TiBE conferences aim to bring together researchers and students working on Evolutionary Biology. Held in an informal but stimulating scientific atmosphere, these conferences provide an excellent opportunity for strong interaction and brainstorming between students and more experienced researchers.

This year, TiBE2018 will be devoted to HOST-PARASITE INTERACTIONS. The conference will take place on 5-7 December, 2018 at CIBIO-InBIO facilities in Vairao, Portugal. It will include plenary talks, oral communications and poster sessions.

For more details on the program, registration and abstract submission, please visit: <https://cibio.up.pt/tibe/details/tibe2018> or contact us at [tibe@cibio.up.pt](mailto:tibe@cibio.up.pt)  
 perera@cibio.up.pt

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**Ventura California Speciation  
Mar10-15**

**MEETING REGISTRATION ANNOUNCEMENT:**

We are pleased to announce SPECIATION 2019, the third Gordon Research Conference (GRC) dedicated exclusively to speciation research. The conference will be held at the Four Points Sheraton / Holiday Inn Express, Ventura, CA during the week of March 10 - 15, 2019, co-chaired by Rebecca Safran (University of Colorado, USA) and Katie Peichel (University of Bern, Switzerland).

The conference will be directly preceded by a two-day Gordon Research Seminar (GRS) on March 9 - 10, co-chaired by Martin Garlovsky (Sheffield University, USA) and Sheela Turbek (University of Colorado, USA), that offers opportunities for early-career scientists to get involved at the forefronts of modern speciation research.

Please follow this link to learn more about these conferences and to register. <https://www.grc.org/speciation-conference/2019/> Invited presentations and discussion sessions at both the GRC and GRS will cover a broad array of timely topics in speciation research.

Please send questions to [Rebecca.Safran@colorado.edu](mailto:Rebecca.Safran@colorado.edu)

Sincerely

Rebecca Safran, Katie Peichel, Martin Garlovsky, Sheela Turbek

Dr. Rebecca Jo Safran

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Research Lab: [www.safran-lab.com](http://www.safran-lab.com) Research Blog:  
<http://www.barnswallowproject.com> Climate Change:  
[www.insidethegreenhouse.org](http://www.insidethegreenhouse.org) NO tolerance for hate  
and social injustice

Rebecca J Safran <[rebecca.safran@colorado.edu](mailto:rebecca.safran@colorado.edu)>

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**Warsaw Evolution Sep26-28**

Dear All,

We warmly invite you to take part in the 6th Polish Evolutionary Conference (26-28th September 2018), which will take place at the Centre of New Technologies in Warsaw. More information about the conference and registration options are available here:

<http://pec2018.cent.uw.edu.pl/> Key dates:

- June 15, 2018

Abstract Submission Closes

-July 4, 2018

Discounted Early-Bird Registration Closes

- August 31, 2018

Online Registration Closes

-September 26, 2018

PEC 2018 Begins

With best wishes,

The Organising Committee PEC 2018

You can contact us at [\\*pec2018@cent.uw.edu.pl](mailto:*pec2018@cent.uw.edu.pl)\* if you have any questions or queries.

Joanna Sudyka <[joanna.sudyka@cent.uw.edu.pl](mailto:joanna.sudyka@cent.uw.edu.pl)>

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### Brno CzechRepublic EvolInfectiousDiseases

The Laboratory for infectious diseases common to humans and (non-human) primates based at the Institute of Vertebrate Biology Czech Academy of Sciences and University of Veterinary and Pharmaceutical Science Brno is searching for a PhD candidate for highly ambitious topic with applications to conservation of critically endangered iconic mountain gorillas.

Title: Epidemiology of helminth infections in great apes with emphasis on mountain gorillas in Virunga Massif in Rwanda

Background: In non-human primates gastrointestinal parasites are typically asymptomatic, but habitat reduction and fragmentation can alter the transmission and increase host susceptibility, which may exacerbate the effects of infection. There is considerable concern

that in fragile or threatened non-human primate populations, these cascading effects can significantly affect species survival. Due to effective conservation efforts, the population of critically endangered mountain gorillas (*Gorilla beringei beringei*) at Virunga has been steadily increasing. Fast increase of the whole population and increase in the home range overlap in particular can lead to elevated risks of changes in pathogens' epidemiology.

Project: The student will investigate the dynamics of parasite-host system and impact of parasites in several gorilla populations at individual and population level and causal-effects events with focus on mountain gorillas at Virunga in Rwanda . The study will benefit from (i) complex sampling design conducted on Rwandan, Ugandan and Congolese populations of mountain gorillas in collaboration with Mountain Gorilla Veterinary Project and Dian Fossey Gorilla Fund International and (ii) our previous long-term research on western lowland gorillas, providing extensive set of genomics/metagenomics data for planned statistical analyses.

Funding: research costs and partial salary (in add to a governmental stipend) covered by a grant by Czech

Science Foundation.

Qualifications: Applicants with master degree in biological or veterinary should have fair background in statistics, knowledge of molecular methods and she/he is preferably expected to have experience in analyses of next-generation sequence data. Parasitological background is advantageous. Previous experience with ape or non-human primate research is not needed. We expect strong motivation and commitment, willingness to quickly learn new methods, analytical thinking, good communication skills and ability for both independent and team-work. The successful candidate will participate in a PhD program at Masaryk University in Brno (parasitology). The starting date is fall 2018.

Important note: this is not a PhD with a strong field component, most of the work is focused on laboratory and data analyses.

If interested, please, send (1) CV including a list of publications, (2) motivation letter, and (3) contact details for 2 references to Klara Petrzekova (petrzekova@ivb.cz) immediately, latest mid-May.

Mgr. Klara J. Petrzekova, Ph.D. Institute of Vertebrate Biology, Czech Academy of Sciences Kvetna 8 603 65 BRNO, CZECH REPUBLIC phone:+420-543422549 fax:+420-543211346 <http://www.ivb.cz> <http://www.hpi-lab.com/en> Klara Judita Petrzekova <petrzekova@ivb.cz>

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## CIRAD Montpellier Evolution Viruses

We have a PhD position available, starting no later than September 2018, at CIRAD, research unit ASTRE, Montpellier, France.

The PhD student will work on the virulence of Peste des petits Ruminants Virus in relation to variability of host response.

Peste des Petits Ruminants virus (PPRV) is highly pathogenic to small ruminants (e.g. goats, sheep), but susceptibility of hosts vary widely among viral strains and host breeds. This project focuses on host-pathogen interactions, and more specifically the modulation of host immune response, during infection of small ruminants by PPRV, and how these interactions can explain variability in pathogen virulence and host susceptibility. The project will combine in vitro and in vivo approaches. Virus infection and replication will be studied,

and critical genes products and their networks involved in resistance to PPRV will be identified using a system immunology approach.

This project will benefit from a close collaboration between the research unit ASTRE of Cirad (Montpellier, France) and the Institute of Virology and Immunology (Berne, Switzerland). The PhD student will be mainly based in Montpellier (France), but will stay in Berne for several months for training and to carry out some of the \*in vitro\* and all the \*in vivo\* experiments under the supervision of Dr Artur Summerfield.

We are looking for a highly motivated student interested in virology and immunology. Previous experience in these fields is an advantage. The student has to be willing to work in high confinement facilities. The student will be based in Montpellier, but will stay at least once for several months in Berne, Switzerland. Knowledge of French is not necessary but may help in everyday life. Active knowledge of written and spoken English is needed.

Please contact us for more details about the thesis project and necessary documents for the application. Candidates must send a PDF document including\* their CV and grade sheets and rank\* (rank/total number of students) \*from their Master\*'s degree\*.\*

Applications must be received before May 7th, 2018: contact

arnaud.bataille@cirad.fr, or/and philippe.totte@cirad.fr

Arnaud Bataille <bataille.ama@gmail.com>

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## ClarkU AnnelidEvoDevo

The lab of Dr. Néva Meyer at Clark University (<http://wordpress.clarku.edu/nmeyer/>) is looking for a PhD student to study annelid central nervous system development with the goal of gaining a better understanding of how nervous systems evolved. Research will be carried out on the annelid *Capitella teleta*, but can be expanded to include other spiralian. The molecular mechanisms underlying annelid and spiralian development are not well understood and multiple features including the spiral cleavage program make spiralian a great group of animals to study evolution of animal body plans. Furthermore, the research community that studies evolution of spiralian body plans is small but rapidly growing and is very welcoming and collaborative. Potential research topics in our lab include investiga-

tion of the molecular control of neural fate specification. We have a stable lab colony of *Capitella teleta*. Techniques used in the lab include microinjection of embryos, qRT-PCR, immunohistochemistry, imaging of live and fixed tissue, quantification of phenotypes using ImageJ, and gene knockdown and misexpression by injection of morpholinos and mRNA.

Students are encouraged to develop a project that matches their learning and career objectives and will enter Clark University's Biology PhD program. Previous experience in molecular biology and/or working with marine larvae is desirable. PhD students will be guaranteed funding for five years, with a possible extension through teaching and research assistantships. A start date of September 2018 is preferable.

Clark University is a small liberal arts research university located in Worcester, MA. Worcester has a nice combination of urban and outdoor activities and is in close proximity to a variety of New England destinations.

Please email a brief description of why you are interested in the position and a CV to: nmeyer@clarku.edu

Néva P. Meyer, Ph.D. Assistant Professor Clark University Department of Biology 950 Main Street Worcester, MA 01610

Neva Meyer <NMeyer@clarku.edu>

cal data from both terrestrial and marine environments, especially coral reef systems. The group of Landscape Ecology is a young and dynamic team of researchers, dedicated to advance interdisciplinary science.

The candidate must hold a master degree in environmental sciences, mathematics or, physics with demonstrated knowledge in programming (e.g. in R, C). Knowledge of ecological modelling, differential equations, dynamical systems, and/or other forms of ecological modelling is an advantage. The successful candidate should also have strong collaborative skills, proven abilities to publish at a high international level, and a good English level. A professional diving licence would be an advantage.

We look forward to receiving your online application including a statement of interest mentioning how the skills fit the project, a CV, the names of two references and copies of degree certificates until May 1st, 2018. Expected starting date: June-July 2018. Please note that we exclusively accept applications submitted through our online application portal. Applications via email or postal services will not be considered.

For further information about the group please visit our websites at ETH Zurich and WSL ([www.landecology.ethz.ch](http://www.landecology.ethz.ch)). Questions regarding the position should be directed to Prof. Dr. Loic Pellissier by email, [loic.pellissier@usys.ethz.ch](mailto:loic.pellissier@usys.ethz.ch) (no applications).

Pellissier Loïc <[loic.pellissier@usys.ethz.ch](mailto:loic.pellissier@usys.ethz.ch)>

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## ETH Zurich SpeciesDiversity

The Research Group of Landscape Ecology at ETH Zurich and the Swiss Federal Institute for Forest, Snow and Landscape Research WSL conducts research on the processes shaping and maintaining species diversity within landscapes and seascapes. The team combines field measurements and modelling to evaluate how extant ecosystems are expected to respond to global changes. We seek a PhD student in spatial eco-evolutionary modelling. We offer an international research environment with the opportunity to conduct highly competitive research in environmental sciences. The project aims at investigating how biodiversity dynamics shape ecosystem processes (e.g. primary productivity) over geological times using a novel spatially-explicit model developed within the group. The project will be global in scope and span both terrestrial and marine ecosystems. The successful PhD student will also participate to several field campaigns to gather empiri-

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## France MicrobialAdaptation

As part of the MOPGA/Campus France program, we are searching for candidates for a PhD project on the impacts of warmer climates on the structure and functioning of microbial communities across an experimental food web.

The job description can be found at <https://doctorat.campusfrance.org/CF201812479>. With the selected candidate, we will apply to the MOPGA/Campus France program for which we have been pre-selected. Twenty projects on 94 MOPGA projects will be selected.

To apply you must send to [ppv.sec@univ-tlse3.fr](mailto:ppv.sec@univ-tlse3.fr) a CV and motivation letter in English, including the names of 2-3 referees.

The deadline is unfortunately very soon. Applications must be received online not later than 27th April 2018. Informal enquiries may be made by email to



julien.cote@univ-tlse3.fr

Supervisors: Julien Cote, Lucie Zinger, Joël White

– Dr Julien Cote 118 route de Narbonne 31062  
Toulouse cedex 9 France laboratoire Evolution & Diver-  
sité Biologique UMR 5174 CNRS UPS phone: +33  
(0) 5 61 55 61 97 Université Toulouse 3 - Paul  
Sabatier email: julien.cote@univ-tlse3.fr website: <http://www.julien.cote.fr/> <http://themetatron.weebly.com/>  
Julien Cote <julien.cote@univ-tlse3.fr>

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## JagiellonianU-Krakow TardigradeEvolution

\*PhD studentship in tardigrade evolution\*

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

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

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

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

Depending on the achievements and performance of the successful candidate, the tax-free monthly stipend will vary from 4 000 to 7 000 PLN (typically, cost of life in Kraków for a PhD student is ca. 2 500 PLN).

Deadline for applications: 20th May 2018.

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

LM@tardigrada.net

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## LaReunion CropPathogenEvolution

As part of a collaboration between CIRAD (La Réunion & Montpellier) and the National Museum of Natural History (MNHN Paris), we are looking for a motivated and talented PhD student to work on the following topic: Improving our understanding of crop pathogen evolution and emergence using ancient DNA .

In order to better control current diseases of plants and prevent future epidemics, it is crucial to develop an improved understanding of the factors underlying pathogen emergence, adaptation and spread. Recent developments in DNA sequencing technology now enable the recovery of historical genomes dating back to previous centuries. The aim of this PhD is to reconstruct the history and evolution of some of the current most devastating crop pathogenic bacteria using historical genomes issued from herbaria collections. The major novelty of this project lies in the reconstruction of complete genomes from herbarium dried plant specimens as well as in their analyses with sophisticated and dedicated population genetics methods. This project is expected to lead to major advances in molecular epidemiology of plant infectious diseases, through both innovative molecular and statistical approaches. The student will benefit from a collection of infected plant sampled from several herbaria worldwide and will be given the opportunity to extend it. While focused on a well-defined question, the project offers exposure to theoretical, computational and molecular biology and thus represents an ideal training for a student to become a well-rounded biologist. The work will combine lab work



(ancient DNA extraction, enrichment and sequencing using innovative molecular biology techniques), bioinformatics (NGS data analysis) and population genomic inferences (phylogenetic, comparative genomic 'A').

The hired PhD will be expected to start between September and December 2018. This project will be funded through an ANR project and has also been shortlisted to benefit from a MNHN fellowship. The student will join the dynamic "Emerging pathogen genomics and epidemiology" research team based at UMR PVBMT in La Réunion Island (<https://umr-pvbmt.cirad.fr/en>). Frequent scientific interactions and short/mid-length exchanges with our collaborators in Montpellier (UMR BGPI/IPME) and Paris (MNHN) are to be expected.

Although the most sought-after qualities are enthusiasm, curiosity, creativity and dedication to the project, the ideal student would have already acquired some specific skills as detailed in the attached document. To apply, send a CV, cover letter and contact details of at least one academic referee to [adrien.rieux@cirad.fr](mailto:adrien.rieux@cirad.fr), [nathalie.becker@mnhn.fr](mailto:nathalie.becker@mnhn.fr) and [lionel.gagnevin@cirad.fr](mailto:lionel.gagnevin@cirad.fr) as soon as possible. Priority will be given to students applying before May the 11th (ten days before the due date for the MNHN fellowship). Do not hesitate to contact us for other informations.

[adrien.rieux@cirad.fr](mailto:adrien.rieux@cirad.fr)

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## LundU 2 EcoImmuneCosts

PhD position advertised in the ERC Advanced Grant Project 'EcoImmuneCosts' (PI: Dennis Hasselquist), Lund University (Sweden):

Mild disease, immune function and aging: the role of telomere length and degradation

Requirement profile Connections between (mild) disease, the immune system and aging has become a hot topic in evolutionary biology and ecology in recent years. In the present project, the main aim is to investigate relationships between mild disease, immune responses and aging/aging markers and how these three factors are associated with reproductive and life history strategies in studies on birds, with special emphasis on telomeres, and with the great reed warbler as model species. Main focus will be on; (i) long-term studies (>30 years) of a natural, wild population of great reed warblers (*Acrocephalus arundinaceus*) at lake Kvismaren SSE Orebro, in southern Central Sweden, and (ii) a long-term malaria

infection experiment on great reed warblers in Bulgaria.

Project description The PhD candidate will analyze longitudinal data on early life telomere length (eTL) to investigate whether, for example, eTL is predictive of malaria infection and/or whether eTL is associated with recovery from illness, as well as how disease recovered versus chronically infected birds differ with respect to telomere shortening, aging and reproductive performance. The project also aims at looking at the different life history strategies of great reed warblers (e.g., pace-of-life hypothesis). Furthermore, the project aims to study sex differences in long-term effects (immune responses, (Mhc) gene expression, physiological health) of experimentally infected great reed warblers which will be kept in aviaries. The project involves extensive field work with great reed warblers in lake Kvismaren, NÅrke, which is part of the ongoing long-term population study. The PhD candidate is also expected to carry out a substantial amount of laboratory work, particularly qPCR analyses of telomere length and infection analyses (malaria and other microorganisms). He/she will analyse long-term data that previously have been collected (DNA samples, reproductive performance and Darwinian fitness data etc) and own data collected during the PhD studies.

Required Qualifications - Master degree in biology, with specializations in animal ecology, evolutionary/behavioural ecology and molecular ecology. - High motivation and a sincere interest in this particular project is crucial. - It is highly desired that the applicant has considerable experience of analysing DNA data, in particular telomere length and malaria parasite analyses. - Laboratory experience from molecular techniques (in particular qPCR, but also PCR and Sanger sequencing) is desirable - Analytic skills and an interest in analysing life history and fitness data in combination with DNA data are requested. - It is a requirement that spoken and written English is excellent. - Experience from fieldwork with birds is very important, and experience of field work on great reed warblers an extra plus.

Lund University, Faculty of Science, Department of Biology Lund University was founded in 1666 and is repeatedly ranked among the world's top 100 universities. The University has 40 000 students and 7 400 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.

Last application date 2018-05-14

More information and application portal: <https://lu.mynetworkglobal.com/what:job/jobID:205649/-type:job/where:1/apply:1> Questions can be directed to: Dennis Hasselquist, professor, +46 46 222 37 08, [dennis.hasselquist@biol.lu.se](mailto:dennis.hasselquist@biol.lu.se)

PhD position advertised in the ERC Advanced Grant Project 'EcoImmuneCosts' (PI: Dennis Hasselquist), Lund University (Sweden):

Telomere length, immune responses and immune costs

Requirement profile Eco-immunology targets one of the great challenges in biology and medicine - how the immune system has evolved to optimize protection and minimize immunopathology (incl. autoimmune) costs. Recent research suggests that seemingly harmless pathogens and short-term episodes of immune system activation entail delayed ('hidden') fitness costs. However, the mechanisms mediating these costs are still unknown. The project thus aims to explore these mechanisms and a major target is to experimentally test if accelerated telomere degradation is a causative mechanism through which small immune costs can accumulate and be translated

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## McGillU EvolutionaryBioinformatics

The fish population genetics and genomics (FPG2) lab in the Department of Natural Resource Sciences at McGill University is seeking applications from students interested in pursuing a PhD in bioinformatics, comparative phylogenomics, and population genomics. Part of the work will consist of de novo assembly and annotation of genomes from generated long read sequences, as well as, performing extensive population RAD and/or RNA sequencing surveys. Although fieldwork experience is not required, a strong potential exists for students to participate in sample collections in Arctic coastal and

offshore marine environments, as well as in more local areas.

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

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

- <http://www.mcgill.ca/internalawards/> - <http://www.mcgill.ca/gps/funding/students> To apply, please send a current c.v., unofficial copies of academic transcripts, brief description of your research interests (~ 1/2 page), and contact information for 2-3 referees. For a September start date, applications should be sent by May 11th 2018 (very soon!, sorry :()), while a January start date is also acceptable with a deadline of July 1st. Electronic applications (PDF only please) can be sent to:

[denis.roy@uconn.edu](mailto:denis.roy@uconn.edu) (Starting at McGill September 2018)

Thank you,

Denis Roy Assistant Research Professor Department of Natural Resources and the Environment/Center for Environmental Sciences & Engineering University of Connecticut 1376 Storrs Road, Unit 4087 Storrs, CT 06269-4087 FPG2 Lab webpage: <http://denisroy.weebly.com>  
Denis Roy <[denisroy1@gmail.com](mailto:denisroy1@gmail.com)>

## MonashU FairyWrenAdaptation

PhD scholarship to study effects of increasing temperature in a tropical endangered fairy-wren

In the Behavioural and Evolutionary Ecology of Birds Group (<https://sites.google.com/site/petersresearchgroup/>) @ Monash University, Melbourne, Australia, a PhD position is available to study how ambient temperatures affect physiology and behaviour of purple-crowned fairy-wrens *Malurus coronatus* using a combination of existing and newly-collected data. This is an endangered bird inhabiting the riparian zone of the monsoonal tropical savannah.

Field work will be taking place at AWC Mornington Wildlife Sanctuary in the Kimberley region of NW-Australia. The research group has been studying a fully colour-banded, known-age population since 2005, with extensive information on individual life-histories. This project will investigate how birds deal with the very high temperatures this tropical endangered species experiences. The research will focus on effects of high temperatures on metabolic rate, condition, heat stress, foraging behaviour, use of microsites and molecular aging. Additionally, the project will assess which individual attributes (age, sex, social status, morphology, genetic background) and environmental parameters (social group size, habitat) affect individual variation in response to increasing temperatures. The work will consist of behavioural observation, capture and handling of birds, metabolic rate measurements

The research is funded through a Discovery Project grant of the Australian Research Council (DP18) to Assoc Prof Anne Peters.

Monash University is a member of Australia's Group of Eight coalition, and is internationally recognized for excellence in research and teaching. The School of Biological Sciences is home to a collegial and interdisciplinary research environment, with strengths in ecology, genetics and evolutionary biology. The Monash doctoral program includes additional training opportunities beyond the research program that enhance employability post degree. Monash is located in Melbourne, one of the most liveable cities in the world and a cultural and recreational hub.

Requirements and further information Applicants must have self-motivation, enthusiasm, a background in be-

havioural and evolutionary ecology, a passion for studying wild animals in their natural environment, strong quantitative skills and an excellent work ethic, experience with (tropical) fieldwork and/or mistnetting highly desirable, a full driver's licence is required.

Successful students will be offered a stipend (living-allowance) scholarship provided tax free for three years, with the possibility of a six-month extension. Expenses for research, coursework, and conference attendance are covered; relocation assistance is available. For international students, cost of tuition fees and Overseas Student Health Cover are covered.

In order to be eligible, students must have four-year degree with relevant research experience, outstanding grades, and excellent English. Evidence of published research is a plus.

The application process takes place in two stages. Send your initial application to Anne Peters ([anne.peters@monash.edu](mailto:anne.peters@monash.edu)), consisting of: a letter of motivation; a CV; overview of your academic results, and translation if required, preferably indicating cohort rank or percentiles; English test results if required; and the names and contact details of 3 academic references. Deadline is 1 June 2018.

After a review of all applications, you may be contacted for a skype or personal interview. If you are selected for a PhD position, you will be sent an invitation to submit a formal application through the Monash University web portal. Start date is September or earlier.

See <https://sites.google.com/site/petersresearchgroup/> for further details. Contact Anne ([anne.peters@monash.edu](mailto:anne.peters@monash.edu)) if you would like further information on the project or the application process.

Anne Peters Associate Professor | Future Fellow School of Biological Sciences 108, 19 Rainforest Walk (enter via 25 Rainforest walk) Monash University VIC 3800, Australia phone: +61 3 9905 6287

<https://sites.google.com/site/petersresearchgroup/>

<http://scholar.google.com/citations?user=-jpoOPNEAAAAJ>

Anne Peters  
<[anne.peters@monash.edu](mailto:anne.peters@monash.edu)>

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## Montpellier Spatial Population Genomics

Important change : DeadLine is extended until May, the 4th.

Our group “Statistical and evolutionary population genomics” < <https://www6.montpellier.inra.fr/-cbgp.eng/Research/Thematic-groups/Statistical-and-evolutionary-population-genomics> > at the CBGP (INRA Lab, Montpellier, France) < <https://www6.montpellier.inra.fr/cbcp.eng/> > has a great opportunity to get funding for a PhD starting in September-December 2018 on the development and test of new inference methods in spatial population genetics/genomics based on simulations. Dead Line for student application is very soon - 22 of April 2018 - and only for non-french students. This funding is part of the project “Make our Planet Great Again” from our President Macron.

A detailed description of the PhD project as well as information on how to apply are available here : <https://doctorat.campusfrance.org/en/CF201812445> We are looking for master student with background and/or strong interest in evolutionary biology, population genetics/genomics and statistics/physics/mathematics matching the expected skills detailed below.

Interested candidates can contact me (Raphael Leblois, see contact below),— and send a CV and a motivation letter.

Funding will depends on the adequation between the applicant skills and project requirements.

Best regards,

Raphael

\*Skills required:\* General training at the Master level in evolutionary biology, bio-statistics or bioinformatics with a good background or a willingness to open up to statistics, bioinformatics and stochastic models of evolution. A good knowledge of population genetics concepts and of one or more programming languages (C++, R) will be a plus.

\*Keywords :\* landscape genomics, dispersal and connectivity, past demographic changes, simulation-based statistical inference, environmental change, biodiversity scenario prediction

\*Raphael LEBLOIS\*\*\*\*\* \*Centre de Biologie et Gestion des Populations (CBGP, UMR 1062)\* 755 avenue du campus Agropolis, Campus International de Baillarguet CS 30016, 34980 Montferrier-sur-Lez cedex France

\*Tel : +33 (0)4 99 62 33 31\* \*Fax : +33 (0)4 99 62 33 45\*

\*raphael.leblois@inra.fr\*\*\*

\*<http://raphael.leblois.free.fr>\* Raphaël Leblois  
<raphael.leblois@inra.fr>

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## Paris-Nice EvoDevo

Graduate Position: Paris-Nice. Evolutionary Genetic-OfDevelopment Second call: April 7, 2018

Two PhD positions are available in the context of a research project between the laboratories of Henrique Teotonio (Institut de Biologie, Ecole Normale Supérieure, Paris; <http://www.ibens.ens.fr/-spip.php?rubrique28&lang=en>) and Christian Braendle (Institut de Biologie Valrose, Nice; <http://www.braendlelab.net>).

The project will characterize the effects of different breeding systems on the evolution of *C. elegans* hermaphrodite germline development. The key objectives are (1) to perform experimental evolution under different sex ratios of males, females and hermaphrodites; (2) to characterize the genetic basis of hermaphrodite germline traits through genetic transformation methods and a genome-wide association study; and (3) to determine how natural selection at candidate loci depends on hermaphrodite germline developmental evolution.

Candidates are expected to have a master’s degree in evolutionary biology and an understanding of the fundamental problems of quantitative genetics, population genetics and developmental genetics, including QTL and GWAS mapping. Candidates with experience in computer programming, experimental evolution, developmental phenotyping and statistical analysis of large data sets are preferred. The PhD students will be expected to conduct full-time independent research in both the Teotonio and Braendle labs.

The PhD positions are funded by the National Agency of French Research (ANR) for three years, subject to an initial evaluation after 6 months, with a potential one-year extension. Successful applicants can start their PhD in summer-fall 2018.



To apply, send a CV, a letter of motivation, and the contact information for two referees as a single PDF file to Henrique Teotonio (teotonio@biologie.ens.fr) and Christian Braendle (braendle@unice.fr), with subject PhD-ANR. Informal inquiries are welcome.

For relevant background information see: Carvalho et al. 2014. <http://doi.org/10.1186/1471-2148-14-117> Pouillet et al. 2016. <http://doi.org/10.1111/evo.13032> Noble et al. 2017. <http://doi.org/10.1534/genetics.117.300406> Teotonio et al. 2017. <http://doi.org/10.1534/genetics.115.186288> braendle <Christian.Braendle@unice.fr>

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## SarsCentre Norway OriginEvolutionSynapticProteins

PhD position: Origin and Evolution of Synaptic Proteins

<http://www.sars.no/jobs/2018-3861-phd.Burkhardt.php>

There is a vacancy for a PhD position at the Sars International Centre for Marine Molecular Biology ([www.sars.no](http://www.sars.no)) in the research group headed by Dr. Pawel Burkhardt. The position is for a fixed-term period of 4 years and is subject to funding on the Sars Centre core budget. The Sars Centre belongs to the University of Bergen and is partner of the European Molecular Biology Laboratory (EMBL) ([www.embl.de](http://www.embl.de)). The place of work will be at the Sars Centre. The starting date is negotiable but preferably no later than 01 September 2018.

About the project/work tasks: The goal of the Burkhardt group is to reconstruct the evolutionary origin of synapses and neurons. The group is particularly interested in studying synaptic protein homologs in choanoflagellates, sponges and ctenophores. We are looking for a highly self-motivated and enthusiastic PhD student with interests in evolutionary biology, neurobiology and cell biology. The project will focus on when the protein signalling complexes required for synaptic activity first evolved and how they functioned at a molecular level (Burkhardt et al, 2011 PNAS; Burkhardt et al, 2014 MBE; Bhattacharyya et al, 2016 eLife). The successful candidate will undertake research with the possibility to use a variety of techniques, ranging from super resolution immunofluorescence and electron microscopy, various biochemical methods to X-ray crystallography to study synaptic protein homologs in choanoflagellates. The successful candidate will work in close association

with the group leader and other lab members with the aim to eventually contribute to the further development of the project in line with her/his interests.

Qualifications and personal qualities: - The applicant must hold a master's degree or the equivalent or must have submitted his/her master's thesis for assessment prior to the application deadline. It is a condition of employment that the master's degree has been awarded - Routine experience in standard molecular and cellular biology techniques is required Practical experience in biochemical techniques (protein purification, Co-IPs) and with different fluorescence imaging techniques is highly desirable - Specific experience with choanoflagellates is beneficial, but not essential - The ability to work both independently and in a structured manner, cooperate with others and possess high motivation and enthusiasm is essential - Proficiency in both written and oral English

About the PhD: The duration of the PhD position is 4 years, of which 25 per cent of the time each year comprises required duties associated with research, teaching and dissemination of results. The employment period may be reduced if you have previously been employed in a recruitment position.

About the research training: As a PhD Candidate, you must participate in an approved educational programme for a PhD degree within a period of 4 years. A final plan for the implementation of the research training must be approved by the faculty within three months after you have commenced in the position. It is a condition that you satisfy the enrolment requirements for the PhD programme at the University of Bergen.

We can offer: - A professional, challenging and international working environment - Well-equipped, modern laboratories and facilities - Salary at pay grade 50 (Code 1017/Pay range 20, alternative 8) in the state salary scale. Currently equal to NOK 436.900. Further promotions are made according to qualifications and length of service in the position - Enrolment in the Norwegian Public Service Pension Fund (SPK) - A position in an inclusive workplace (IA enterprise) - Good welfare benefits

Your application in English must include: - A brief account of the applicant's research interests and motivation for applying for the position - The names and contact information for two reference persons. One of these must be the main advisor for the master's thesis or equivalent thesis - CV - Transcripts and diplomas showing completion of the bachelor's and master's degrees, or official confirmation that the master's thesis has been submitted - Relevant certificates/references - A list of any works of a scientific nature (publication

list)

The application and appendices with certified translations into English or a Scandinavian language must be uploaded at Jobbnorge.

Application Deadline: 02 May 2018.

General information: Detailed information about the position can be obtained by contacting: Group Leader Pawel Burkhardt, tlf.: +47 55 58 43 57, email: Pawel.Burkhardt@uib.no

The state labour force shall reflect the diversity of Norwegian society to the greatest extent possible. Age and gender balance among

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### SimonFraserU AvianEvolutionaryPhysiology

PhD/MSc positions. Fall 2018 or Spring 2019. Diet or exercise? How do birds cope with transitions in workload associated with parental care or fledging? I am looking for multiple MSc or PhD students to join my lab as part of my long-term NSERC-funded work on avian evolutionary physiology. We work within a strong life-history framework: several potential projects are available integrating behaviour and physiology of exercise or training during parental care and post-fledging activity to explain costs of reproduction and survival. This work will take advantage of an automated radio-tracking system we set up in 2015 for European starlings, and/or a training system for captive-breeding zebra finches. General requirements: Strong academic background (GPA >3.0 and >3.5 for PhD), a commitment to graduate school and basic research, and a genuine interest in integrating evolutionary biology with behaviour, and physiology. Experience with radio-telemetry, blood sampling, banding, GIS or physiological analysis an advantage but not essential. This work will be based at SFU with fieldwork in the Lower Mainland, BC.

For more information contact: Tony D. Williams, Dept. Biological Sciences, Simon Fraser University, Burnaby, V5A1S6, Canada, [tdwillia@sfu.ca](mailto:tdwillia@sfu.ca); Lab web page <https://tonydwilliamslab.weebly.com/> Dept. of Biological Sci-

ences Simon Fraser University 8888 University Drive Burnaby, BC Canada, V5A 1S6

Tony Williams <[tdwillia@sfu.ca](mailto:tdwillia@sfu.ca)>

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### SorbonneU Paris NovelMicrobialLineages

The 'Adaptation, Integration, Reticulation, Evolution' team at Sorbonne Universite, Paris, France is searching for the right candidate for either the following PhD topic—: Networks approaches to characterize novel microbial lineages and divergent defense/communication mechanisms from metagenomes of extreme environments. OR the following PhD topic—: Networks approaches to characterize divergent microbial lineages and novel genes encoding primary metabolisms from metagenomes of extreme environments. — There are good chances (circa 40%) that one of these grants will be funded, but the candidate will have to pass an audition in late May/early June to ensure this. — There will be in fact two separate auditions since each project (one focusing on communication mechanisms/ the other focusing on primary metabolisms) has been preselected in a separate instance.

Supervisors for this project will be Philippe Lopez and Eric Bapteste, and the first project will also be co-supervised by Yanyan Li (Museum National d'Histoire Naturelle, Paris, France). If interested, please send a mail to [philippe.lopez@upmc.fr](mailto:philippe.lopez@upmc.fr).

A brief summary of the first project can be found below—:

Our knowledge on the evolution of important gene families has so far largely relied on the comparative analysis of sequences from cultured microbial organisms, which represent a minor fraction of Life on Earth. However, the growing amount of molecular data from environmental samples or single cells is now providing important additional data to test whether genetic diversity in environmental sequences is significantly larger than genetic diversity in the gene families of cultured organisms. This project aims at finding very divergent homologs of proteins of interest (see below) in environmental data.

The Lopez/Bapteste lab owns unique metagenomic datasets from under-explored extreme environments (Dallol, Lake Tirez, Lost Hammer), as well as the corresponding samples collected and stored. This lab also masters sequence similarity network methods, that allow



to analyze metagenomic and genomic data and to investigate highly divergent gene forms and relationships of distant homology. These graphs allow for mathematical analyses of genetic diversity over dozens of millions of sequences, providing a powerful framework to address the evolution of divergent genes and genomes.

The Li/Bourguet-Kondracki lab is specialized in the functional studies of molecular mechanisms involved in the microbial communication, defense and adaptation to the environment, using multi-disciplinary approaches (biochemistry, microbiology). This team will provide expertise in guiding the selection of genes involved in microbial communication and defense to study and will provide experimental validation of newly-identified gene families identified by bioinformatics.

This project, at the interface of bioinformatics, evolutionary microbiology/ecology and biochemistry will mine publicly available and original environmental datasets to:

- identify new forms of microbial defense and communications genes, e.g.— those involved in quorum sensing, two-component systems as well as antibiotic production and resistance genes.
- identify new lineages hosting these genes, with a particular focus on microbes belonging to still undetected deep-branching microbial lineages—
- sequence these new lineages through design of original primers and single cell genomic studies.—

Philippe Lopez <philippe.lopez@upmc.fr>

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## SoutherIllinoisU EvolutionPoisonFrogs

Evolution of South American Poison frogs (genera *Ameerega* and *Ranitomeya*) Zoology Department, Southern Illinois University Carbondale, Carbondale, IL.

A graduate position (prefeed PhD, also considering master's students) is available to study the evolution of S. American poison dart frogs. Neotropical poison frogs are a species-rich family (Dendrobatidae) that exhibit a diversity of mating systems, parental care strategies and phenotypes. The Brown lab is looking for a student to develop a research program studying ANY core aspect of the lab's research. The ideal student will be prepared to conduct field-based research, have some experience in molecular ecology/population genetics, genomic and/or

geospatial analyses. This position includes several trips to South America and fully funded lab work.

As follows are a few key projects that could be your graduate research:

1. Speciation, species boundaries and hybridization in the *Ameerega bassleri* complex: insights from natural history, acoustic and morphological data, geospatial data, sub-genomic and paleoclimatology. This group is a highly diverse group of three species with dramatic phenotypic variation across its range. It also has experienced several historical hybridization events among the taxa that have muddled and complicated their evolutionary histories. This research will be aimed to understand factor driving and maintaining speciation in natural situations.

1. Phylogeography and spatial biodiversity patterns of the poison frog genus *Ranitomeya*: insights from sub-genomic data, geospatial analysis and phylogenetics. The thumbnail poison frogs are some of the most amazing species on earth— half the taxa are involved in Mullerian mimicry, they exhibit intensive parental, and they often display incredible phenotypic variation among populations... This group in an endless fountain of evolutionary questions.

1. The genetic consequences of future climate change: spatially explicit predictions of within-species genetic diversity using climatic, demographic, and genetic data. This research will expand upon a lab methodology that accounts for climatic, geographic, and biological complexity. This framework is promising for understanding evolutionary consequences of climate change and guiding conservation planning.

For more information on the Brown Lab please visit the lab website at: <http://www.jasonleebrown.org> and the Zoology Department at SIUC <http://www.zoology.siu.edu>. Students will find all the brains of a nationally ranked research university and all the heart of a small college at SIUC.

Carbondale is located in southern Illinois and provides a close link to many forested areas and lakes. The regional landscapes varies from bottomlands to uplands with rolling hills, bluffs, and rugged topography. This makes it perfect home for outdoor lovers (when they are not in the rainforest of S. America).

Interested students are encouraged to contact Dr. Brown ([jason.brown@siu.edu](mailto:jason.brown@siu.edu)) ASAP. Please include a brief description of your research interests related the Brown Lab, a CV, and names of two references (with contact info). Competitive funding options are available. US and Canadian students only. For full consideration, application due date is May 15th 2018. Start date of

position is August 2018 (preferred) or January 2019.

Jason Brown <jason.brown@siu.edu>

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## StockholmU Biodiversity

Dear colleagues,

We are looking for a highly motivated PhD-student to join our new interdisciplinary project on The relationship between climate, biodiversity, disease and coffee yield in Southwestern Ethiopia.

For more information see the project description (below) and the following link:

<https://www.su.se/english/about/working-at-su/> and don't hesitate to contact me directly by email, (closing date is 25 May 2018)

My best,

Ayco Tack & Kristoffer Hylander

ayco.tack@su.se

Project description

The Department of Ecology, Environment and Plant Sciences invites applications for a four-year PhD position as part of a project on The relationship between climate, disease and coffee yield: Optimizing management for smallholder farmers.

High-profile studies have warned for the threat of climate change and fungal disease on world coffee production at a global scale. However, few studies have targeted the opportunities and challenges of smallholder coffee farmers to face such changes. For this we need detailed insights on the link between climate, disease and yield, and how the farmers can improve their livelihood by optimal management. This project focuses on the link between climate, diseases, management and the livelihood of smallholder farmers in southwestern Ethiopia. Within the study area, coffee is grown in the shade of natural trees, and the farmer therefore has the unique opportunity to influence the link between the macroclimate and the microclimate by managing the shade cover.

The overarching aim of the PhD project is to understand the relationship between management, macro- and microclimate, disease levels, and yield, and use these insights to optimize management decisions by smallholder farmers. The project is strongly interdisciplinary, including climate modelling, farmer interviews, field sur-

veys and field experiments. More specifically, we aim to: i) use dataloggers to model the spatial and temporal variation in the macro- and microclimate, and explore future climate scenarios under different carbon-emission levels, ii) use field surveys to link climatic variation and management to disease levels and coffee yield, iii) conduct a questionnaire to understand the decision-making process by the farmer, which may be influenced by observations of past and present yield, disease levels, the macro- and microclimate and perceived ecosystem services, and iv) use a manipulative field experiment using shading and irrigation to validate the effectiveness of adaptive management.

Ayco Tack Assistant professor Department of Ecology, Environment and Plant Sciences

Stockholm University SE-106 91 Stockholm, Sweden Visiting address: Svante Arrhenius Väg 20A, room N420 Phone: + 46-(0)8-163959 Mobile: + 46-(0)70-4942557 ayco.tack@su.se

[www.plantmicrobeinsect.com](http://www.plantmicrobeinsect.com) [www.su.se/profiles/atack](http://www.su.se/profiles/atack)  
Ayco Tack <ayco.tack@gmail.com>

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## Tahiti OysterGenomicSelection

Graduate position: PhD - Exploration of the potential of genomic selection in the black-lip pearl oyster, *Pinctada margaritifera*

WHERE: Centre Ifremer du pacifique, BP 49, 98719 Taravao, Tahiti, Polynésie Française.

WHAT: Graduate Position (PhD)

Scientific context: Within French Polynesia, the aquaculture of the silver-lip pearl oyster, *Pinctada margaritifera*, is dedicated to the production of the highly valued Tahitian pearl. The culture of these Tahitian pearls represents the second most valuable economic resource for French Polynesia after tourism. Today, there are 536 producers in 26 islands and atolls covering a total operating sea area of 7800 hectares. The production of cultured pearls is carried out through a transplant involving two genomes: one from a donor oyster, and one from a recipient oyster. During this process, the donor oyster is sacrificed for a portion of its mantle tissue. This piece of mantle tissue is then inserted into the gonads of a recipient oyster along with a spherical nucleus. The cells from the grafted tissue then form a mineralizing pearl sac in which after 15 to 22 months of culture, a pearl will be produced through the deposition

of successive layers of aragonite around the nucleus. At harvest, the quality of the pearl is defined by a range of characters including: 1) its weight / diameter, 2) its surface defects (number of blemishes and imperfections), 3) its luster (dull or highly lustrous), 4) its commercial grading (A, B, C, D or reject), 5) its color components (hue, saturation and darkness), and 6) its shape. The quality of a pearl is conditioned by a very complex set of intrinsic (genetic) and extrinsic (environmental) factors. Recent studies have confirmed the roles played by the donor oysters graft in determining the color of the pearls, as well as the effect the recipient oyster has on pearl size (Blay et al., 2017, Ky et al., 2017). Genomic selection for *P. margaritifera* in French Polynesia is still in its infancy. The general ease of accessing the abundant wild mother-of-pearl resources in the Polynesian lagoons (Lemer et al., 2011, Lemer and Planes, 2012) has indirectly hindered the development of hatcheries which are an integral part of developing a genetic selection program. However, pearling is having an environmental impact by reducing the abundance of this natural resource. This coupled with the overproduction of pearls and the subsequent reduction in their quality, has raised awareness of the need for sustainable management of pearl production. Furthermore, the identification and analysis of the expression of biomineralization genes associated with the growth and quality of the pearls produced (Joubert et al., 2010; Joubert, 2011), provides a panel of target genes that may influence the quality of pearls. These molecular tools can offer indications of adaptive processes involved in biotic and abiotic interactions and their impact on the industry (Joubert et al., 2014). Although these standard “candidate gene” approaches have shown a genetic basis leading to the formation of the pearl, they have not been able to provide an answer from the point of view of the selection of lines and the potential “trade off” associated with them. With genome assembly and ongoing transcriptome analyzes in progress, the thesis project aims to provide practical and theoretical tools for the genomic selection of the black-lip pearl oyster. This will be conducted in partnership with SCA Regahiga (Gambier archipelago), the first French Polynesian pearling company with a hatchery, DRMM and CRIOBE (CNRS / EPHE). More specifically, the objectives of the thesis are: 1. To estimate the level of inter- and intra-family genetic differentiation using SNPs markers (the SNPs panel will be developed as part of the AmeliGEN project). Automated batch genotyping will allow the optimization of crosses to maintain the genetic diversity and identify families. 2. To lay the foundations necessary for the establishment of a genetic selection program for the black-lip pearl oyster within an operational hatchery. This will be done through the comparative

analysis of grafts made from individuals originating from natural populations (wild S), first (G1), or second (G2) generations. These comparisons will make it possible to estimate the potential for genetic progress and to evaluate the non-genetic components involved in the transmission of the “pearl” phenotype. This component will also assess the importance of genotype-environment interactions. 3. To identify and study the expression of the key biomineralization genes involved in the growth potential of pearl oysters and their associated pearl phenotype. This will be conducted through the transcriptome analysis (RNA-Seq) of experimental batches of pearl oysters.

The originality and innovative nature of the research:

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## TempleU Bioinformatics

A new PhD program in Bioinformatics is accepting applicants for Fall 2018. <http://phdbioinform.cst.temple.edu/> Accepting applications until May 1, 2018.

Jody Hey [hey@temple.edu](mailto:hey@temple.edu) Director, Center for Computational Genetics and Genomics <https://ccgg.temple.edu> Professor, Department of Biology <https://bio.cst.temple.edu/~hey> Department of Biology (rm 206) Temple University 1900 N. 12th Street Philadelphia, PA 19122

Jody hey <[tuf29449@temple.edu](mailto:tuf29449@temple.edu)>

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## UBern EvolutionaryGenomics

PhD position in Ecological Genomics

Motivated students of plant evolution are invited to apply for a PhD position within our projects on the ecological genomics of duplicated genes.

Responsibilities This research will extend our understanding of plant adaptation and speciation across natu-

ral landscapes. It will contribute to answering fundamental questions in evolutionary biology such as: What are the main molecular drivers of genome evolution? How do ecological constraints shape genomes? What is the significance of whole-genome duplication for biodiversity? The PhD project will experimentally address the phenotypic and transcriptional plasticity in populations of Buckler Mustard from different environments. In particular, the candidate will generate high-throughput sequence data from experimental populations of diploid and polyploid lineages and assess the impact of duplicated genes along with environmental changes on adaptation to contrasted ecological niches. In collaboration with a postdoc focused on the molecular underpinnings of genome dynamics, the candidate will disentangle the contributions of genomic and environmental factors in driving radiation in the Alps.

**Requirements** The project necessitates to proactively deal with multiple tasks going from field work to in silico analyses. The ideal candidate will thus be well organized and creative, collaborative and used to handle large datasets towards integrated results. A solid background in evolutionary genomics and practice in computational biology represent strong assets. Experience with field work and molecular routines such as nucleic acid extraction and RT-qPCR is a plus. Excellent presentation in (written and oral) English is crucial. A master degree in a relevant field and a valid (international) driver's license is required.

**Further information** We offer a stimulating environment within an international research community benefitting from excellent infrastructure at the Institute of Plant Sciences, University of Bern. The working language is English. Most of the candidate's time will be dedicated to research, with ample opportunities for training within and beyond various doctoral programs. There is additionally the possibility of supervising undergraduate students. This position is funded by the Swiss National Science Foundation for a maximum of four years. The anticipated starting date is July 2018 (or soon thereafter). Please, send your application as a single pdf to Prof. Christian Parisod ([christian.parisod@ips.unibe.ch](mailto:christian.parisod@ips.unibe.ch)). It must include: (i) a letter describing your past research experience and explaining your particular skills and motivation for this position, (ii) an abstract of your master thesis, (iii) a current CV (with publications; if any), and (iv) contact details of two referees. Applications should be submitted before May 31st 2018, but will be considered until the position is filled.

Christian Parisod Institute of Plant Sciences - University of Bern Altenbergrain 21 - 3013 Bern - Switzerland Phone : +41 (0)31 631 4949 e-mail : [christian.parisod@ips.unibe.ch](mailto:christian.parisod@ips.unibe.ch) <http://www.ips.unibe.ch/>

[research/ecogen](http://research/ecogen) [christian.parisod@ips.unibe.ch](mailto:christian.parisod@ips.unibe.ch)

## UBielefeldGermany FunctGenomics- BirdSpermCompetition

PhD position in Evolutionary Ecology and Functional Genomics

A PhD position in evolutionary ecology and functional genomics is available at the Faculty of Biology at Bielefeld University in the Evolutionary Biology group (with PD Dr Tim Schmoll, see [http://www.uni-bielefeld.de/\(en\)/biologie/Evolutionsbiologie](http://www.uni-bielefeld.de/(en)/biologie/Evolutionsbiologie) in collaboration with the Department of Animal Behaviour (with Dr Peter Korsten, see <http://www.unibielefeld.de/biologie/-animalbehaviour>). The position is available immediately for 36 months and is funded by the German Research Foundation (DFG) within the recently approved collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

The goal of this project (project B04 of the collaborative research centre) is to test how male Zebra Finches conform to their social niche as set by the prevailing level of sperm competition. This will allow us to understand how individual variation in sexual competition generates individual variation, and covariation, in both competitive traits and parenting behaviour. The successful candidate will closely work together with another PhD student to (i) quantify male social niche conformance by analysing adjustment of sexual competitiveness including behavioural (e.g. aggression) and ejaculate (e.g. sperm motility) traits; (ii) identify the underlying mechanisms of social niche conformance on the hormonal (via endocrinological profiling) and the gene expression (via RNAseq) levels; (iii) assess the adaptive significance of niche conformance under a niche match/mismatch paradigm; and (iv) test for trade-offs between investment in sexual competitiveness versus paternal care. A sub-project A will primarily focus on male social niche conformance through adjustment of behavioural traits and the hormonal mechanisms underlying niche conformance. A sub-project B will primarily focus on male social niche conformance through adjustment of ejaculate traits and the gene expression underlying niche conformance. Note that the position offered here is exclusively for sub-project B.

The collaborative research centre: The position will be



embedded within a larger collaborative research centre (SFB) comprising 18 principle investigators, 8 postdocs and 16 PhD students based at Bielefeld University, the University of Münster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programmes. Full details of the SFB can be found at [www.uni-bielefeld.de/biologie/crc212](http://www.uni-bielefeld.de/biologie/crc212). Main responsibilities Research tasks (90%): - Designing and conducting laboratory experiments in which zebra finch males are exposed to different levels of sperm competition - Maintaining a zebra finch stock population and breeding of experimental birds - Processing of tissue samples for transcriptomic analyses - Bioinformatic processing of high-throughput sequencing data to quantify gene expression - Assisting in setting up a computer-assisted sperm analysis (CASA) system - Phenotyping sperm samples using CASA and other methods - Assisting in taking behavioural recordings - Statistical analyses of experimental data - Collaborating with other research groups in the collaborative research centre - Writing scientific publications for international peer-reviewed journals

Organizational tasks in the research groups and collaborative research centre (10%)

Applicants' profiles We are seeking a bright, highly motivated and creative student with - a university degree in a relevant discipline with specializations in one or more of the following fields: bioinformatics, transcriptomics/genomics, animal behaviour, behavioural ecology, behavioural physiology, evolutionary ecology, and/or veterinary science, - a keen interest in using molecular genetic methods to answer behavioural and life history questions, - experience with bioinformatic processing of high-throughput sequencing data or a keen interest in acquiring relevant skills, - experience with statistical analysis (preferably using R), - ability to work both independently and as part of a team, and - excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage: - publications in peer-reviewed international journals, - experience with sperm phenotyping including CASA - experience with large-scale research projects.

Remuneration

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## UCalgary VertebrateEvolutionaryBiol

The Rolian lab at the University of Calgary is seeking highly motivated graduate students (MSc or PhD) with an interest in skeletal evolution in mammals, to start as soon as possible. The core of the Rolian Lab's research program is an artificial selection experiment targeting increases in limb bone length in mice. This unique resource, known as Longshanks, was developed to study skeletal evolution in 'real time', from genomics to development to phenotypic coevolution and whole organism performance. Students will be able to develop specific projects in accordance with their own interests, and with the long-term goals of the Rolian lab. Individuals with a background and interest in vertebrate evolutionary biology, developmental biology and/or biomechanics are particularly encouraged to apply.

The University of Calgary is one of Canada's leading research-intensive universities, with diverse faculty working on evolutionary, developmental and skeletal biology. Funding is available through the lab and through teaching assistantships, although it is expected that students will also apply for competitive external and internal grants (e.g. NSERC). Calgary is a world-class city near the Canadian Rockies, with excellent amenities and year-round opportunities for recreation and culture.

More information on the Rolian lab can be obtained at: <http://www.rolianlab.com>, where links to our most recent projects on Longshanks can also be found under Publications. Information on admission requirements to pursue graduate studies at the U of C can be obtained at: <http://www.ucalgary.ca/future-students/graduate-apply> Interested candidates should email Dr. Campbell Rolian ([cprolian@ucalgary.ca](mailto:cprolian@ucalgary.ca)) by May 20<sup>th</sup> 2018, with a brief description of their research interests, background preparation and current studies/work. Please note that the deadline for admissions varies by program, with the earliest possible start date of Fall 2018.

Campbell Rolian <[cprolian@ucalgary.ca](mailto:cprolian@ucalgary.ca)>

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## UCalgary Wildlife Evolutionary Genetics

Graduate student positions (M.Sc./Ph.D.) in wildlife evolutionary genetics and ecology. Faculty of Veterinary Medicine, University of Calgary.

I am seeking highly motivated graduate students with interests in wildlife biology, quantitative genetics, genomics, and/or evolutionary ecology of host-parasite interactions to join my group at the University of Calgary.

The main research focus in my lab (<https://sites.google.com/site/jocelynpoisant/home>) is to understand the causes and consequences of contemporary adaptive evolution in free-living vertebrates, with a particular interest in health-related phenotypes and multivariate genetic constraints. Current opportunities include studying various trait/topics including complex gastro-intestinal parasitic nematode infections (the 'nemabiome'), coat color, and risk aversion, mating success, adaptive evolution, stress physiology, pedigree-free (genomics) quantitative genetics, and genomic signatures of selection using the Sable Island horse long-term population study as a model system. There are also similar opportunities in other study systems.

Ideal candidates will have demonstrated skills or interest in at least some of the following: molecular ecology, quantitative genetics, population genomics, parentage analyses, long-term individual-based studies of free-living animals, evolutionary ecology, community ecology, multivariate statistics, DNA metabarcoding, or bioinformatics.

Students will be based at the Faculty of Veterinary Medicine at the University of Calgary where they will benefit from interactions with a large community of researchers focussing on host-parasite interactions, animal health, and bioinformatics, as well as close collaborations with the University of Saskatchewan (Philip McLoughlin) and the University of Exeter (Alastair Wilson).

Students should enjoy curiosity-driven research, working in teams, and generally be comfortable contributing to physically demanding field work. Financial support is available for 2 years for MSc and 4 years for PhD (minimum of \$CA22,000/year). While all qualified candidates will be considered, priority will be given to Canadians who are competitive for external awards (e.g. NSERC).

Start date is flexible, but would ideally be between September 2018 and September 2019.

Information about applying for graduate studies in the Faculty of Veterinary Medicine at the University of Calgary is available at <http://www.vet.ucalgary.ca/graduate-postgraduate/future-graduate-students>. Interested students should send a brief email outlining research interests, along with a CV and unofficial transcripts to [jocelyn.poisant@ucalgary.ca](mailto:jocelyn.poisant@ucalgary.ca).

Jocelyn Poissant Assistant Professor Dept. of Ecosystem and Public Health, Faculty of Veterinary Medicine University of Calgary, Calgary, AB Office: TRW 2D24

Web: <https://sites.google.com/site/jocelynpoisant/>  
Twitter: @jocelynpoisant @SI\_Horses

[Jocelyn.Poisant@ucalgary.ca](mailto:Jocelyn.Poisant@ucalgary.ca)

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## UCapeTown Evolutionary Cost Breeding

Taking the heat: how do parent birds mitigate costs of breeding at high temperatures?

MSc/PhD research at the FitzPatrick Institute of African Ornithology, Department of Biological Sciences, University of Cape Town

We invite applications for the above full-time research scholarship at the FitzPatrick Institute, a world-renowned, national Centre of Excellence (CoE) in ornithological research with a strong emphasis on post-graduate studies. The successful applicant will focus on understanding whether & how Fork-tailed Drongos *Dicrurus adsimilis* balance trade-offs between parental care and thermoregulation in order to maintain reproductive output in the face of harsh thermal conditions in the Kalahari Desert. The candidate will be supported and supervised by Dr Susie Cunningham and Dr Tom Flower, and will work under the aegis of the Hot Birds Research Project and the Fork-tailed Drongo Project.

Fork-tailed Drongos are pair-breeding passerines that nest during the hottest time of year in the Kalahari Desert, when air temperatures regularly approach or exceed 40°C. Preliminary data suggest adult drongos struggle to balance thermoregulatory, foraging and parental demands at high air temperatures; yet nestlings maintain growth rates even on hot days, suggesting parents may somehow buffer them from these costs. Major lines of investigation for this study include: how adults



alter provisioning behaviour with temperature; whether they can compensate for reduced provisioning during hot periods; how they regulate their own and offspring's body temperature; whether costs to offspring manifest in ways other than reduced mass gain. The project sits at the intersection of the fields of behavioural ecology and ecophysiology, drawing on behavioural ecology theory (including central place foraging theory and the economics of balancing energy and water budgets); and principles of thermal biology. The drongo population at the study site (Kuruman River Reserve) is fully habituated, facilitating an experimental approach. The project is offered as an MSc with scope to be upgraded to a PhD depending on the interests and progress of the successful candidate. Under exceptional circumstances, we will also consider applications from candidates already holding an MSc who would like to undertake the project as a PhD.

Candidates should have an appropriate BSc Honours/MSc degree with excellent records. Field experience involving data collection is essential as the candidate will be required to often organize and conduct field work independently. As drongos nest high in camelthorn trees it is important to have a good head for heights. Experience in statistical data analysis and writing skills would be favoured to ensure an efficient start. The successful candidate will form part of an established and supportive research team.

The value of the scholarship is R95 000/R125 000 per year for up to two years for MSc/for up to three years for PhD. Renewal each year will be contingent on satisfactory academic progress. Adequate project running costs are available.

To apply, please send a CV (including your academic record & names and contact details of two referees) and a short motivation letter to Hilary Buchanan at [hilary.buchanan@uct.ac.za](mailto:hilary.buchanan@uct.ac.za) (subject 'Your surname' [project name] MSc/PhD). Informal enquires can be directed to Dr Susie Cunningham: [susie.j.c@gmail.com](mailto:susie.j.c@gmail.com) or Dr Tom Flower [tompflower@gmail.com](mailto:tompflower@gmail.com).

For more information on the FitzPatrick Institute visit [www.fitzpatrick.uct.ac.za](http://www.fitzpatrick.uct.ac.za). For more information on the Hot Birds Research Project visit <https://hbresearchproject.wixsite.com/hbresearchproject> and [www.facebook.com/hotbirdsresearchproject/](https://www.facebook.com/hotbirdsresearchproject/) Closing date: 6 May 2018 (possible interviews to be held in mid-May)

Thomas Flower <[tflower@sfu.ca](mailto:tflower@sfu.ca)>

## UEdinburgh Evolutionary Genetics

Funded PhD studentship in Evolutionary Genetics  
"Causes and consequences of mutational variation in the mammalian genome"

Supervisors Prof Peter Keightley and Dr Konrad Lohse, University of Edinburgh, UK.

Spontaneous mutations are the ultimate source of genetic variation and are therefore central in evolutionary genetics. For example, spontaneous mutation is fundamental for understanding the genetic basis of quantitative variation, the threat posed by declining population size in conservation biology and the distribution of nucleotide variation in the genome. We are recruiting a PhD student to join our team attempting to address these and other unanswered questions. We work extensively on the house mouse as a model system, but our research is not restricted to this species.

The PhD will be part of an ERC Advanced Grant entitled "An integrated approach to understanding the impact of de novo mutations on the mammalian genome", a key component of which is to carry out the first large-scale mutation accumulation (MA) experiment in a mammalian species (the house mouse). Such an experiment consists of maintaining independent MA lines, bred by full-sib mating, for many generations in the near-absence of selection. Different lines will accumulate different mutations and diverge at the molecular and phenotypic levels. The PhD project is expected to be within some or all of the areas described below. However, the project is flexible and can be tailored to the interest of the applicant.— Applicants are strongly encouraged to contact the supervisors ahead of application to discuss the project.— 1. The nature of variation from new mutation (a) Theoretically, inbred lines should harbour little genetic variation. At mutation-drift balance, expected nucleotide variation is the product of the mutation rate per base pair and the effective population size ( $N_e = 4$  for full-sib mating). There are, however, several factors which could lead to inbred lines harbouring more variation than expected.— We will test this by quantifying nucleotide variation in the inbred MA line progenitors by deep genome sequencing and bioinformatic analysis.

(b) The extent and nature of variation in the mutation rate have been little studied. We will address these questions by large-scale deep sequencing and bioinformatic

analysis of house mouse MA lines of different strains and potentially families of wild house mice.

(c) The relationship between nucleotide and phenotypic variation arising from mutation are largely unknown. Phenotypic divergence between MA lines quantifies the new mutational variation. We will relate the accumulation of phenotypic differences among lines to differences in the accumulation of mutations in different genomic site classes.

2. Understanding variation in diversity across the genome.

Genetic diversity varies across the genome, but the causes of this variation are poorly understood. It is clear that variation in diversity is caused by interactions between mutation, natural selection, recombination and genetic drift. We will explore avenues of research that might help tease apart these factors. (a) Are patterns of diversity across the genome consistent between different species with different population sizes? It will be especially relevant to determine how diversity relates to the rate of recombination and the local density of functional genomic elements. (b) Are there signals in genomic polymorphism data, for example in the joint frequency distribution of linked sites that can differentiate between different forms of selection? We will explore how new analytic results under coalescent approximations to selection can help to better quantify genome-wide selection.

Further Information —

The project is funded by a grant from the European Research Council (ERC) over 5 years, and there is a substantial budget for staff, genome sequencing, consumables and travel to conferences.— Our ERC project is a collaborative effort with Prof Diethard Tautz, Max Planck Institute for Biology, Plön, Germany, where the MA lines are being bred.

There will be several training opportunities, including attendance of bioinformatics courses and courses in population and quantitative genetics and statistics run as part of the Institute of Evolutionary Biology's MSc in Quantitative Genetics and Genome Analysis.

Prospective applicants are encouraged to contact Peter Keightley <peter.keightley@ed.ac.uk> to discuss the project in the first instance. Formal applications to be made via <http://www.ed.ac.uk/biology/prospective-students/postgraduate/pgp/how-to-apply> by 21 May 2018.

– The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

“peter.keightley@ed.ac.uk” <peter.keightley@ed.ac.uk>

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## UGroningen Experimental Evolution Microbes

PhD position: Experimental Ecology and Evolution of Microbial Infectious Ecosystems

Organisation Founded in 1614, the University of Groningen enjoys an international reputation as a dynamic and innovative centre of higher education offering high-quality teaching and research. Flexible study programmes and academic career opportunities in a wide variety of disciplines encourage the 30,000 students and researchers alike to develop their own individual talents. As one of the best research universities in Europe, the University of Groningen has joined forces with other top universities and networks worldwide to become a truly global centre of knowledge. The Groningen Institute for Evolutionary Life Sciences (GELIFES) GELIFES, the largest institute of the Faculty of Science and Engineering (FSE) fills a special niche in the life sciences by covering and integrating mechanistic, evolutionary and ecological approaches, aiming to understand adaptation on all levels of biological organisation. Researchers pursue fundamental questions while collaborating with partners from nature conservation, industry, medicine and other realms of society. Our research fields include ecology, conservation biology, evolutionary biology, behavioural biology, chronobiology, genetics and genomics, neurobiology, physiology and theoretical modelling, using a wide array of research tools. Research levels range from molecular and organismal to populations and ecosystems, performed under laboratory, semi-natural and field conditions. Job description We are looking for a talented and enthusiastic quantitative microbiologist for a fully funded 4-year PhD position. The PhD candidate for this project will be working at the Microbial Population Biology group in Groningen. PhD candidates will receive excellent training through cutting-edge research projects, advanced courses and training opportunities, complemented by workshops on generic research, transferable skills and teaching. As a PhD candidate, you are committed to conduct independent and original scientific research, to report on this research in international publications and presentations, and to present the results of the research in a PhD dissertation, to be completed within 4 years. Project summary Polymicrobial infections can be viewed as ecosystems in which the community members interact. It is an open question how ecological interactions

affect the evolution of the community members. In this project we will address the role of these interactions on the evolution of the community members, and the development of antibiotic resistance. In the project we will use polymicrobial urinary tract infections as a model system to study these eco-evolutionary interactions by means of experimental ecology and evolution. The work will consist of a combination of microbial growth experiments, molecular biology and biochemistry, sequencing and bioinformatics, data analysis and modeling. Qualifications Specific requirements: MSc with specialization in microbiology, ecology or evolution, quantitative biology, skills in data management and analysis, statistics and programming. In addition to specific qualifications outlined above, the candidate has a good command of English (oral and written), is enthusiastic and a team-worker, has a passion for science, is highly motivated to work within the field of microbial ecology and evolution at the interface with medicine, possess excellent communication skills and the ability to write scientific papers and deliver presentations.

Conditions of employment The University of Groningen offers a salary of euro 2,222 gross per month in the first year to a maximum of euro 2,840 gross per month in the final year (salary scale Dutch Universities), based on a full-time position (1.0 FTE) excluding a 8% holiday allowance and a 8.3% end of the year bonus. The position offered is for four years. Each successful candidate will first be offered a temporary position of one year with the option of renewal for another three years. Prolongation of the contract is contingent on sufficient progress in the first year to indicate that a successful completion of the PhD thesis within the contract period is to be expected. A PhD training programme is part of the agreement and the successful candidate will be enrolled in the Graduate School of the Faculty. The conditions of employment are available at the University of Groningen website under Human Resources: <https://www.rug.nl/about-us/work-with-us/> Supervisor Dr Marjon de Vos The preferred starting date is 1 December 2018. Application You may apply for this position until 20 May 23.59h / before 21 May 2018 Dutch local time, by means of the application form (click on "Apply" on the advertisement on below mentioned university website). Interviews are scheduled to take place on 5 June 2018 in Groningen.

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## UHighlandsIslands UK EnvironmentalMetabarcoding

A fully funded 3.5 year PhD studentship is available with the Rivers and Lochs Institute (RLI) and the Scottish Association for Marine Science (SAMS) at the University of the Highlands and Islands.

### Project description

The farming of fish is expanding rapidly in order to meet the ever increasing demand for food by a rapidly growing human population. The FAO estimates that the world population will grow from 7.5 billion to 9.7 billion by 2050 and currently aquaculture supplies more than 50% of all fish for human consumption. Salmon farming is a massive industry with major production centres in Norway, Chile, UK and Canada. In Scotland, it constitutes the largest food-based export market, worth pounds 500 million per year and this is set to double by 2030. Salmon farming operations must demonstrate, to the Scottish Environmental Protection Agency (SEPA), compliance with environmental standards around their operations. Currently, environmental monitoring is expensive and time-consuming and not conducive to optimising a site's potential. Whilst most Scottish salmon aquaculture is marine-based, a significant proportion occurs in freshwater lochs where the impacts are poorly understood. There is not a common approach to monitoring across the two aquatic environments.

Salmon farming impacts the seabed below and around the farm where farm-derived organic waste accumulates. The current method of assessing impact is by interpreting patterns in the spatial distribution of benthic assemblages of organisms using traditional morphology-based identification. This is expensive, time consuming and relies on a dwindling number of taxonomic experts. Often by the time the assessment is complete, fish in the cages have been harvested, resulting in an inability to implement immediate change in response to any environmental impact. This morphology-based approach is implemented for marine fish cages, with no equivalent assessment for freshwater aquaculture that occurs in Scotland. Similar monitoring in freshwater could help the industry by demonstrating environmental stewardship across both habitat types, realise production potential, maintain environmental standards, and reduce the costs for regulatory compliance, thereby allowing

the industry to grow responsibly.

Recent innovations mean that it is possible to assess entire biological assemblages by extracting DNA from environmental samples (e.g. from sediments) and identifying the source organisms, using high-throughput next generation DNA sequencing in an approach referred to DNA metabarcoding. Metabarcoding can complement and potentially overcome limitations of morphologically-based methods by targeting different species, sampling greater diversity and increasing taxonomic resolution. The use of DNA metabarcoding is rapidly expanding, however questions still remain on the spatial and temporal scales of inference compared to other methods in addition to issues around data interpretation.

This studentship will extend an ongoing UHI-industry-SEPA project by developing and comparing the use of this technology at both marine and freshwater farming operations by addressing the following questions: (i) what is the influence of fish farms on the taxonomic diversity of marine and freshwater benthic assemblages? (ii) which (if any) organisms can be used as indicators of environmental impact and (iii) how does the biological assemblage change over the farm production cycle and how can this be used to predict regulatory compliance?

#### Location and Supervisory Team

The student will be based in the Rivers and Lochs Institute at the new Inverness Campus as part of a team of researchers focusing on aquatic biodiversity, conservation and management with Dr Mark Coulson (Rivers and Lochs Institute, Inverness College UHI) as Director of Studies. Dr. Coulson has 15 years of experience in molecular ecology and applied population genetics, fisheries management and environmental DNA (eDNA). He helped to establish a state-of-the-art molecular genomics facility encompassing NextGen sequencing systems, qPCR, and other high throughput DNA fragment analysis instrumentation.

The PhD will be co-supervised by Tom Wilding (SAMS, Nr Oban, Scotland). Dr Wilding has 20 years of impact monitoring, experimental design and statistical modelling experience. Dr Wilding will provide 'aquaculture-industry' context to the project, provide guidance on experimental design, sampling methodology, bioinformatics and statistical modelling. The student will have opportunities to join boat-based marine sampling conducted by SAMS. A third supervisor from SEPA will also be appointed to provide regulatory context to the PhD.

This PhD offers the successful candidate the opportunity to join a team of experienced, dynamic researchers that are developing revolutionary methodolo-

gies for ecosystem-monitoring applicable to any environment. The student will gain experience in field-sampling, laboratory-based

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## ULausanne 2 MicrobialEvolution

PhD position in microbiota research/microbial genomics/evolution

Starting date: flexible

Length of contract: 1 year, renewable, maximum 4 years.

Work percentage: 100%

Workplace: Department of Fundamental Microbiology, University of Lausanne, Switzerland

Qualification:

MSc. PhD position applicants should have a Master thesis in microbial genomics, bioinformatics, or microbiology. Prior research experience in large-scale sequence data analysis or microbiology wet-lab experimentation would be desirable. A good command of the English language, a high personal motivation to excel in science and a curious mind are required. We offer a stimulating environment in a young international research group combining computational (i.e. microbial genomics) and experimental approaches to study microbial symbiosis. The focus of the project can be adapted to the interests of the applicant.

Work description:

We are looking for an outstanding and highly motivated candidate to join our research group to work on the bee gut microbiota. The scope of the project is to understand how gut communities are structured in terms of functional and genetic diversity. Which processes govern community assembly and resilience? How do gut communities evolve and adapt to changing environments? The doctoral student will address this question using computational (metagenomics, transcriptomics, metabolomics) and/or an experimental approaches, depending on the interests and skill set of the applicant.

We are part of the Department of Fundamental Microbiology, a highly collaborative, multidisciplinary, and



team-oriented scientific environment. Our group consists of a good mix of bioinformaticians and wet-lab biologists from all over the world, funded through the University of Lausanne, the Swiss National Science Foundation and the European Union (ERC-STG, Marie Skłodowska-Curie Actions). We are equipped with state-of-the-art infrastructures enabling cutting-edge research with access to many core facilities located on campus (microscopy, proteomics, sequencing facilities). We have strong ties to other Departments within the University, such as the Department of Ecology and Evolution, and also actively collaborate with other research teams within and outside of Switzerland. Last but not least, our Department is situated on a beautiful campus at the shore of Lake Geneva with a great view of the Alps and with plenty of opportunities for outdoor activities.

For recent publications from the lab, please visit the lab webpage at <http://wp.unil.ch/engellab>. At least 80% of the working time will be dedicated to personal research. The remaining of the working time may be dedicated to teaching (organization and supervision of student practicals).

How to apply:

Please submit your full application including motivation letter, CV, list of publications (if available), copy of the Master thesis (if available) and the names and addresses of two referees via the official UNIL career portal. Only applications through the official website will be taken into account. Please use the following link to apply: <https://wp.unil.ch/engellab/open-positions/> For questions concerning the application, position, or research topic, or in case of problems with accessing the UNIL career portal using the above link, please do not hesitate to contact us: Philipp.Engel@unil.ch.

The application should be written in English.

Application deadline:

We will start to evaluate applications beginning of April. The deadline for submitting an application: 30.05.2018.

PhD position in community ecology/microbial genomics of Swiss cheese starter cultures

Starting date: flexible

Length of contract: 1 year, renewable, maximum 4 years.

Work percentage: 100%

Workplace: Department of Fundamental Microbiology, University of Lausanne, Switzerland

Qualification:

We are looking for a highly motivated candidate with a

master degree in bioinformatics, genomics, food sciences, life sciences or in other related sciences. Experience with microbiology or biotechnology methods is pivotal. Experience in bioinformatics is a plus.

You will be employed at the Department of Fundamental Microbiology, University of Lausanne on the terms of the doctoral regulations of the Doctoral School of the Faculty of Biology and Medicine.

Work description:

We are looking for an outstanding and highly motivated candidate to join our research group to work on bacterial communities of cheese. Cheesemaking relies on the use of lactic acid bacteria. Undefined mixed cultures are applied for the majority of traditional Swiss cheeses. History of the practical application shows that these cultures are very robust and reliable acidifiers. However, so far, little is known about

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## ULausanne FungalSymbionts

PhD student position 'V Epigenetic versus Genetic and Variation in Fungal Symbionts and How it Affects Plant Growth (Uni. Lausanne, Switzerland)

Job Description: A PhD student position is available in the Sanders' group to study the role of epigenetic versus genetic variation in mycorrhizal fungi on plant growth. Our research indicates that variation in mycorrhizal fungi is associated with large differences in plant growth. We will study this in more detail to find out which aspects of genetic or epigenetic variation in these fungi causes high growth rates in plants (especially cassava).

It is intended that the results of this project will be combined with research in the field where our work is leading to real solutions to increase production of food in areas of the world where starvation is a major problem. More information about our work can be found at <http://people.unil.ch/iansanders/> The project is part of a wider collaboration between the University of Lausanne, Dr Marco Pagni at the Vital-IT center of the SIB Swiss Institute of Bioinformatics and Prof. Alia Rodriguez at the National University of Colombia.

Your skills and qualifications: Candidates must be highly motivated, have a MSc (or expect to have very soon), and have an interest in one or more of the following fields: genetics; plant or fungal molecular biology; epigenetics; quantitative or population genetics. Sound knowledge of bioinformatics would be an advantage and an interest in solving problems in an analytical way. The successful candidate should also have very good interpersonal communication skills and an ability to work well in a team.

Job information: The position is available from 1st December 2018. A PhD at the University of Lausanne takes between 3 and 5 years. The contract is initially for 1 year, renewable.

Most of the PhD student's time will be dedicated to research, and there is additionally the possibility of supervising master students.

Applications: To apply you must upload a CV and motivation letter in English, including the names of 2-3 referees, to the University of Lausanne job portal at:

<https://bit.ly/2JnksHa> Applications must be received online not later than 5th May 2018. Informal enquiries may be made by email to [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch).

NOTE: We are currently seeking a postdoctoral researcher with the same profile but the hiring of the two people should be complementary, i.e. one more laboratory-based and one more computational/bioinformatics based.

Ian Sanders <[ian.sanders@unil.ch](mailto:ian.sanders@unil.ch)>

4x4 field vehicle and a specialized mobile lab trailer for preparing samples. In addition to our fieldwork in the Rocky Mountains, foothills and prairie regions of western Canada, opportunities are available for students to travel to and collaborate with researchers at other institutions in Canada, USA, Chile and Australia and attend national and international conferences.

The University of Lethbridge offers competitive scholarship funding, including tuition waivers, for applicants based on grades and research experience. Potential students must have a background in biology, psychology or neuroscience, some research experience (of any kind) and a valid driver's license. No fieldwork experience is required, but applicants should be prepared to conduct fieldwork in rural and remote locations. For application deadlines see: <https://www.uleth.ca/graduate-studies/> Start dates are flexible, but the deadlines for graduate school applications are May 1st and October 1st.

To apply, send: 1) a c.v.; 2) unofficial copies of academic transcripts; and 3) a brief description of your research interests to: [andrew.iwaniuk@uleth.ca](mailto:andrew.iwaniuk@uleth.ca). More information about our lab can be found at: <http://scholar.ulethbridge.ca/iwaniuk/home> Andrew N. Iwaniuk Associate Professor Canada Research Chair in Comparative Neuroanatomy Canadian Centre for Behavioural Neuroscience University of Lethbridge Lethbridge AB T1K 3M4 Canada ph. +1 403 332 5288 fax +1 403 329 2775 <http://scholar.ulethbridge.ca/iwaniuk/> "andrew.iwaniuk@uleth.ca" <[andrew.iwaniuk@uleth.ca](mailto:andrew.iwaniuk@uleth.ca)>

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## ULethbridge EvolutionaryNeurobiology

The Iwaniuk lab at the University of Lethbridge is currently seeking applications from students interested in pursuing a MSc or PhD on testing the social brain hypothesis in ground squirrel species. Graduate students will have the opportunity to work with several ground squirrel species in Alberta, BC, Manitoba and Montana. Dedicated lab facilities include microtomes, cryostat, fluorescent microscope, a high-resolution digital slide scanner (Olympus VS-120), and the latest in stereology and neuron tracing software (StereoInvestigator and Neurolucida). Confocal and electron microscopy are also available within the Canadian Centre for Behavioural Neuroscience at the University of Lethbridge. Field research is supported by a brand new

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## UMontpellier ModellingEvolution

We have a PhD position available, starting no later than September 2018, at the Institut des Sciences de l'Evolution, University of Montpellier, France.

The PhD student will work on analyzing and developing theoretical models describing the evolution and shifts in distribution of species confronted to climate change. A particular focus of the work will be the evolution of phenological traits and the effect of assortative mating on adaptive responses to a changing environment.

The thesis will be jointly supervised by Ophelie Ronce and Celine Devaux, on the evolutionary biology side, and by Matthieu Alfaro, on the mathematical side.

We are looking for candidates with a good background in evolutionary biology and ecology, interest for adapta-



tion to climate change, taste for formal approaches, and skills in modeling (ranging from computer programming to use of various mathematical models for analytical predictions).

Please contact us for more details about the thesis project and necessary documents for the application. Retained candidates must apply through the University PhD program online system, which requires some preparation.

Applications must be received before May 7th, 2018:— contact [ophelie.ronce@umontpellier.fr](mailto:ophelie.ronce@umontpellier.fr), or/and [celine.devaux@umontpellier.fr](mailto:celine.devaux@umontpellier.fr)

Best regards

Ophelie Ronce

[ronce.ophelie <ophelie.ronce@univ-montp2.fr>](mailto:ronce.ophelie<ophelie.ronce@univ-montp2.fr>)

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## UMontpellier SleepingAdaptation

Please find below a description for a PhD thesis under the MOPGA program (Make Our Planet Great Again). The salary is not yet secured but the odds to obtain such a grant are fair and will depend on the good fit between the PhD topic and the candidate profile.

If you are interested, please send a CV and a motivation letter, before May 4th, to: [marie.charpentier@umontpellier.fr](mailto:marie.charpentier@umontpellier.fr)

The adaptive significance of sleep: Testing the immune theory in a natural primate population.

Abstract

The adaptive significance of sleep: Testing the immune theory in a natural primate population.

Abstract

The functional significance and the physiological mechanisms of sleep remain unsolved. A largely untested assumption is that sleep evolved to sustain immune defences and protect against diseases. We propose to study the mechanistic and functional relationships between sleep and the immune system using long-term individual monitoring of nonhuman primates in combination with field experiments and laboratory analyses. In particular, we propose to identify i) the different factors causing sleep variation within and across individuals; ii) the mechanistic, physiological and immunological pathways that relate sleep to immunity and conversely; and iii) the short- and long-term consequences of both

chronic and acute lack of sleep on animal physiology, behaviour and fitness. We propose to attain these three objectives in two populations of mandrills ( *Mandrillus sphinx* ) showing contrasted lifestyles and different constraints acting on individual sleep. In particular, we will perform a fine-grained description of sleep architecture and quality in the two studied populations. We will study how and why sleep naturally varies across individuals under normal vs. altered conditions (natural vs. captive populations) and how it changes when individuals face both parasite challenges (considering a large range of parasites) and experimental disruptions of their sleep (through deparasitation events). Additionally, we will study the physiological consequences of normal vs. experimentally-disrupted sleep on cytokine production. Finally, sleep variation in normal vs. in altered conditions will be related to individual health and fitness thanks to long-term monitoring of the two populations.

Candidate desired profile

Biologgers will be equipped on 90 individuals for a full year generating billions of data (acceleration, temperatures). We are therefore looking for a highly motivated PhD student with a strong experience and background in bio-informatics. The student will manage the database associated to the project and will take care of the data generated by the biologists. Strong competencies in statistics are also mandatory. Candidates with no experience in bio-informatics will not be considered. Fieldwork in Gabon is not planned within the framework of this PhD project.

If you need more information, please contact me.

Marie

Dr Marie Charpentier, Director of Researches, CNRS

Institut des Sciences de l'Évolution-Montpellier UMR 5554 Place Eugène Bataillon cc 065 34095 Montpellier cedex 05, France

Projet Mandrillus: [www.projetmandrillus.com/](http://www.projetmandrillus.com/)

Marie Charpentier <[marie.charpentier@umontpellier.fr](mailto:marie.charpentier@umontpellier.fr)>

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## UppsalaU MolecularEvolution

PhD position in Molecular evolution

see: <http://www.uu.se/en/about-uu/join-us/details/?positionId=204544> for advertisement

Within this PhD project you will study how unicellular eukaryotes (protists) adapt to new environments. Mainly the group diplomonads and their relatives will be studied. These organisms are found in oxygen-poor environments, some of which are pathogens for humans and other animals, while others are free living. We are interested in how this diversification has taken place and more generally how eukaryotes adapt to different environments.

Bioinformatic methods that will be used are assembly of genomic sequences and comparative genomic analyzes of various types. The project may also contain laboratory work.

Duties: Research in the project and teaching up to 20%.

Requirements: Master degree in Bioinformatics, Molecular biology, Biotechnology, or equivalent. Experiences in bioinformatic work in Linux/equivalent environment and script programming are desired. Experience of analysis of large-scale sequence data is an advantage. Experience in laboratory work is an advantage, but not a requirement. Strong written and oral communication skills are required. Assessment of personal suitability will be an important aspect in the selection.

Application: Application should include a brief description of research interests and relevant experience (1 page), a CV, copies of diplomas and certificates, a copy of your master thesis or equivalent, and at least one letter of reference.

For further information about the position please contact Jan Andersson, ICM, e-mail: [jan.andersson@icm.uu.se](mailto:jan.andersson@icm.uu.se). For information about the research group, please visit <http://www.icm.uu.se/molecular-evolution/andersson-lab/>. Rules governing Ph.D. candidates are set out in the Higher Education Ordinance Chapter 5, §§1-7 and in Uppsala university's rules and guidelines <http://regler.uu.se/search/?hits=30&languageId=1&search-language.en=English> Uppsala University strives to be an inclusive workplace that promotes equal opportunities and attracts qualified candidates who can contribute to the University's excellence and

diversity. We welcome applications from all sections of the community and from people of all backgrounds.

Pay: According to local agreement for PhD students and teaching assistants.

Starting: Summer 2018

Working hours: 100 %

You are welcome to submit your application no later than 2018-05-07, UFV-PA 2018/1457.

Are you considering moving to Sweden to work at Uppsala University? If so, you will find much information about working and living in Sweden at [www.uu.se/joinus](http://www.uu.se/joinus). You are also welcome to contact the International Faculty and Staff Services at [ifss@uadm.uu.se](mailto:ifss@uadm.uu.se).

We decline offers of recruitment and advertising help. We only accept the application the way described in the advertisement.

Jan Andersson, Ph.D Associate Professor in Microbial Evolutionary Genomics < <http://www.icm.uu.se/-molecular-evolution/andersson-lab/> > Programme Director for the MSc Programme in Molecular Biotechnology Engineering Department of Cell and Molecular Biology Uppsala University, BMC, Box 596 SE-751 24 Uppsala, Sweden Tele: +46-70-1679598 E-mail: [Jan.Andersson@icm.uu.se](mailto:Jan.Andersson@icm.uu.se)

Jan Andersson <[Jan.Andersson@icm.uu.se](mailto:Jan.Andersson@icm.uu.se)>

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## USheffield EvolOfUnstructuredProteins

We are seeking a highly motivated and enthusiastic PhD student to work on disease mutations in unstructured protein regions.

Deadline: Monday, May 14, 2018

Enquiries and application: <https://www.findaphd.com/-search/ProjectDetails.aspx?PJID=97197> Project Description

There are proteins that are well characterized with regard to their three dimensional structure. In particular it is known that parts of them act as "functional" units, e.g. active and binding sites or functional domains. However, within proteins, regions of intrinsically disorder occur and these are characterized by a lack of a well-defined three-dimensional structure. Although these disordered regions do not show a particular higher conformational state, they are known to be functionally

important, such as through their involvement in protein-protein interactions or DNA/RNA binding. In a recent work we have shown that there is ongoing positive selection that contributes substantially to the evolution of human long intrinsically disordered protein regions. Furthermore, these protein regions are enriched in post-translational modification sites as well as regions and motifs (annotated sequence stretches of biological importance), but surprisingly disease mutations tend to occur much less frequently in disordered regions (Uversky et al., 2014), with the exception of mutations associated with musculoskeletal diseases.

This timely project aims to understand why disease mutations tend to be less frequent in disordered protein regions. The focus of this project will lie on the exceptional group of mutations involved in musculoskeletal diseases that are enriched in disordered protein regions by comparing them to those involved in other disease groups. Fundamental will be a novel genomic comparative approach currently developed in the Gossmann lab targeted at the identification of the evolutionary properties of disease-associated sites. Furthermore, in collaboration with Daniel Rigden from the University of Liverpool, we will conduct molecular dynamic simulations to investigate three dimensional features of disease associated mutations on protein flexibility and protein-ligand interactions. Furthermore we will exploit machine learning approaches to predict protein disorder on the single site residue effects. Experimental evidence and the underlying mechanistics of disease candidate sites can then functionally be tested in a fly model in collaboration with the Mirre Simons lab at the University of Sheffield. This will ultimately gain insights into whether disease mutations are genuinely less likely to occur in disordered protein regions or whether our lacking understanding of disease properties associated with disordered protein regions has led to an under-annotation in the respective databases.

For this highly innovative, collaborative and interdisciplinary PhD the respective candidate should have a strong background in biology, molecular biology and genetics as well basic programming knowledge or at least a strong interest in computational approaches to investigate fundamental biological problems. A background in bioinformatics is of advantage, however all necessary approaches will be taught during the duration of the PhD. This project will take advantage of multiple biological “big” data sets, such as the 1000-Genome project, Uniprot, large-scale mammalian phylogenies and their respective whole genome information, as well as PDB and several secondary databases.

Funding Notes

This studentship is part of the MRC Discovery Medicine North (DiMeN) partnership and is funded for 3.5 years. Including the following financial support: Tax-free maintenance grant at the national UK Research Council rate Full payment of tuition fees at the standard UK/EU rate Research training support grant (RTSG) Travel allowance for attendance at UK and international meetings Opportunity to apply for Flexible Funds for further training and development Please carefully read eligibility requirements and how to apply

– Toni Ingolf Gossmann, Leverhulme Early Career Fellow

Department of Animal & Plant Sciences Western Bank University of Sheffield Sheffield, S10 2TN United Kingdom

Tel: +44 (0) 1142220062

“t.gossmann@sheffield.ac.uk”

<t.gossmann@sheffield.ac.uk>

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## USheffield ScienceInformationBias

We are seeking a highly motivated and enthusiastic PhD student to work on information bias in modern life sciences.

Deadline: Monday, May 14, 2018

Enquiries and application: <https://www.findaphd.com/-search/ProjectDetails.aspx?PJID=97183> Project Description

Modern life sciences are increasingly driven by next-generation sequencing and whole genome/transcriptome/proteome/metabolome wide-association studies. Such ‘modern life science’ associates large-scale datasets with phenotypes or diseases of interest to discover their underlying biology to be used in medicine. With such discovery-based science a lot of progress can be made, however, there is a large dependency for interpretation on currently known information. This information bias generates self-fulfilling prophecies, biased research directions and interpretations. We know that the level of information is heavily biased - for example, because, certain genes, diseases or species have been hotspots of research (<https://www.nature.com/articles/d41586-017-07291-9>). Even worse, such study bias reinforces information bias further and it is often unclear what the reliability of the initial information was in the first place. Here we propose a statistical approach that incorporates

information bias in both quantity and quality to objectively distil biology of interest and to flag up important currently unknown biology.

The techniques used to achieve this will involve machine learning (principle component and cluster analysis), evolutionary genomics, data imputation and reliability weighting (as in meta-analysis). Moreover, the student will help generate a user-friendly GUI for the community. For proof of principle we will utilise one database, Flybase (*Drosophila melanogaster*), that is very well annotated and has the largest quantity of in depth information not available for other organisms. The methods generated will however be applicable to any database, including human databases. In addition, the use of flies will allow the student to put the software generated to the test using two large experimental datasets that we have generated in my lab: experimental GWAS in flies for longevity and neurodegenerative disease. Candidate genes identified by the student can subsequently be tested for causality using functional genetics of flies.

Modern life science generates a tremendous amount of data that is close to incomprehensible except to study the top associations with the outcome (e.g. disease) of interest. Currently such top associations, or 'hits', are compared to a database of current knowledge on the gene level. Such data mining can be rewarding, but also imposes strong information bias. The beauty of modern life science is that it has the potential to be unbiased and can be highly informative about mechanisms, especially in disease or for complex phenotypes such as ageing. The project we propose is therefore exceptionally timely. Biological interpretation from large scale, often costly, studies that are currently generated is impeded by our current inability to assess current knowledge objectively, intuitively and in an integrated fashion.

We seek a hard-working passionate student with a quantitative mind-set and an interest in the biology of disease and ageing. Several educational backgrounds are suitable for this project and include, but are not exclusive, to bioinformatics, computational science and biomedical science. The techniques that are listed can all be learned within the PhD and no prior experience with these is essential. The broad scientific expertise and commitment of the supervisors ensures ample support and a vibrant environment for the student.

Links: <http://simons-lab.group.shef.ac.uk> <http://toni-gossmann.staff.shef.ac.uk> Funding Notes

This studentship is part of the MRC Discovery Medicine North (DiMeN) partnership and is funded for 3.5 years. Including the following financial support: Tax-free maintenance grant at the national UK Research Council rate

Full payment of tuition fees at the standard UK/EU rate Research training support grant (RTSG) Travel allowance for attendance at UK and international meetings Opportunity to apply for Flexible Funds for further training and development Please carefully read eligibility requirements and how to apply on our website, then use the link on this page to submit an application: View Website

#### References

Simons MJP. Questioning causal involvement of telomeres in aging. *Ageing Res Rev.* 2015 1;24(Pt B):191-6.

Garratt M, Nakagawa S, Simons MJP. Comparative idiosyncrasies in life extension by reduced mTOR signalling and its distinctiveness from

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## UTechnologySydney Australia RealTimePhylogenetics

Project description: We are looking for a talented PhD student to develop methods for real-time analysis of bacterial and viral outbreaks. The project will be part of a larger effort with international collaborators in the UK and USA that aims to develop methods that efficiently and accurately analyse data streams being generated by laboratories around the world. The project will provide the student experience in statistical modeling, programming, bioinformatics, and evolutionary biology.

Requirements: Undergraduate or postgraduate degree in bioinformatics, computer science, statistics, engineering or a related quantitative field.

Knowledge and skills to be developed: Bayesian statistics Phylogenetics and evolutionary biology Software development in R, Python, Java, C or C++ Production software engineering Linux command-line, HPC and cloud computing Excellent written and oral communication skills

Project supervisors: Associate Professor Aaron Darling and Dr. Mathieu Fourment

Research environment: This role is within the itthree institute in the Faculty of Science, one of the largest



faculties at UTS, which is Australia's top ranked young university, with a particular focus on research translation. The ithree institute brings together a team of scientists with diverse skill sets who collectively address key challenges in the understanding and control of infectious diseases in humans and animals.

Commencement date: Applicants would be expected to commence studies in the Spring 2018 or Autumn 2019 terms (August 2018 or March 2019).

Contact: Informal enquiries can be sent to [aaron.darling@uts.edu.au](mailto:aaron.darling@uts.edu.au) or [mathieu.fourment@uts.edu.au](mailto:mathieu.fourment@uts.edu.au)

Dr. Mathieu Fourment ithree institute University of Technology Sydney [mathieu.fourment@uts.edu.au](mailto:mathieu.fourment@uts.edu.au)

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## UToronto TurtleSexDetermination

MSc/PhD position in Evolutionary Ecology and Global Change Biology,

The Rollinson group at the University of Toronto ([www.njal.rollinson.com](http://www.njal.rollinson.com)) is seeking a highly-motivated graduate student to study temperature-dependent sex determination in Snapping turtles. The candidate would leverage two decades of data on primary sex ratios and incubation temperatures collected in Algonquin Park, and would develop and validate a model that predicts historical and future sex ratios. The candidate would also perform fieldwork in Algonquin Park at the historic Wildlife Research Station, and would be responsible for curating and contributing to the long-term dataset on sex ratios. The ideal candidate would have an interest in evolutionary ecology and quantitative methods, a strong statistical background, and be familiar with the programming language R. Candidates that have a demonstrated ability to learn quickly and an interest in modelling are also encouraged to apply.

The position begins in September 2018, with the possibility of performing some research in Algonquin Park in summer 2018. The position is funded, however the candidate will be expected to apply for NSERC funding in the fall of 2018. The position will remain open until it is filled.

Please apply by emailing your (unofficial) transcripts, a writing sample, and your CV to [njal.rollinson@utoronto.ca](mailto:njal.rollinson@utoronto.ca).

Njal Rollinson Assistant Professor Ecology & Evolutionary Biology / School of the Environment Earth Science Building Office ES3051 University of Toronto Phone: 416-978-3665 Research Homepage: [www.njalrollinson.com](http://www.njalrollinson.com)

Njal Rollinson <[njal.rollinson@gmail.com](mailto:njal.rollinson@gmail.com)>

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## UWesternSydney EvolutionSexDifferences

PhD position available at Western Sydney University (Hawkesbury Campus) in the Hawkesbury Institute for the Environment (HIE) working with Professor John Hunt. The HIE has rapidly become a research leader in environmental and ecological research, with a strong reputation for delivering research outcomes of the highest quality. We are now offering a research scholarship to a highly motivated PhD candidate to work within a research group addressing the role of diet and sexual conflict in the evolution of sex differences in the lifespan of decorated crickets (*Gryllobates sigillatus*). This project will use replicate experimental populations of crickets that have been evolving for 30 generations on specialized diets differing in the ratio of protein to carbohydrates and total nutritional content. This project will examine how dietary adaptation and sexual conflict influences the evolution of sex differences in lifespan and ageing and identify the mechanisms responsible for these differences. The project provides an exciting opportunity to test new concepts on the link between nutrition, sexual conflict and lifespan/ageing, and to develop key core skills in behavioural ecology, nutritional ecology, quantitative genetics, genomics and chemical ecology. The project will provide the opportunity to work with an internal supervisor on the project, Dr Alexie Papanikolaou, with expertise in genomic analysis, as well as a USA-based collaborator, Prof Scott Sakaluk, with vast experience in sexual conflict research and working with decorated crickets.

We welcome applicants from a range of backgrounds, who are keen to apply their skills to key issues in evolutionary biology. In particular, the project is suitable for candidates with strong interests in ecology, evolution, nutrition, sexual conflict, lifespan, ageing and/or entomology.

The successful applicant should:

\* hold qualifications and experience equal to one of the following (i) an Australian First Class Bachelor (Hon-



ours) degree, (ii) coursework Masters with at least 25% research component, (iii) Research Masters degree, or (iv) equivalent overseas qualifications.

\* demonstrate strong academic performance in subjects relevant to ecology, evolution, nutrition, lifespan/ageing and entomology.

\* have an understanding of the importance of sexual conflict and evolution more generally.

\* be willing to learn new techniques in nutrition, quantitative genetic and genomic analysis and chemistry.

\* be enthusiastic and highly motivated to undertake further study at an advanced level. International applicants must also meet English language proficiency <<https://www.western-sydney.edu.au/international/home/apply/admissions/entry-requirements>>.

\* Domestic students will receive a tax-free stipend of \$30,000 per annum to support living costs, supported by the Research Training Program (RTP) Fee Offset.

\* International students will receive a tax-free stipend of \$30,000 per annum to support living costs. Those with a strong track record will be eligible for a tuition fee waiver.

\* International students are eligible for Overseas Student Health Cover.

Support for conference attendance, fieldwork and additional costs as approved by School/Institute.

How to Apply:

1. Contact Professor John Hunt (J.Hunt@westernsydney.edu.au) to discuss your eligibility, the project requirements and your intention to apply.
2. Complete the scholarship application form (PDF, 222.11 KB) <[https://www.westernsydney.edu.au/\\_data/assets/pdf\\_file/0005/733487/Project-Scholarship\\_Application\\_Form.2017.pdf](https://www.westernsydney.edu.au/_data/assets/pdf_file/0005/733487/Project-Scholarship_Application_Form.2017.pdf)>.
3. Compile your CV, contact information for two referees and a one-page proposal stating your experience and how your research interests align with the project aims.
4. Ensure all documentation is certified according to Western Sydney University requirements <[https://www.westernsydney.edu.au/currentstudents/current\\_students/applying\\_to\\_study/certifying\\_documents](https://www.westernsydney.edu.au/currentstudents/current_students/applying_to_study/certifying_documents)>.
5. All applications and supporting documentation must be submitted directly to the Graduate Research School as follows:

\* Use the email subject line: <GRS TO UPDATE>

\* Submit to [grs.scholarships@westernsydney.edu.au](mailto:grs.scholarships@westernsydney.edu.au)

\* All attached documents must be submitted as PDF.

\* In the body of your email, include your full name, your student ID (if you are a current or previous Western Sydney University student) and the full title of the scholarship.

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

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## 23andMe PopulationGenetics

Population Geneticist - Ancestry Research Mountain View, CA, United States

We are seeking colleagues with extensive training and experience in statistical and population genetics to join our highly productive, world-class Ancestry Research & Development team. Our team develops novel methods for the interpretation of 23andMe customer genetic data in order to provide insight into ancestry and to establish relationships between individuals. We are seeking team members who are excited to develop cutting edge features that will reach millions of people.

Successful candidates will work within and across teams to support our research and development efforts. The job requires strong computational and statistical skills, a deep understanding of human genetics, and excellent writing abilities.

Full details: <https://www.23andme.com/careers/ons96fwO/> Requirements: Ph.D. in Population Genetics, Statistical Genetics or a related field (e.g., Genetics, Computer Science, Statistics, Bioinformatics, Physics, Mathematics). Evolutionary or population genetics research experience; focus on human population genetics is a plus. Experience in algorithm development or machine learning approaches essential. Hands-on experience working with very large data sets in Python or R; experience with C/C++ is a plus. At ease in a Linux environment. Excellent written and verbal communication skills. Enthusiasm for working in a highly collaborative environment.

23andMe, Inc. is the leading personal genetics company. Our mission is to help people access, understand and benefit from the human genome.

23andMe has over 2 million customers worldwide

with ~85 percent consented to participate in research. 23andMe is located in Mountain View, CA. More information is available at [www.23andme.com](http://www.23andme.com). At 23andMe we value a diverse, inclusive work force and we provide equal employment opportunity for all applicants and employees. All qualified applicants for employment will be considered without regard to an individual's race, color, sex, gender identity, gender expression, religion, age, national origin or ancestry, citizenship, physical or mental disability, medical condition, family care status, marital status, domestic partner status, sexual orientation, genetic information, military or veteran status, or any other basis protected by federal, state or local laws. 23andMe will reasonably accommodate qualified individuals with disabilities to the extent required by applicable law.

Adam Auton <[aauton@23andme.com](mailto:aauton@23andme.com)>

## BrownU ResAssist EvolutionaryDevelopment

Brown University Research Assistant position for Cell and Developmental Biology

Location: Brown University, Molecular Biology Cell Biology Biochemistry Department (Providence, RI)

We are looking to hire an excellent full-time research assistant who is encouraged to conduct her/his independent research under PI's supervision. The area of research includes developmental biology, molecular biology, evolutionary developmental biology, live imaging, proteomics, RNA-IP-seq, CRISPR genome editing technology. Basic skillset and knowledge in molecular biology (e.g. cloning, PCR) and a good accomplishment in her/his undergraduate work is prerequisite. Other necessary trainings (e.g. microinjection, confocal imaging,

proteomics) will be provided by the PI. The successful individuals will be given own projects to conduct and finish (hopefully with lead author publications) within one-two years of appointment. This is an excellent job opportunity for individuals who seek to proceed to graduate school or medical school with a good record of research accomplishment in near future. Any interested individuals should contact the PI via e-mail: mamiko\_yajima@brown.edu. Please enclose your CV, title of your thesis, and name of your thesis advisor. Reviews will begin immediately and continue until position is filled. \*To be noted, the University does not support a Visa for this position.

Mamiko Yajima <mamiko\_yajima@brown.edu>

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### DrexelU Philadelphia CollectionManager

Dear colleagues,

The Invertebrate Paleontology Department of the Academy of Natural Sciences of Drexel University is searching for a Collection Manager. The Academy is the oldest natural science research institution and museum in the Americas, and is situated within Philadelphia's scenic Museums District on the Ben Franklin Parkway. The Invertebrate Paleontology collection consists of over 1 million specimens, ~ 75% of which are fossil mollusks, including ~5,000 types, with strengths in Mesozoic and Cenozoic mollusks from the US Atlantic and Gulf Coastal Plains and from Britain.

Qualifications: Candidates should have at least a Master's Degree in either museum studies, invertebrate paleontology, vertebrate paleontology, or zoology. Candidates with a Bachelor's degree and extensive experience will also be considered. Experience in collections operations and digitization initiatives are required. Familiarity with collections management software, such as Specify or Arctos, and with national and international collections digitization efforts, such as iDigBio, ALA, GBIF, is desirable, as is experience in grant writing for collections management.

For Further Details on the Position and to Apply: Applicants may see the full job posting and must apply online at

[www.drexeljobs.com/applicants/-](http://www.drexeljobs.com/applicants/-)

Central?quickFind&107 Applicants will need to provide a CV, letter of interest, and, if selected for

the second round, names and contact information for three references. Position is open until April 30 2018. Questions about the position should be directed to Dr. Jocelyn Sessa (jsessa@drexel.edu)

The Academy of Natural Sciences of Drexel University is especially interested in qualified candidates who can contribute to the diversity and excellence of the academic community.

Thank you,

—  
Mariangeles Arce H., PhD

Collection Manager

Ichthyology Department

The Academy of Natural Sciences of Drexel University

1900 Benjamin Franklin Parkway

Philadelphia, PA 19103

215-299-1128

“Arce Hernandez,Maria” <maa383@drexel.edu>

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### MaxPlanck Tuebingen MouseGeneRegulationEvolution

GENETIC MAPPING IN MOUSE INTERSPECIFIC HYBRIDS USING IN VITRO CROSSES

Friedrich Miescher Laboratory, Max Planck Campus, Tübingen, Germany

One postdoctoral position and one staff scientist position (both for 2 years in the first instance) are available in the Chan Lab at the Max Planck Institute in Tübingen as part of a prestigious 1.5M EUR European Research Council grant investigating the role of gene regulatory network evolution in mice by studying “in vitro” genetic crosses.

The goal of our research is to adopt cutting-edge tissue culture techniques for studying evolutionary divergence in gene networks. We have developed a system to use mitotic recombination, as opposed to meiotic recombination through breeding, to generate genetic diversity in F1 interspecific hybrid mouse ES cells under tissue culture conditions (Lazzarano et al., PNAS, 2018). This allows us to create recombinant cell lines of effectively unlimited size at low costs within a matter of weeks. We now aim to use these “in vitro recombinant” panels

to obtain phenotypic measurements via tissue engineering, organ-on-a-chip or droplet microfluidic single-cell methods.

We're looking for highly motivated individuals for the following roles:

1) Postdoc: You should be about to earn, or have recently earned your PhD in the areas of genetics, molecular biology or regenerative medicine. You should demonstrate expertise in tissue culture techniques. You should be able to demonstrate promise in early career success in a first author publication or preprint ready for submission. A background in genetic mapping or GWAS will be advantageous. A background in evolutionary biology will be helpful, but not a requirement. We are interested in candidates who are keen to apply and develop new genetic tools and technologies. Passion for research, team spirit and enthusiasm are essential.

2) Staff scientist: You should hold a Bachelors-equivalent degree or higher qualifications in the areas of genetics, molecular biology or regenerative medicine. We are looking for a strong track-record and demonstrated research experience and training, particularly in tissue culture and aseptic techniques. You will be a central team member assigned to work closely with a postdoc in carrying out work mainly using tissue culture, tissue engineering and microfluidics techniques. We will provide training on advanced tissue engineering techniques and microfluidics device fabrication, including but not limited to flow or microfluidics models to assay expression and tissue phenotypes. You will also operate flow cytometry instrument(s) in the context of tissue differentiation and single-cell studies. You will assist in generating DNA and RNAseq libraries to help dissect the genetic architecture of gene expression evolution in mouse or human tissue models.

We are a multidisciplinary team that focuses on the systems biology of development and evolution in mice, combining population and functional genomics with molecular biology and tissue engineering techniques to study the evolution of gene regulatory network in mouse and its close relatives. Our research group is funded by the European Research Council (ERC) and the Max Planck Society and is located on the Max Planck Campus in Tübingen, Germany. Our campus hosts world-class research groups and operates state-of-the-art sequencing and other core facilities. English is the working language. All seminars and communications are in English.

The position is available for an initial 2 years with the possibility of extension. Salary and benefits are according to the German public service pay scale (TVöD Bund up to and including E13) and are commensurate with training and experience.

The Max Planck Society seeks to increase the number of women in areas where they are underrepresented, and therefore explicitly encourages women to apply. The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. For more information please see: <http://fml.tuebingen.mpg.de/chan-group/-open-positions> Reference Lazzarano et al., Genetic mapping of species differences via in vitro crosses in mouse embryonic stem cells. Proc Nat Acad Sci, 2018. doi: 10.1073/pnas.1717474115

Consideration of applications will begin on 15th April 2018, and will remain open until filled.

Please send your application with:

1. a statement of research interests and why you have applied for this position, 2. your CV, and 3. reference contacts (3 for postdocs and 2 for staff scientists)

to Dr. Frank Chan at [frank.chan@tue.mpg.de](mailto:frank.chan@tue.mpg.de).

Frank Chan Max Planck Research Group Leader  
Friedrich Miescher Laboratory of the Max Planck Society  
Max-Planck-Ring 9 72076 Tübingen Germany

T: +49 (0)7071 601 888 F: +49 (0)7071 601 801 @:  
[frank.chan@tue.mpg.de](mailto:frank.chan@tue.mpg.de)

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## MfN Berlin Biodiversity

Biodiversity research for the 21 century - at the Museum für Naturkunde Berlin

The Museum für Naturkunde Berlin, Leibniz Institute for Evolution and Biodiversity Science (MfN), is developing a new cutting-edge center for Integrative Biodiversity Discovery. By 2020 this program will consist of a large team (> 20 staff) of mainly new hires and existing MfN biodiversity experts. We expect this new program to develop into a worldwide recognized center for modern collection-based biodiversity discovery and taxonomic expertise, able to strengthen and develop networks and train global biodiversity scientists and leaders. The program aims to significantly contributing to alleviating the global taxonomic deficit and speeding up biodiversity discovery.

Berlin is a dynamic international city at the heart of Europe. The museum has a strong team culture, thrives for scientific excellence and is undergoing a transformation. Developing our science and our public programs we want to address global challenges, respond to scientific opportunities and foster science-society dialogue.

We would welcome you joining our team. The first four new positions in the biodiversity discovery center are now advertised:

Researcher Biodiversity Diptera [<https://www.museumfuernaturkunde.berlin/de/ueberuns/jobs-und-karriere/stellenausschreibungen/wissenschaftliche-mitarbeit-biodiversitaet-0>] Re-

searcher Biodiversity Lepidoptera [<https://www.museumfuernaturkunde.berlin/de/ueberuns/jobs-und-karriere/stellenausschreibungen/wissenschaftliche-mitarbeit-biodiversitaet>] Researcher

Biodiversity Freshwater Arthropods [<https://www.museumfuernaturkunde.berlin/de/ueberuns/jobs-und-karriere/stellenausschreibungen/wissenschaftliche-mitarbeit-biodiversitaet-von>]

Researcher Bioeconomy & Biodiversity <https://www.museumfuernaturkunde.berlin/de/ueberuns/jobs-und-karriere/stellenausschreibungen/wissenschaftliche-mitarbeit-biooekonomie>

For further info about the place, its history, its future and 'character' please see - our website: <https://www.museumfuernaturkunde.berlin/en>

Brain Scoop videos: <https://www.youtube.com/watch?v=3DneHO3-PUxVY>, <https://www.youtube.com/watch?v=YEMGMJMqjto>, and <https://www.youtube.com/watch?v=6qbU5U8m18E>

thomas.vonrintelen@mf.n.berlin

## MinotStateU TeachingEvolution

### OPEN POSITION: TENURE-TRACK ASSISTANT PROFESSOR OF BIOLOGY

Position Summary Minot State University's Department of Biology invites application for an assistant professor of biology. Position starts August 2018. The applicant is expected to teach an introductory-level biology course for non-majors, upper-level courses in the applicant's area of expertise, and develop a research program involving undergraduates.

Responsibilities The applicant is expected to teach lectures and labs in the department and involve undergraduates in research experiences. The applicant is also

expected to advise students, to serve the department, university, or the public, as well as produce scholarly articles or books in his or her field. The department is interested in adding a faculty member who will expand our areas of expertise. Terrestrial or aquatic ecologists who can provide field experiences or animal physiologists who can teach Human Anatomy & Physiology with a cadaver lab are particularly encouraged to apply.

Minimum Qualifications The successful candidate must have earned a Ph.D. in biology.

Preference Qualifications Preference will be given to candidates with teaching experience and an established record of research.

Compensation Commensurate with qualifications and experience. Benefits package includes employer-paid full family health coverage, retirement plan, and tuition waiver benefits.

Application Documents Please submit cover letter, CV, names and contact information for three references familiar with your teaching and/or research, three letters of support from colleagues who can speak to your teaching and/or research, a statement of teaching philosophy, and a statement of research interests.

Additional Information Review of applications will begin April 16 and continue until position is filled.

If you have questions about the position, programs, or Minot State University, please contact:

Alex Deufel, Ph.D. Chair, Department of Biology alexandra.deufel@minotstateu.edu

The state of North Dakota has an open records law; therefore, your application could be subject to review upon request. A criminal history background check must be satisfied prior to employment. According to NDCC 15-10-13.2, all faculty members are required to take an oath (or affirm) to support the constitutions of the United States and North Dakota.

MSU is an equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity or national origin. Women, minorities, veterans and individuals with disabilities are encouraged to apply. This position is subject to North Dakota Veteran's Preference.

"Adam, Peter J" <PADAM@nwmissouri.edu>



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## NewPhytologist Editorial Assistant

The New Phytologist Trust is recruiting an Editorial Assistant to work on its journals, New Phytologist, and Plants, People, Planet.

We are looking for an enthusiastic individual with a passion for plant science, excellent English language skills, good organisational skills and a flair for teamwork. This post offers an excellent opportunity to join a vibrant journal team at an exciting and innovative time for the publishing industry.

Salary: 21,585 to 24,983 Closing Date: Tuesday 29 May 2018 Interview Date: To be confirmed

More information and application form here: <https://hr-jobs.lancs.ac.uk/Vacancy.aspx?ref=N1605> Informal enquiries should be directed to Sarah Lennon, Executive Editor: [s.lennon@lancaster.ac.uk](mailto:s.lennon@lancaster.ac.uk)

Kind regards, Mike

Dr Mike Whitfield Development Coordinator, New Phytologist

New Phytologist Central Office, Bailrigg House, Lancaster University, Lancaster, LA1 4YE, UK Tel: + 44 1524 592839; Fax: + 44 1524 594696 [newphytologist.org](http://newphytologist.org) Twitter: @NewPhyt Facebook: [fb.com/NewPhytologist](https://www.facebook.com/NewPhytologist)

The New Phytologist Trust, registered charity number 1154867

2016 Impact Factor 7.33

Get behind the science < <https://www.newphytologist.org/blog> > Read all about it on the New Phyt blog.

New Phytologist Symposia in 2018 < <https://newphytologist.org/symposia> > The biology of wood: from cell to trees

“Whitfield, Mike” <[m.whitfield@lancaster.ac.uk](mailto:m.whitfield@lancaster.ac.uk)> “Whitfield, Mike” <[m.whitfield@lancaster.ac.uk](mailto:m.whitfield@lancaster.ac.uk)>

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## NHM Geneva Entomology Research Officer

The Natural History Museum of Geneva (MHNG) encompasses collections covering all animal phyla and is especially strong in entomology, where the collections are among the top-10 largest in Europe, with about 10 million specimens. The MHNG holds a large number of type specimens that play an important role as reference material in ongoing research projects. Researchers from the MHNG regularly receive grants from the Swiss National Science Foundation and other funding bodies to fund international research projects on biodiversity.

**\*Job description\*** We are seeking a Research Officer in entomology to manage and develop entomological collections and research along with two other Research Officers doing collection-based research on insects. The selection committee will consider applications from specialists in all holometabolous orders of insects. This position of Research Officer will include responsibility for part of the entomological collections, in particular those associated with the appointee's personal interests. The appointee will be expected to participate actively in a broad range of museum outreach activities, such as public communications and media interaction, exhibitions, and citizen science programs. She/He will also be a major actor of programs for the study, conservation and valorisation of local and regional biodiversity. The appointee will develop and engage in collaboration with other similar institutions, both nationally and internationally. She/He is expected to be active in applying for external funding in fields such as taxonomy, systematics, biogeography or biodiversity science, ideally with an emphasis on evolutionary biology.

**\*Required qualifications\*** The appointee shall hold a doctoral degree in entomology or equivalent. Experience in managing natural history collections, and an understanding of the importance and role of collections and research in museums are mandatory.

**\*Meriting\*** It is also desirable that the candidate has postdoctoral experience as well as a strong research record. Participation in student supervision and knowledge of the European fauna are considered further assets.

**\*Candidates should submit a cover letter describing their interest in the position, including but not restricted to experience with natural history collections and future**

research plans, as well as a full curriculum vitae, a list of publications, and a list of three references.\*

Application materials should be combined in a single file (pdf) and sent before the 21st of May 2018 by email to [recrutement.mhn@ville-ge.ch](mailto:recrutement.mhn@ville-ge.ch) or by post mail to Dr. Nadir Alvarez, head of the Unit of Research and Collections, Museum of Natural History, route de Malagnou 1, Case postale 6434 - 1211 Genève 6. The appointee is expected to start on the 1st of September 2018. Salary will range between 95750 CHF and 158564 CHF per annum depending on the experience of the appointee.

J. Mariaux

Jean Mariaux <[mariauxj@gmail.com](mailto:mariauxj@gmail.com)>

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### NSF Program Director

Interested candidates with significant expertise in bioinformatics or with deep knowledge regarding postdoctoral fellowships are invited to apply for the position of Program Director in the Division of Biological Infrastructure (DBI) of the National Science Foundation. Applicants must have a Ph.D., at least six years of experience, and be interested in enabling research and education in the biological sciences. Further information is given at the following link: <https://dbiblog.nsfbio.com/2018/04/aksakai@uci.edu> <[aksakai@uci.edu](mailto:aksakai@uci.edu)>

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### RiceU Technician

The Saltz lab at Rice University seeks a full-time lab manager/technician. The lab manager will be responsible for facilitating scientific experiments with fruit flies (primarily by maintaining stocks), coordinating logistics of the day-to-day lab operations, and contributing intellectually to lab meetings and other scientific conversations. The ideal candidate will be passionate about science and have exceptional time-management skills and attention to detail. This is a great position for a recent college graduate interested in obtaining research experience for a year or two before moving onto graduate school or something else. The position would start in July or August of 2018. You can learn more about our research here: <https://saltzlab.wordpress.com>

. To apply, please send me ([Julia.b.saltz@rice.edu](mailto:Julia.b.saltz@rice.edu)) your resumé/CV, names and contact information for a few references, and a few sentences about why you are interested in the position.

– Julia B. Saltz Assistant Professor Biosciences at Rice University 6100 Main Street, MS-170 Houston, TX 77005 [julia.b.saltz@rice.edu](mailto:julia.b.saltz@rice.edu) [Saltzlab.wordpress.com](http://Saltzlab.wordpress.com)  
[jbsaltz@gmail.com](mailto:jbsaltz@gmail.com)

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### SouthAfrica ResearchManager

Position as research assistant and as research manager (July 2018-November 2019)

at the striped mouse project in South Africa,

We are looking for an extremely motivated and independent biology student with a master's degree to join the striped mouse project in July / August 2018 at least until November 2019 and for a maximum of 3 years, first as research assistant (until October 2018) and afterwards as research manager. This position is suitable for somebody who would like to gain experience in field work and scientific management. Assistants / managers get free accommodation at the station and a compensation to cover their daily costs. Travel costs can be refunded by up to an additional R 12 000 / year. As such, the position compensates for all arising costs but does not represent a real employment.

As research manager you will work closely together with the station manager and both managers will share 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). Our current research manager will leave the project in October 2018. The new research manager will be instructed by the present research manager.

Skills needed: Good experience in field work and must good knowledge of behavioural ecology or a similar field of research. Experiences in working with small mammals, radio-tracking, blood sampling, living at a remote location are of advantage.

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!

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 (August to November) during periods when other students are present at the research station.

Primary duties research manager / secondary duties station manager

- . Data:
- Weekly data entry
- Weekly data check
- Monthly data backup
- Monthly data report
- Training and supervision of field assistants
- Training of students and postdocs
- Support for students and postdocs
- Management of transmitters
- Management of field and laboratory supplies

Primary duties station manager / secondary duties research manager

- Technical support research station:
- Water system incl. sewage system
- Solar system
- Gas bottles replacement
- House and furniture
- Running of the respirometry laboratory
- Management of the captive colony
- Management of the research station car
- Management of bank account and cash box
- Management of research station supplies

Compensation:

- Free accommodation.
- A monthly compensation of R 3 500, which is sufficient to pay all costs of living. This compensation will rise to

R4 700 per month in November 2018, when the research assistant takes over the research manager position. - For travel costs, R12 000 per year can be refunded, but proof (receipts) must be presented for this. This refund is only payable after October 2019 and will not be paid if the person leaves earlier than agreed. - You will become an honorary researcher at the University of the Witwatersrand in the group of Prof. N. Pillay. - Scientific co-authorship will be possible if the manager contributes to the success of projects by not only collecting the majority of data, but also by data analysis and writing of the manuscript.

Responsibilities:

- The manager has to cover the costs to get to the station, including travel costs and visa fees. For this, a refund can be paid (see above).
- The manager needs to arrange for a health insurance covering him / her during the stay. A copy must be sent to C. Schradin before travelling to the stations.

Place and project: Succulent Karoo Research Station (SKRS) in the Goegap Nature Reserve near Springbok in the Northern Cape of South Africa. The research projects are on the socio-ecology of small mammals, studying ecological and physiological reasons of social behaviour, behavioural flexibility, and physiological adaptation.

Period: The new manager is expected to start in July / August 2018 and to

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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>

## St Andrews Aquaculture Genetics- Breeding Manager

Full time, permanent

Starting salary 25,000-30,500 per annum

Xelect Ltd is seeking to appoint a dynamic breeding programme manager to be based at our headquarters in St. Andrews in Scotland. The person appointed would be working directly with and supervised by our Senior Breeding Programme Manager and would be expected to liaise with the rest of the Xelect team of managers,

quantitative geneticists, bioinformaticians and molecular biologists. This exciting new role would be ideal for somebody with a keen interest in aquaculture breeding and genetics looking to develop their knowledge and expertise in this rapidly advancing field.

Duties would primarily involve liaison with our clients to review, plan and manage the contracted breeding programmes. This will involve extensive overseas travel. The position would require a comprehensive understanding of the laboratory processes involved including SNP genotyping as well as conduct of the post-laboratory processing and statistical analysis and subsequent compiling of reports and presentations. The successful candidate would be expected to have excellent organisational and time management abilities, be effective within a team and hold outstanding interpersonal skills. See [www.xelect.co.uk](http://www.xelect.co.uk) for further details.

Essential skills:

A minimum of a M.Sc. relating to aquaculture, fish reproduction or animal breeding.

Knowledge and experience of hatchery and broodstock systems for finfish and / or shellfish species.

Experience working with aquaculture industry.

Excellent data management and computer literacy skills.

Willing to travel and experience working within other countries.

Laboratory skills in molecular biology including DNA extraction and qPCR techniques.

Basic knowledge of programming platforms including R and Linux.

Desirable skills:

Ph.D. relating to aquaculture, fish reproduction or animal breeding.

Proficiency of programming platforms R and / or Linux.

SNP and microsatellite genotyping techniques.

Ability to converse in another language. Knowledge of one or more of Arabic, French, Mandarin, Spanish or Turkish would be a distinct advantage.

Peer reviewed publications in the field of aquaculture, reproduction or genetics.

Further details about the position and the company are available upon request. To apply please send a current CV and a covering letter, along with contact details of two referees to [info@xelect.co.uk](mailto:info@xelect.co.uk). Informal enquires should be made to Dr Tom Ashton or Professor Ian Johnston (01334 845204). Closing date Friday 4th May. [marie.smedley@xelect.co.uk](mailto:marie.smedley@xelect.co.uk)

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## StockholmU Experimental Evolutionary Biology

Experimental and Evolutionary Biology Tenure Track Position

as Assistant Professor \*\*

\*at the Department of Zoology < <http://www.zoologi.su.se/en/index.php> >\*\*. Closing date:—28—June—2018.\*

The Department of Zoology has a long history of basic and applied research on animals ranging from insects to large mammals, at five divisions: Animal Ecology, Ethology, Population Genetics, Functional Animal Morphology and Systematic and Evolutionary Zoology. The Department has a staff of around 100 employees, of which about 40 are PhD students. In addition, the Department keeps a research station (Tovetorp) south of Stockholm with facilities for various field and laboratory experiments. The advertised position will be affiliated to the Division of Functional animal morphology, which has a long tradition of research in neuroscience, endocrinology, reproductive biology, and more recently insect sensory physiology and behaviour, as well as genomics and the evolution of life history traits of insects. At present the organisms under study are insects, particularly *Drosophila*, *Bactrocera*, bumblebees and butterflies, and the water flea *Daphnia*, for all of which rearing facilities are available. Access to state-of-the-art imaging equipment, as well as genomics and bioinformatics resources are provided by affiliated core facilities.

\*Subject\*\* \*Functional animal morphology

\*Subject—description\*\* \*Experimental biology with a focus upon the physiology or functional morphology of animals

\*Main responsibilities\* Research and in addition some teaching and supervision.

\*Qualification requirements\*\* \*In order to qualify for the position of assistant professor, the applicant must have completed a doctoral degree in Sweden or an equivalent degree from another country. In the first instance, an applicant should be considered who has received such a degree no more than five years before the deadline for applications. However, an applicant who has received such a degree earlier may be considered under special

circumstances.

All teaching positions at Stockholm University require the ability to collaborate and the general ability and suitability to perform one's duties.

**\*Assessment criteria\*\*** \*In the appointment process, special attention will be given to research skills. Teaching skills will also be considered. The assessment of research skills will focus primarily on merits within the subject area of the position.

**\*Terms of employment\*\*** \*For this position the assistant professor is employed until further notice, but no longer than six years. The contract may be extended to a maximum of eight years under special circumstances, such as due to sick leave or parental leave.

An assistant professor may, on application, be promoted to a permanent position as associate professor. Specific criteria for promotion from assistant professor to associate professor have been established by the Faculty of Science < <http://www.science.su.se/english/> >.

An application for promotion to associate professor should be submitted to the faculty at least nine months before the appointment as assistant professor expires. At the time of promotion, the candidate is expected to be able to carry out teaching and administrative duties that require proficiency in Swedish.

**\*Additional information\*\*** \*This position, in Swedish "biträdande lektor", is a tenure track position and the qualification requirements and terms of employment are regulated by the Higher Education Ordinance (SFS 2017:844).

Since most lecturers at the department are men, applications from women are particularly welcome. Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

**\*Contact\*** Further information about the position can be obtained from the Head of the Department, Professor Linda Laikre, telephone: +46 8 164283, [linda.laikre@popgen.su.se](mailto:linda.laikre@popgen.su.se).

For questions regarding the application process, please contact administrator Katarina Gustafsson, telephone: +46 8 16 22 92, [katarina.gustafsson@su.se](mailto:katarina.gustafsson@su.se).

**\*Application\*** <https://www.su.se/english/about/working-at-su/jobs?rmpage=job&rmjob=5426&rmlang=UK>\*\* /Stockholm University - our education and research produce results./

– Linda Laikre Professor, Head of Department Head of Division of Population Genetics Director of Studies in Population Genetics Department of Zoology Stockholm University SE-106 91 Stockholm,

Sweden phone: +46 8 164283, +46 705 254574  
email: [linda.laikre@popgen.su.se](mailto:linda.laikre@popgen.su.se) [www.zoologi.su.se](http://www.zoologi.su.se) [twitter.com/zoology\\_su](https://twitter.com/zoology_su)

Linda Laikre <[linda.laikre@popgen.su.se](mailto:linda.laikre@popgen.su.se)>

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## SwedishGotland FieldAssist MayJune2018

We offer expenses-paid field assistant positions in a long-term project conducted in the wild collared flycatcher population on the Baltic island of Gotland (Sweden). Assistants will have their accommodation and other expenses covered, we also offer a salary add-on depending on experience and declared period of work in the project. Lodging will be provided in a large house rented for the period of the field season.

Basic duties: performing nest-boxes checks and monitoring of breeding pairs; ringing of nestlings; capture of adult individuals, ringing and basic morphological measurements. Prior experience with wild birds handling and a valid driving license will be an advantage. The work is not especially exhausting but sometimes requires long hours in the woods, in diverse weather conditions.

Period of work: half of May until end of June/first days of July, or a shorter period within this time window.

For more details and to apply please contact: Lars Gustafsson (Uppsala University) [lars.gustafsson@ebc.uu.se](mailto:lars.gustafsson@ebc.uu.se) or Szymon Drobnik (Jagiellonian University) [szymek.drobnik@uj.edu.pl](mailto:szymek.drobnik@uj.edu.pl).

Szymek Drobnik <[geralttee@gmail.com](mailto:geralttee@gmail.com)>

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## TexasParksWildlife FishGeneticistBioinformaticist

We have a single opening for a geneticist/bioinformaticist that will work with a team of 3 other fisheries research biologists. The position will support research into the biology, population genetics, and genomics of marine organisms on the coast of Texas and greater Gulf of Mexico. There is broad latitude in devising individual projects and working through



the team; however most projects at our facility have the common objective of supporting management and conservation of coastal resources in the Gulf.

The position closes April 20. Information and application instructions can be found at the link below:

<https://www.governmentjobs.com/careers/tpwd/-jobs/2042738/natural-resources-specialist-i-ii-iii-iv-geneticist-bioinformaticist>

Joel Anderson

Natural Resource Specialist

Perry R. Bass Marine Research Lab

Texas Parks and Wildlife

Ph: 361-972-5483

Fax: 361-972-6352

Joel Anderson <Joel.Anderson@tpwd.texas.gov>

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## UBern EvolutionaryBiology

The Institute of Ecology and Evolution (IEE), Faculty of Science, University of Bern, is seeking highly motivated applicants for a

Lecturer (Dozent I, 100%) position in Community Ecology ad interim >From 1 February 2019 to 31 July 2020

Responsibilities:

Applications are sought from scientists with an outstanding research record and pertinent teaching experience in Community Ecology. The candidate will be expected to teach various courses in community ecology and to supervise students, including BSc and MSc theses. We are searching for an active researcher who can serve as a model for students in ecology and evolution. Collaborations with other researchers of our institute are highly welcome. Senior researchers are also encouraged to apply.

Requirements:

The candidate should have a PhD and habilitation (or equivalent) in community ecology or a related field, and several years of postdoctoral research and teaching experience. The successful candidate will take responsibility for teaching community ecology at undergraduate and graduate levels. All graduate and advanced undergraduate teaching at the IEE is in English.

Further information: We offer a very stimulating, multi-

national research community with excellent infrastructure. Information about the institute can be found at [www.iee.unibe.ch](http://www.iee.unibe.ch) Applications must be submitted by e-mail before 15 May 2018 as one PDF file to [susanne.holenstein@iee.unibe.ch](mailto:susanne.holenstein@iee.unibe.ch) and should include a letter of motivation with a short research plan for the employment period, a CV including the funding history, a list of previous teaching and supervised BSc, MSc and PhD students, a list of publications, and the names and contact information of two referees. Appointment will be as a lecturer (Dozent I, temporary). The starting date for the position is February 1st 2019. For further information, please contact the institute secretary, Susanne Holenstein.

Prof. Dr. Michael Taborsky Acting Director IEE

University of Bern Institute of Ecology and Evolution  
Baltzerstrasse 6 3012 Bern +41 (0)31 631 45 11

“[susanne.holenstein@iee.unibe.ch](mailto:susanne.holenstein@iee.unibe.ch)”

<[susanne.holenstein@iee.unibe.ch](mailto:susanne.holenstein@iee.unibe.ch)>

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## UCollege Dublin SpeciesDiversity

University College Dublin is seeking to appoint a Lecturer / Assistant Professor in Macroecology, to the School of Biology & Environmental Science.

\*Closing Date: 17:00hrs (local Irish Time) on Tuesday, 1 May 2018.\*

Details and application link available here:

<http://www.jobs.ac.uk/job/BIX459/lecturer-assistant-professor-in-macroecology/>

\*Position Summary:\* We are looking for a candidate who uses applied or theoretical macroecology approaches to provide insight and understanding into the patterns and processes shaping species diversity, ecological systems and community ecology. The successful candidate should have interests in animal study systems and proven field skills, and will be expected to lead an original and innovative scientific research programme and contribute to the development of the discipline areas of ecology and zoology. Classic ecological questions amenable to study through the techniques of macroecology, and relevant to this post, include questions of species richness, latitudinal gradients in species diversity, the species-area curve, range size, body size, and species abundance. The candidate should complement and engage with current academic staff and research

programmes within the School and wider UCD community.

Jon Yearsley <jon.yearsley@ucd.ie>

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## ULjubljana Slovenia ConservationBioinformatics

Researcher - Bioinformatics (with relation to Genetics, Ecology and Wildlife Conservation)

University of Ljubljana, Biotechnical Faculty, Dpt. of Biology, Animal Ecology Research Group

Application Deadline: 7 May 2018, or until the position is filled

A full time post-doc or doctorate researcher position is available at Dpt. for Biology, Animal Ecology Research Group. We encourage applications from highly-motivated post docs or researchers with good programming skills. We will also consider candidates with the required skill set but without a finished PhD, with a possibility to enroll in graduate studies at our institution.

Starting date: as soon as possible, but no later than June 2018.

Duration: 1 year, with possibility of extension.

Location: Ljubljana, Slovenia.

Keywords: Bioinformatics, Genetics, Wildlife Conservation, Ecology, Brown bear, Ursus arctos, Eurasian lynx, Lynx lynx.

### JOB DESCRIPTION

We invite applications from highly motivated candidates with advanced computer programming / informatics background and passion for wildlife ecology and conservation. The work will be related to two international Life projects, LIFE DINALP BEAR and LIFE LYNX, with strong emphasis on conservation genetics of brown bear (*Ursus arctos*) and Eurasian lynx (*Lynx lynx*).

Specifically, the candidate will work on programming a stochastic simulation system for brown bear population dynamics in Northern Dinaric Mountains and stochastic genetics / population dynamics simulations of lynx population augmentation. Some programming work will also be required in optimization/programming of bioinformatics pipelines for analysis of next-generation sequencing data.

Since we're a multidisciplinary and dynamic group, the candidate will also have a possibility to engage in other activities of the group (e.g. fieldwork, other research) when the main obligations will permit. The candidate will also have the opportunity (but not obligation) to develop hers/his own personal research interests within the scope of the work we do. We are looking for candidates that are able to work independently on specific tasks but still function as a part of the team. The working language is English, everyone in the research group speaks it and we have other foreigners working with us.

### RESEARCH GROUP DESCRIPTION

We're a dynamic, multidisciplinary group that combines "classic" approaches in animal ecology and conservation with molecular genetics and social sciences. While some of our projects are oriented in basic ecology, much of our work is conservation oriented, mainly in conservation of European large carnivores: the wolf, the bear and the lynx. We have considerable laboratory, computing and field resources, and engage in a variety of research projects.

Some of our past/current projects (the ones that have nice webpages :o )

<http://fp7hunt.net/> <http://www.volkovi.si> <http://dinalpbear.eu> <https://www.lifelynx.eu/> EXPECTED SALARY, LIVING

The total net salary would be between 1100pounds 'V 1500pounds , depending on the academic title (different for BSc, MSc or PhD).

The salary is not great compared to western European countries, but enough for a decent living in Slovenia. Living costs in Slovenia are not that high, and Ljubljana is a nice place to live 'V there are both mountains and the Adriatic Sea close by. A one to two hour drive can take you sailing / swimming / diving / windsurfing / fishing in summer, and a 1/2 hour drive skiing in winter, or hiking / rock climbing in summer. The city is very green, and wildlife areas start right at the outskirts (we've had bears enter city proper). It's a small city which makes it easy to move around, it's relatively bike-friendly, but being a capital we get much more culture (concerts, events, festivals...) than most other cities of this size. It's also clean and safe.

<https://www.visitljubljana.com> REQUIRED SKILLS AND LEVEL

The skills listed below are a must to apply to this position. Please list references or some verifiable information, or explain how we can confirm your proficiency.

Biology / Life Sciences or Mathematics / Statistics / Computer sciences background, with appropriate

achieved degree (typically a PhD, but MSc and BSc candidates will be considered).

Computer programming, advanced level. Our preferred programming languages are R, Python and C/C++. Since we do a lot of our simulation programming and analysis in R, any candidate should be either already an advanced R user or demonstrably (e.g. through showing proficiency in another programming language) willing/able to learn R to an advanced level through self-study in a very short time.

Linux use and administration, intermediate/advanced  
 We have a small HPC running CentOS Linux as our primary number cruncher which we

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## Umassachusetts Amherst EvolBiol VisitingProf

Visiting Assistant Professor (NTT) - Biology

The Biology Department at the University of Massachusetts Amherst ([www.bio.umass.edu/biology/](http://www.bio.umass.edu/biology/)) invites applications for one full-time non-tenure track position (renewable up to three years) starting fall semester 2018. The Visiting Assistant Professor will be provided with research support and mentoring through placement in an active research lab. Candidates should have completed the Ph.D. by the beginning of the appointment. Exceptional promise in research and a commitment to outstanding teaching at all levels of the curriculum are expected. Applicants must review the list of potential sponsoring laboratories/mentors (<https://www.bio.umass.edu/biology/vap-mentors>). In addition to their research role, the Visiting Assistant Professor will have a mentored teaching load of two-courses per year.

Candidates must have a Ph.D. in biology or a related discipline. In their materials, the candidate should describe how their program of research is a strong fit with one of the research laboratories available for sponsoring the candidate, and show evidence of teaching excellence and the ability to work with diverse populations/students.

Potential applicants must contact their chosen mentor,

who must be chosen from the list of eligible mentors at (<https://www.bio.umass.edu/biology/vap-mentors>). Applications should include a cover letter, curriculum vitae, a statement describing their teaching philosophy, experience, and interests, as well as the names of at least three references. Also, please arrange to have a letter from your proposed faculty mentor sent directly to Lisa Barry at [lisab@bio.umass.edu](mailto:lisab@bio.umass.edu). Applicants should apply by the priority deadline of May 7, 2018 in order to ensure consideration.

The University of Massachusetts Amherst is an Affirmative Action/Equal Opportunity Employer of women, minorities, protected veterans, and individuals with disabilities and encourages applications from these and other protected group members. The Biology Department is committed to sustaining a diverse, inclusive community of faculty, students, and staff with the conviction that such an environment catalyzes learning and cultivates ethical, informed, and prepared citizens. We are especially interested in qualified candidates whose teaching and service reflect engagement with varied perspectives and constituencies. Because broad diversity is essential to an inclusive climate and critical to the University's goals of achieving excellence in all areas, we will holistically assess the many qualifications of each applicant and favorably consider an individual's record working with students and colleagues with broadly diverse perspectives, experiences, and backgrounds in educational, teaching or other work activities. We will also favorably consider experience overcoming or helping others overcome barriers to an academic degree and career.

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## UNewMexico LabFieldTechnician

The Rudgers & Whitney Labs at the University of New Mexico are looking for a technician / supervisor to work on projects related to the ecology and evolution of plant-microbe-animal interactions.

<https://unm.csod.com/ats/careersite/jobdetails.aspx?site=13&c=unm&id=3451> Req 3451.

Duties will include work in both field and laboratory settings on projects examining the ecology and evolution of plants, plant-animal and plant-microbe interactions. Position includes lab management and training/working with our undergraduate team. Candidates should have B.A./B.S. in biology (or related field) and some hands-

on field and/or lab experience. Training will be provided, but experience with DNA techniques (PCR, sequencing), plant care and greenhouse maintenance, plant identification and vegetation sampling, insect identification, soil science, and/or microbial methods is a bonus. The position is full-time and term-limited (12-36 months). This position would be an excellent fit for someone planning on graduate study in Ecology & Evolutionary Biology, as there will be the opportunity to gain experience in a number of research areas and to co-author papers.

Kenneth Whitney <whitneyk@unm.edu>

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## UOregon EvolutionDataCenter ManagerProgrammer

The Phillips lab in the Institute of Ecology and Evolution at the University of Oregon is seeking a Manager for a Data Coordination Center (DCC) (Research Assistant/Associate) for the three-institute consortium project, the Caenorhabditis Intervention Testing Program (CITP). UO Job #522103.

<http://careers.uoregon.edu/cw/en-us/job/522103/-data-center-manager-and-developer> The Phillips lab conducts research on the structure and evolution of the genes and genomic elements underlying complex phenotypic traits such as behavior, sexual reproduction, life history, stress resistance, and longevity. Through a consortium with Rutgers University and the Buck Institute, they form the Caenorhabditis Intervention Testing Program (CITP). The CITP aims to find robust and reproducible chemical interventions to extend life by testing the effects of chemical compounds across many strains of the nematode *Caenorhabditis* and in multiple laboratories across the country. This is an opportunity to help translate discoveries in basic science to help improve the quality of life and human health.

The key responsibilities of the DCC Manager and Developer include: - Maintaining and updating the project data pipeline from assorted lifespan and healthspan experiments at the three institutions to the centralized Filemaker Pro 16 database. - Working with the PIs and technicians to simplify data quality control and metadata validation. - Working with project scientists to provide reports and output files for statistical analyses. - Writing or updating existing scripts that allow smooth exporting and importing of data from one platform to another, as well as defining new data types as the project implements new health-related measures. -

Working with the consortium institutes on any system-wide updates to software, operating systems, or specific experimental needs. We are testing a major upgrade to our Automated Lifespan system which requires updating our operating system to Scientific Linux 7. - Helping to maintain the systems integrity and integration of existing laboratory data acquisition systems, including our scanner-based automated lifespan machines.

The CITP project focuses on screening various compounds for their ability to extend the lifespan and “healthspan” of 21 isolate strains of three species of nematode worms in the genus *Caenorhabditis*.

Minimum Requirements - BSc, MSc (for Assistant) or PhD (for Associate) in computer science, engineering, mathematics, biology or a related field. - Proven competence with Filemaker, MySQL, R and standard data formats in Excel. - Experience working with scientific data in a multi-institutional or multi-department environment.

Professional Competencies - The ability to work as a member of an exciting, interactive team. - Excellent communication skills. - Excellent time management skills requiring little direct supervision. - An interest in the biology of aging, age-related diseases, or pharmacology.

The University of Oregon is proud to offer a robust benefits package to eligible employees, including health insurance, retirement plans and paid time off. For more information about benefits, visit <http://hr.uoregon.edu/-careers/about-benefits>. The University of Oregon is an equal opportunity, affirmative action institution committed to cultural diversity and compliance with the ADA. The University encourages all qualified individuals to apply, and does not discriminate on the basis of any protected status, including veteran and disability status.

UO prohibits discrimination on the basis of race, color, sex, national or ethnic origin, age, religion, marital status, disability, veteran status, sexual orientation, gender identity, and gender expression in all programs, activities and employment practices as required by Title IX, other applicable laws, and policies. Retaliation is prohibited by UO policy. Questions may be referred to the Title IX Coordinator, Office of Affirmative Action and Equal Opportunity, or to the Office for Civil Rights. Contact information, related policies, and complaint procedures are listed on the statement of non-discrimination.

In compliance with federal law, the University of Oregon prepares an annual report on campus security and fire safety programs and services. The Annual Campus Security and Fire Safety Report is available online at <http://police.uoregon.edu/annual-report>. Patrick C.

Phillips, Ph.D. Acting Executive Director | Professor of Biology Phil and Penny Knight Campus for Accelerating Scientific Impact <https://www.uoregon.edu/accelerate> <https://www.uoregon.edu/~pphil>

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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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## UPittsburgh Tech AmphibianEvolution

The Richards-Zawacki Lab (<http://www.rzlab.pitt.edu/>) in the University of Pittsburgh Dietrich School of Arts & Sciences is seeking a Laboratory Technician/Manager that will manage the maintenance of laboratory equipment, purchase supplies, and supervise animal (amphibian) care and undergraduate lab assistants. The incumbent will be responsible for generating and analyzing molecular data for ongoing projects on the topics of amphibian ecology, evolution, and conservation, and providing technical assistance to other personnel involved in these projects who are using similar techniques.

Management experience and excellent communications skills, as well as experience with basic molecular and microbiology techniques, are preferred. The incumbent will train new personnel who are recruited to the project and supervise the efforts of undergraduates. This includes regular meetings with personnel and supervision of notebook keeping. The incumbent will report to the primary investigator and work in collaboration with the primary investigator to manage laboratory activities.

The Dietrich School of Arts & Sciences is committed to building a culturally diverse staff.

Excellent interpersonal and relationship-building skills and the ability to work effectively with a wide range of individuals and constituencies in support of a diverse community.

Please see the full position posting for more information and to submit an application: <https://www.pittsource.com/postings/157180> For questions about the position, please contact Corinne Richards-Zawacki ( [clz17@pitt.edu](mailto:clz17@pitt.edu) )

Corinne L. Richards Zawacki, Ph.D. email: [cori.zawacki@pitt.edu](mailto:cori.zawacki@pitt.edu) Associate Professor, Department of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

“At night I went out into the dark and saw a glimmering star and heard a frog and nature seemed to say, well do not these suffice?” - Ralph Waldo Emerson

Cori Zawacki <[cori.zawacki@pitt.edu](mailto:cori.zawacki@pitt.edu)>

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## URhodeIsland ResTech 1yr

Looking for a full-time lab technician that would like to join the shared lab of Hollie Putnam ([putnam-lab.com](http://putnam-lab.com)), Jon Puritz ([marineevoco.com](http://marineevoco.com)) and Carlos Prada (<https://www.carlosprada.org>) at the University of Rhode Island. This is a one year position with the possibility of renewal. We are looking for someone with molecular biology and marine field experience. You can find the full add here: <https://jobs.uri.edu/-postings/3278> Carlos Prada Assistant Professor Department of Biological Sciences University of Rhode Island 120 Flagg Road Kingston, RI 02881 [P] 401-874-5767 [prada@uri.edu](mailto:prada@uri.edu) <http://www.carlosprada.org> Carlos Prada <[prada@uri.edu](mailto:prada@uri.edu)>

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## UVienna TheoEvolutionaryBiology

Dear all,

The Faculty of Life Sciences at the University of Vienna seeks applications for the position of a Full Professor in Theoretical Evolutionary Biology.

The extended deadline for application is May 8, 2018.

Vienna is not only one of the most livable cities in the world, it also offers a great scientific environment, in particular for Evolutionary Biology.

Please find details of the position under:

<http://personalwesen.univie.ac.at/en/jobs-recruiting/-professorships/detail-page/news/theoretical-evolutionary-biology/> Best wishes

Uli Technau



Univ.-Prof. Dr. Ulrich Technau Dept. for Molecular Evolution and Development Centre for Organismal Systems Biology Faculty of Life Sciences University of Vienna Althanstrasse 14 1090 Wien

Tel. +43-(1) 4277-57000 Mobile: +43-664-6027757000  
Website: <http://molevodevo.univie.ac.at> Nick BARTON <nick.barton@ist.ac.at>

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## UVirginia Daphnia Technician

The Department of Biology is looking to hire a Research Technician in the Bergland lab at the University of Virginia which uses *Daphnia* to study ecological and evolutionary genetics. Current projects in the lab include the adaptive evolution of predator induced phenotypic plasticity through time and space in *Daphnia*.

The technician will assist with ongoing research projects as well as day-to-day lab activities. Responsibilities of the position include, but are not limited to, ordering materials and supplies, maintenance of laboratory *Daphnia* stocks, training and management of undergraduate work study students, DNA and RNA extractions, performing phenotyping assays, data management, and assisting with field collections locally. Ideally, we seek an enthusiastic individual who works well with others and has a willingness to learn and take on new challenges.

This position is restricted and is contingent upon the availability of funding.

This position is open until filled.

To apply, search for position 0622981 at UVA's HR department website: [jobs.virginia.edu](http://jobs.virginia.edu)

posted by: Alan Bergland [aob2x@virginia.edu](mailto:aob2x@virginia.edu)

"Bergland, Alan Olav (aob2x)" <[aob2x@virginia.edu](mailto:aob2x@virginia.edu)>

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## WashingtonU Teaching Evolution

Dear Colleagues

we are looking for a lecturer to join our team in Principles of Biology starting in Fall 2018. The description of the position is attached.

If you know of PhD-level folks interested in teaching full

time with strong expertise in evolutionary biology, please refer them to this opening # 40052 (google: Washington University job opening #40052). Please share this information with people you think might be qualified and interested.

Kathy

Position description:

We seek a full-time lecturer in Biology who will help with teaching undergraduate laboratory and lecture courses. Specific immediate responsibilities will include co-teaching Principles of Biology each fall, specifically the section on evolution biology and population genetics. In addition, the position entails joining a team of PhD-level lecturers and teaching professors as an instructor in multiple lab sections in each semester that are a required part the Principles of Biology two semester sequence. Additional duties will include additional teaching in an area of interest and strength in the Spring and advising majors in the Biology.

Required Qualifications: Ph.D. In an evolution-related field, demonstrated teaching record.

Preferred Qualifications: Preference will be given to candidates with a demonstrated ability to teach an evolution course for undergraduate students at the introductory level. There is potential for the candidate to develop a new laboratory or other majors course to be offered in spring semesters. Familiarity with and demonstrated use of student-centered, active learning strategies is strongly preferred.

"Losos, Jonathan" <[losos@wustl.edu](mailto:losos@wustl.edu)>

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## Worcester MA Visiting Prof Evolution

College of the Holy Cross

Department of Biology

Two Full-Time Visiting Faculty Positions in Biology (Ecology, Evolution and Organismal Biology)

GENERAL INFORMATION

The Department of Biology at the College of the Holy Cross invites applications for two visiting full-time faculty appointments in Ecology, Evolution and Organismal Biology for the 2018-19 academic year to begin in August 2018. We are seeking candidates who can contribute to the teaching of courses such as General

Ecology (with lab), Evolution, Environmental Science, and courses dealing with specific groups of organisms (e.g., entomology, ornithology). More detailed information is available at the Biology Department website: (<https://www.holycross.edu/academics/programs/-biology/faculty-staff/visiting-assistant-professor>). Visiting full-time faculty teach three courses each semester, with a lab section counted as a full course, and are eligible for travel support and reimbursement of relocation costs within the College's published policies. All full-time appointments offer competitive salaries and include full benefits.

#### QUALIFICATIONS

Candidates must demonstrate commitment to, and excellence in, undergraduate teaching as informed by current practice and scholarship in the field. Strong preference will be given to candidates who have completed a Ph.D.

Please submit a cover letter, current curriculum vitae, statement on teaching expertise and interests, transcripts, and two confidential letters of recommendation. In your cover letter, please address the ways you might contribute to and further the College's core commitment to diversity and inclusion that is part of its mission as a Jesuit, undergraduate liberal arts college. For more information, please visit <http://www.holycross.edu/-mission> and <http://holycross.edu/diversity>. < <http://holycross.edu/campus-life/diversity-and-inclusion> > To learn more about faculty life at the College, applicants are encouraged to visit <http://holycross.edu/join>. The College of the Holy Cross uses Interfolio to collect faculty

job applications electronically. Please submit all application materials to <https://apply.interfolio.com/49857>. For full consideration, candidates are encouraged to submit their materials by April 13. Contact Karen Ober, Search Chair, (508) 793-3046 or [kober@holycross.edu](mailto:kober@holycross.edu), with any questions related to this search.

#### EQUAL OPPORTUNITY EMPLOYMENT STATEMENT

The College of the Holy Cross is a highly selective Catholic liberal arts college in the Jesuit tradition. It enrolls about 2,900 students and is located in a medium-sized city 45 miles west of Boston. The College seeks faculty members whose scholarship, teaching, advising, and on- and off-campus service demonstrate commitment to the educational benefits of a richly diverse community. Holy Cross aspires to meet the needs of dual-career couples, in part through its membership in the Higher Education Consortium of Central Massachusetts (<http://www.heccma.org>) and the New England Higher Education Recruitment Consortium (<https://new-england.hercjobs.org/>). The College is an Equal Employment Opportunity Employer and complies with all Federal and Massachusetts laws concerning equal opportunity and affirmative action in the workplace.

– Dr. Karen A. Ober Associate Professor Department of Biology College of the Holy Cross Worcester, MA 01610 PH: 508-793-3046 FAX: 508-793-2696 e-mail: [kober@holycross.edu](mailto:kober@holycross.edu)

“Ober, Karen” <[kober@holycross.edu](mailto:kober@holycross.edu)>

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## BangorU TropicalForestBiodiversity

Other: Panama. VolResAssist. Tropical Forest Ecology.  
Bangor University, UK 'V Smithsonian Tropical Research Institute, Panama

We are looking for a highly motivated volunteer research assistant to support us in unravelling the mechanisms driving secondary succession of tropical forests.

Research 'V Hyper-diverse mature tropical rainforests have been largely degraded due to human expansion. Recovering forests present >70% of the global forest cover. These secondary forests can restore some of the original forests' benefits, yet they recover slowly and differ to mature forests in tree species composition. Understanding the mechanisms driving tropical forest dynamics following disturbance is imperative to promote the recovery of ecosystem functionality and mitigate land-use impacts. Species-specific interactions between trees and their natural enemies that have evolved for thousands of years might be the key. Our current project will assess the impact of soil fungi in secondary succession of tropical forests. The project will involve field work and a large greenhouse study in Gamboa, Panama. This collaborative project between Bangor University (UK), Bayreuth University (Germany) and the Smithsonian Tropical Research Institute (USA, Panama) will offer an ideal opportunity to gain research experience in the tropics!

Job Description 'V The intern will assist in a variety of tasks, involving field work (e.g. seed collection), intense manual labour (e.g. soil sieving) and greenhouse work. Working hours will vary strongly between days, but working weeks will never exceed 45 hours. Applicants must be in good physical condition to be able to meet the demands of working sometimes long hours under challenging tropical field work conditions, i.e. high humidity and heat. Ability to drive a 4x4 transmission truck is desirable but not required. We expect the intern to have a strong interest in ecology and to be willing to follow protocols to ensure the quality of data. We are more than happy to help in developing and discussing ideas for own research projects. We will contribute 500

USD to the flight costs. Due to a limited research budget, we cannot offer accommodation, but will help in finding a place to live in Gamboa (rooms in shared flats are available from 200-250 USD per month, including all bills). Start date is between May and August 2018, with earlier availability being preferred. A minimum stay of 3 months is required. For applicants being able to join the project in mid-May, the minimum duration can be negotiated.

Location 'V Gamboa is a small town next to the Panama Canal. With its vibrant scientific community, it presents a stimulating background to develop and exchange research ideas and explore a broad variety of ecological research in the Tropics. Gamboa is an ideal base to discover Panama and Central America: on your daily stroll through the town you can watch huge ships passing by on the canal or discover the forest that starts directly behind the greenhouses with its fascinating wild-life (toucans, gigantic butterflies, agoutis, etc.). Panama City can be reached in 45 min via an adventurous bus ride.

Applicants should send a cover letter, CV and the names and e-mail addresses of at least two professional or academic references to Anita Weissflog (anita.weissflog@bangor.ac.uk). Shortlisted applicants will be invited for a Skype chat.

This position is open from now on. There is no deadline for applications.

I am looking forward to hearing from you! Cheers,  
Anita

anita.weissflog@bangor.ac.uk

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## Brazil VisitingProfessorSystematics

The Post-Graduation Program in Animal Biology of the Federal University of Pelotas, Brazil, has a job opportunity for a foreigner visiting professor in animal ecology, systematics or genetics: Lancado edital para selecao de professores visitantes na pos-graduacao

A PRPPGI lancou, na manha desta terca-feira (17),

o edital para selecao de professores visitantes para os  
progra...

Thanks for sharing!

All the best,

Rafael Antunes Dias Departamento de Ecologia, Zoologia e Genetica, Instituto de Biologia, Universidade Federal de Pelotas, Campus Universitario Capao do Leao, s/no, CP 354, CEP 96010-900, Pelotas, RS, Brasil. Telefone: (53) 3275-7340.

Rafael Dias <rafael\_antunes\_dias@yahoo.com.br>

## MolluscEvolution StudentGrants

Dear all

Unitas Malacologica offers member-supported small grants for student research activities in malacology.

Any project, related to any kind of mollusc, anywhere, in any field of science, will be considered. There is no restriction on how the funds should be spent, though the funds should not be used to supplement the income of the awardee, and we do not support projects with direct commercial or industrial applications.

These awards are generally granted to PhD students who undertake a small, self contained project related to their dissertation research. Awards will be made up to a maximum of 1000 euro (= \$1080 USD). Usually two or three awards are granted each year, and the normal value is around 750 euro.

The next deadline for applications is 15 May 2018.

To apply - submit the application form, and a letter of recommendation, by email to [j.sigwart@qub.ac.uk](mailto:j.sigwart@qub.ac.uk)

The application form and links to reports from past award winners is available at [www.unitasmalacologica.org/projects.html](http://www.unitasmalacologica.org/projects.html) Please note we have also recently updated instructions to join the MOLLUSCA email list [www.unitasmalacologica.org/links.html](http://www.unitasmalacologica.org/links.html) Please spread the word, and good luck to all applicants!

Cheers,

Julia

– Dr Julia Sigwart Queen’s University Belfast, Marine Laboratory <http://www.qub.ac.uk/qml/People/Sigwart> sabbatical address (2015-2018): University of California, Berkeley, Museum of Paleontology

Julia Sigwart <[j.sigwart@qub.ac.uk](mailto:j.sigwart@qub.ac.uk)>

## Namibia Baboon VolFieldWork

We are currently advertising 3 volunteer positions with the Tsaobis Baboon Project (see <https://www.zsl.org/science/research/baboon>) The Tsaobis Baboon Project is a field-based wildlife research programme that studies desert baboons in Namibia. Every year, we recruit a small team of field volunteers to assist with our scientific work.

The Tsaobis Baboon Project is a long-term study of wild desert baboons in Namibia. We are currently recruiting Volunteer Field Assistants for our 2018 field season. These positions combine practical research with training and are entirely field-based. The volunteers are trained by and work alongside doctoral students and postdoctoral researchers, assisting with their studies and contributing to the wider research activities of the Baboon Project.

The fieldwork will primarily involve daily follows of baboon troops on foot, collecting data on the behaviour of individually recognisable animals, together with monthly vegetation surveys, and the capture of both study troops to fit GPS collars and collect measurements and samples. This year, our research focus is on baboon social behaviour and female reproductive strategies.

Three Volunteer Field Assistant positions are currently available, each running for three months from late August to late November. Once the volunteers arrive in Namibia, the Tsaobis Baboon Project covers all their work-related costs, including all meals and accommodation. We will also cover the costs of the volunteers’ research visas and travel insurance. On the successful completion of fieldwork, we also contribute a minimum of pounds 75 towards the cost of the volunteers’ air ticket. The Volunteer Field Assistants will learn and implement a range of research skills related to the study of animal behaviour and ecology. Following training, the fieldwork will primarily involve daily follows of baboon troops on foot, during which they will collect data on the behaviour of individually recognisable animals, together with monthly vegetation surveys and wider ecological monitoring related to the baboons’ environment. This year we will also be briefly capturing our study troops to collect routine measurements and samples. Who are we looking for?

These positions are open to all with an interest in animal

behaviour and ecology. We are particularly keen to hear from applicants who:

- \* Are friendly, easygoing people, happy to live in small team under basic conditions at a remote field site
- \* Are strongly motivated, reliable and committed
- \* Have good levels of physical fitness and stamina - you will be following the baboons on foot from dawn to dusk over mountainous terrain in extreme heat
- \* Show good initiative, with a willingness to learn and show attention to detail
- \* Have a full, clean driving licence.

What do volunteers get out of it?

- \* An amazing opportunity to share the lives of wild baboons in a beautiful desert landscape
- \* An opportunity to learn new skills and gain experience, especially those relevant to research in behaviour, ecology, and conservation
- \* An opportunity to be involved in a long-term project on African wildlife, hosted by an international research institution and conservation charity
- \* Most of our volunteers are graduate students who use their experience on the Baboon Project as a stepping stone on to Masters and PhD degree course

If you would like to apply, you will need to upload a CV and covering letter, using the online application on the following website : <https://volunteeringopportunities-zsl.icims.com/jobs/2032/volunteer-field-assistant%2c-tsaobis-baboon-project/job>

The covering letter should explain why you would like to work on the project, and the CV should include the names of two referees with e-mail contact details. The covering letter and CV should be uploaded as a single PDF document, with the covering letter on a separate page preceding the CV.

Closing date for applications: 10am, Monday 16 April 2018.

Please note: We will notify successfully shortlisted candidates by the evening of Tuesday 17 April, and interviews will be held in London the following week on Tuesday 24 April and Wednesday 25 April. Applicants should keep these dates free for interview, since no other dates will be available. Telephone/skype interviews will be possible for overseas applicants or those that genuinely cannot travel to London to attend the interview.

Jules Dezeure <[jules.dezeure@etu.umontpellier.fr](mailto:jules.dezeure@etu.umontpellier.fr)>

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## Queensland Avian VolFieldAssistants

We are looking for field assistants to help search nests of a small bird, fairy gerygone and large-billed gerygone for PhD project (Australian National University, Canberra). The main objective of this research is to gain a better understanding of the breeding ecology of gerygone species, and the coevolution between gerygone species and little bronze-cuckoo. Research will be conducted in Queensland, Australia. We will be based in Kutini-Payamu (Iron Range) National Park, and Cairns city, and travel to several sites in these areas. Volunteer field assistants are needed from Jul. 'V Nov. or Dec. 2018 for full period. The exact dates flexible but need to be around this time.

Overall duties will include nest searching and monitoring, recording begging calls and adult calls for cuckoos, and data entry. Previous experience with fieldwork is highly desired, and nest searching experience is also preferred, but not required. The large-bill gerygone build nests over the water, and the height of nests varies from 1m to 5m. The fairy gerygone's habitat is mainly at the edges of rainforest, but poorly known (our main work will be to find their nest). The study site is rugged, hot, and venomous snakes and ticks are quite common. Working days are long, with early starts, six days a week. Therefore, applicants must have good physical fitness to walk along the creek with a heavy ladder, withstand harsh conditions at the site, and maintain an energetic attitude despite long hours in hot and humid conditions. Work schedules and duties will vary, so flexibility is a must. Applicants should work well alone and in a small group and have a sense of direction to work in remote areas. Previous experience with fieldwork is highly desired, and nest searching experience is also preferred, but a positive attitude is much more important than tons of field experience.

Housing will be provided, and you can get reimbursed for food and flights up to \$750 AUD per month and assistants will enjoy fantastic wildlife viewing opportunities (Wallabies, platypus, koalas, kookaburra, etc.), proximity to Queensland rainforest and the surrounding field areas.

To apply, send a cover letter detailing interests, previous relevant field research experience, dates of availability and a CV as well as a list of names and



contact information for 2 referees to Hee-Jin Noh (hjnoh891@gmail.com).

Please feel free to enquire with any questions related to the application process or on the project in general.

Hee-Jin Noh <hjnoh891@gmail.com>

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## Query LabFumeHoods

Dear all,

I am reaching out to the EvolDir community for opinions. We are building a molecular/structural botany lab, and as part of it are considering installing three fume hoods. One for DNA extraction, one for RNA extractions/insitu hybridization work, and a third one for anatomy purposes.

We were asked by the architects if we would like duct fume hoods or ductless (recirculating) fume hoods. From the construction side ductless hoods are a cheaper alternative, but none of us (scientists) involved in the lab planning has ANY experience with ductless hoods. So we would like to ask people who have experience with those, three questions:

1. Do they really work? If they do, what kind of procedure you perform?
2. How noisy are them compared with a ductless fume hood? Can you or do you have to have them on at all times?
3. Are they really cheaper when you take into account the filters? How often do you have to change those?

Please feel free to add any comments besides these three questions! We really appreciate your help and if anybody is interested in knowing the answers I get, I will be happy to share them with you.

Best,Alejandra

Alejandra Vasco, Ph.D.Botanical Research Institute of Texas (BRIT)1700 University Drive, Fort Worth, Texas 76107Phone: 817-332-4441 Ext. 262Email: avasco@brit.org

Associate Editor: Systematic Botany, Journal of the Botanical Research Institute of Texas, Revista Mexicana de Biodiversidad

Alejandra Vasco <alevascog@yahoo.com>

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## Science business skills

[TRAINING] Business Skills for Scientists: Apply by April 20

Sustaining Biological Infrastructure (SBI) Summer Training Course

June 19-21, 2018 Washington, DC area

Application deadline: April 20th <http://esa.org/sbi/how-to-apply/> Are you struggling to keep your database, collection, field station, or lab afloat? Do you wish you had more training in business planning and financial management to help you navigate this uncertain funding environment?

The Ecological Society of America's Sustaining Biological Infrastructure (SBI) Training Initiative can help. We have recruited experts from the business world to provide hands-on training tailored to scientists. Join us to learn vital tools for strategic planning, business planning, stakeholder analysis, communication, and financial management. At the end of three days, you will have an action plan ready for your project.

Here's what alumni say about our training:

"Diversifying approaches to funding is important, and I have learned valuable skills that will help with this - not just the sources themselves, but approaches to communication and establishing partnerships as well."

"I feel more equipped to take an organized approach to managing my facility the team of instructors, advisors, and guest speakers was phenomenal."

"I learned financial management and business model preparation more clearly than I thought I ever would! Every bit of the course was perfectly conducted concise, excellent material, presented in interesting ways with interactive pieces, and designed to allow us to network with each other."

"My main objective in taking the course was to get help in developing business and strategic plans. I got much more than that in learning to approach corporations, private foundations, and individual donors."

We will also be training in Fort Collins, Colorado on October 16-18, 2018. If you would like to join our mailing list to learn of future opportunities, please let us know.

For more information: Email: Jill Parsons, [jill@esa.org](mailto:jill@esa.org)

Website: <http://esa.org/sbi/> Jill Petraglia Parsons Science Programs Manager

Ecological Society of America 1990 M Street, NW Suite 700 Washington DC 20036 202.833.8773, ext. 209 202.833.8775 Fax

"Jill P. Parsons" <jill@esa.org> "Jill P. Parsons" <jill@esa.org>

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## Smithsonian Conservation Events

Twitter event: Smithsonian #EarthOptimism2018: April 16-22

#EarthOptimism2018: Sharing Stories of Conservation Success on Social Media - April 16 - 22

The Smithsonian Conservation Commons invites you to celebrate Earth Optimism 2018 with a series of events the week of Earth Day. Here's how to get involved:

- Free Online Conservation Success Storytelling Workshop Begins April 16<sup>th</sup> - #EarthOptimism2018 MOOC
- Take a 5-session workshop through edX.org to learn how to identify and craft conservation success stories to share on Twitter. Enroll here!

- Celebrate Success on Twitter: April 16-22 - #EarthOptimism2018 and #ImAnEarthOptimistBecause. Share your conservation success stories or reasons why you are an earth optimist using #ImAnEarthOptimistBecause. Tag all conservation success stories with #EarthOptimism2018

- Find a Sister Event near you or consider planning your own!!

Celebrate Earth Day with Optimism!

"Coyle, Brian J." <CoyleB@si.edu> "Coyle, Brian J." <CoyleB@si.edu>

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## Software GenomicClineAnalysis R

Dear Evoldir community,

I've just uploaded a new R package to GitHub for Bayesian hybrid index estimation and genomic cline analysis here:—<https://github.com/ribailey/gghybrid>

A synopsis is below. Please feel free to email me with questions or feedback.

Best regards Richard Ian Bailey [richardianbailey@gmail.com](mailto:richardianbailey@gmail.com)

gghybrid

R package for analysis of hybrids and hybrid zones. Currently includes hybrid index and genomic cline estimation for bi-allelic genomic data.

To cite package 'gghybrid' in publications use: Richard Bailey (2018). gghybrid: Evolutionary Analysis of Hybrids and Hybrid Zones. R package version 0.0.0.9000.

Basic functionality of the package is to read in SNP data in the form of structure files or similar, prepare data for analysis, carry out Bayesian MCMC hybrid index and genomic cline estimation, compare models (for either hybrid index or genomic clines) run on the same data set using the widely applicable information criterion (waic), and make plots of hybrid indices or cline curves.

gghybrid can be downloaded from within R using the following two lines of code: `install.packages("devtools"); devtools::install_github("ribailey/gghybrid")` Functions should be run in the following order: `read.data #Read in a data file in structure format or similar# data.prep #Prepare the data for hybrid index and genomic cline estimation# esth #Estimate hybrid indices# plot.h #Plot hybrid indices (optional)# ggcline #Estimate genomic clines# plot.clinecurve #Plot fitted clines (optional)# compare.models #Compare two models (either from esth or ggcline) run on the same data set using the widely applicable information criterion (optional)#`

For usage please see help files for individual functions by typing e.g. `?read.data`.

Synopsis: To understand mechanisms of speciation and the evolutionary impacts of admixture it is vital to identify loci showing restricted or biased introgression among hybridizing taxa. Genomic cline analysis provides a means to do this, by examining patterns of introgression of loci into foreign genomic backgrounds. Here I present a new R package, gghybrid, which allows hypothesis-testing on bi-allelic genomic data through Bayesian hybrid-index (proportion of allele copies coming from one of two parental reference sets) and logit-logistic genomic-cline (Fitzpatrick 2013) estimation. The package takes structure files or similar data tables as input, allows filtering of loci based on parental allele frequencies, and pooling and fixing of parameters followed by model comparison for both hybrid index and genomic clines with the Bayesian widely applicable information criterion (waic). It therefore provides great flexibility in

comparing, for example, populations, transects, genomic regions or gene networks for differing patterns of admixture and introgression. It also allows rapid creation of a genotype table, with genotypes scored according to the parent-of-origin of each allele, and contains plot functions for hybrid index and genomic cline estimates. I use an adaptive algorithm during burnin to optimize multivariate parameter proposal distributions, utilizing both the acceptance rate and the estimated parameter covariance matrix. Furthermore, given the intention for the package to be used on large whole-genome data sets, I employ recursive estimation of posterior distributions to avoid storage of the full set of posterior values and hence improve memory efficiency.

r\_1470 <r\_1470@yahoo.co.uk>

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### SouthAfrica VolResAssist PhysiologyBehaviour

Volunteer Research Assistant position at the Kalahari mole-rat project

We are looking for several volunteer research assistants to carry out exciting experiments with captive Damara-land mole-rats, *Fukomys damarensis* at the Kuruman River Reserve, in the South African Kalahari Desert. Broadly, our research investigates the influence of genes, hormones and social factors on individual developmental, growth and behaviours.

Currently, we are particularly interested in characterizing the phenotypical differences between breeding and non-breeding individuals and to develop an integrated understanding of the causes and consequences of such differences.

Applicants should be available for a period of 6 to 12 months starting as soon as possible. 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 and management (behavioural observations, collection of blood and urine samples). Other general tasks related to animal handling (hormone injections and implants) and husbandry and data handling will also be expected. One of the two applicants should feel comfortable with being involved in experiments requiring the sacrifice of experimental subjects.

Working weeks will not exceed 45 hours.

This position is particularly suited, but not exclusively, for people aiming to carry on their academic education or 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 project using the data available in our existing database.

Costs of food and accommodation while at the project will be covered.

If you are interested in this position send your CV and cover letter stating your availability to Philippe Vulllioud (philippe.vulllioud@gmail.com).

Shortlisted applicants will be invited for a Skype interview.

Deadline: 30th April 2018 (the position will remain open until filled)

philippe.vulllioud@gmail.com

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### SSB Grad Student Research Grant

The Society of Systematic Biologists (SSB) Graduate Student Research Awards assist graduate students conducting research in systematics. These grants are for collection of preliminary data or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Awards will range between \$1000 - \$2000 and approximately 25 awards will be made.

APPLICATION DEADLINE: All application materials are due on May 31, 2018 by 11:59 PM Eastern Standard Time (US).

**\*\* HOW TO APPLY \*\***

Submit all materials via the application form found on the SSB website: <http://www.systbio.org/graduate-student-research-awards.html> The application materials required are:

- + a curriculum vitae
- + brief research proposal including objectives, methods, significance, and schedule
- + budget (\$2,000 limit) and budget justification
- + two letters of recommendation.

Please see the SSB website for further details about the application materials. **\*\* ELIGIBILITY \*\***

Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications. Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply.

Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work.

\*\* CONTACT \*\*

If you have any questions, please contact the Chair of the SSB Awards Committee (Dr. Tracy Heath: awards@systematicbiologists.org).

“Tracy Heath (SSB Awards Director)”  
<awards@systematicbiologists.org>

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## UCalifornia Riverside ResIntern GuppyEvolution

### Research Internships - Evolutionary Biology

Research interns are needed to assist in a multi-disciplinary, multi-investigator, experimental study of the interactions between ecology and evolution in Trinidad, West Indies. The research is led by Professor David Reznick at the University of California, Riverside in collaboration with Joseph Travis (Florida State), Tim Coulson (Oxford), Paul Bentzen (Dalhousie U.), and Ron Bassar (Williams). We seek to integrate multiple biological fields for the study of these interactions in experimental populations of guppies in Trinidad. Duties include assisting in monthly censuses of guppy populations in montane streams. The monthly censuses include long hours in the field and laboratory. There will also be 12 days off between each census when interns can pursue an independent project.

Qualifications: We seek interns who are entertaining the possibility of pursuing graduate studies in some area of ecology and evolution and who wish to gain some additional field research experience before doing so. Research will take place in semi-remote areas of Trinidad sometimes under bad weather conditions. Applicants must be able to live and work well with others. Research will involve carrying heavy packs over slippery and steep terrain. Applicants must be in good physical condition and be able to meet the demands of field research under

these conditions. Ability to drive a standard transmission vehicle is desirable but not required. Applicants with first-aid/first responder training, skills in automobile maintenance, and construction skills are highly desirable. Please address these skills when applying.

Interns will be required to spend a minimum of 3-months in Trinidad, with possibility of extension. There are potential start dates in July 2019 and every month thereafter until early 2020. We will cover all travel and living expenses and provide housing.

Please see our website <[www.theguppyproject.weebly.com](http://www.theguppyproject.weebly.com)> for more information on the project and access to reprints. Be sure to check out our video menu, which includes a “guppy censuses” submenu that details the main tasks associated with the internship.

Applicants should send cover letter, CV and the names and e-mail addresses of three or more professional references to David Reznick (gupy@ucr.edu). At least two of the references should be academics.

Cheers,

Ron

Ron Bassar <[rdbassar@gmail.com](mailto:rdbassar@gmail.com)>

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## ULausanne SIBVirtualSeminar SaraMitri Apr18

Dear all,

We are pleased to announce the next speaker at the SIB Virtual Computational Biology Seminar Series:

Sara Mitri, Evolutionary Microbiology, University of Lausanne & SIB “The ecology and evolution of small bacterial communities” 18 April 2018, 16:00 - University of Lausanne, Genopode building, Auditorium B

The seminar will also be broadcast live for those unable to attend it physically (<https://collab.switch.ch/-sib-cbss/>). For more information about these seminars as well as the upcoming speakers list and previous screencasts, please visit the SIB virtual seminar series webpage: <http://www.sib.swiss/training/-virtual-seminars-series> Important: If you want to remain informed about our upcoming seminars, please subscribe to the dedicated mailing list:<http://lists.isb-sib.ch/mailman/listinfo/sib-virtual-seminars> Looking forward to seeing you all there.

Best regards, Diana Marek

“Diana.Marek@sib.swiss” <Diana.Marek@sib.swiss>

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## ULausanne SIBVirtualSeminar SaraMitre April18

Dear all,

Please find here a gentle reminder of our next speaker at the SIB Virtual Computational Biology Seminar Series:

Sara Mitri, Evolutionary Microbiology, University of Lausanne & SIB “The ecology and evolution of small bacterial communities” 18 April 2018, 16:00 - University of Lausanne, Genopode building, Auditorium B

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Best regards, Diana Marek

“Diana.Marek@sib.swiss” <Diana.Marek@sib.swiss>

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## UMainz FieldAssist ArizonaAnts

UMainz.FunctBasisLifespanFecundity

The Institute of Organismic and Molecular Evolution at the University of Mainz is searching for a field / research assistant (65% TVL E13) for the research project

The functional basis of lifespan and fecundity in Temnothorax ants

We invite applications for a field / research assistant (2 months, extension possible) for an ant collection trip to the Chiricahua Mountains Arizona followed by transfer of ant colonies to lab nests at the Johannes Gutenberg University of Mainz, Germany. Our project aims at understanding the evolution of life history traits such

as lifespan and fecundity and their functional transcriptomic basis. Our model systems are Temnothorax ants, in which workers and queen lifespan vary between one to over twenty years. Field work includes searching for ant colonies in rock crevices and transfer to vials with an aspirator. The position requires a Master degree in Biology. Candidates with an interest in an academic career in Evolutionary Biology will be preferred, as it is likely that the successful candidate could be able to continue to work on this project for his / her PHD. In this project, we will use experiments, RNA-seq and RNAi gene knockdowns and epigenetic inhibitors to study the regulation and connectivity of gene regulatory pathways linked to longevity and fecundity. We are searching for a highly motivated student with a strong background in evolutionary genetics and behavioral ecology. Previous research experience with social insects, ant collection, transcriptomics are advantageous, but not required. Students from every nationality are encouraged to apply. The working language of the laboratory is English. For more information on the position, especially the long-term perspectives, please contact us.

Interested candidates should send an application (as a single pdf e-mail attachment) containing a letter of motivation, a brief statement of their research experience and interests, a curriculum vitae (including grades of their B.Sc and M.Sc), and the names and email address of 2 potential referees to Prof. Dr. Susanne Foitzik (foitzik@uni-mainz.de) or Dr. Barbara Feldmeyer (barbara.feldmeyer@senckenberg.de).

Deadline for applications is May 25th 2018. Skype-interviews will be scheduled on June 5th 2018, on-site interviews about 2 weeks later. Fixed starting date due to the field season in Arizona would be August 11th 2018.

Prof. Dr. Susanne Foitzik foitzik@uni-mainz.de

Dr. Barbara Feldmeyer barbara.feldmeyer@senckenberg.de

“B.Feldmeyer” <b.feldmeyer@googlemail.com>

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## UZurich VolFieldAssist BirdsJapan

Expenses paid field assistant positions to study the role of call combinations in Japanese tits

For the upcoming field season (15 May - 20 July 2018) we are looking for a highly motivated expenses paid field volunteer to join our field project (main respon-



sible Dr. Toshitaka Suzuki, Sokendai & University of Zurich, Switzerland) investigating the role of call combinations in Japanese tits. The study site is located near Karuizawa, Nagano, Japan

Our current project investigates the development of call combinations in juvenile Japanese tits. The work of the field volunteers will be to help with field experiments, behavioural observations, and data management. This work will give insight into exciting experimental field-work and will be carried out partly in managed forests and partly in scenic pristine forests of Central Japan. We will work 5-6 days per week in the field depending on the workload of the experiments. The work is physically strenuous at times.

Qualifications:

- (1) BSc/MSc in Biology, Ecology, Evolution or similar qualification
- (2) Previous field experience, preferably involving playback experiments and behavioural observations
- (3) Ability to work in small teams and sociable personality

- (4) Driving license
- (5) Fluent in English

We will cover for the accommodation, travel expenses from and to the study site (in total up to 650 Euros), as well as the living expenses.

Applications - including a CV, a letter of motivation (1 page) and the name of two referees - should be send to Toshitaka Suzuki: toshi.n.suzuki@gmail.com , preferably in a single PDF.

Applications received until 22 April 2018 will be given full consideration.

-

Toshitaka Suzuki

Department of Anthropology, University of Zurich

Department of Evolutionary Studies of Biosystems, The Graduate University for Advanced Studies

Michael Griesser

Department of Anthropology, University of Zurich

Toshitaka Suzuki <toshi.n.suzuki@gmail.com>

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## PostDocs

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## AarhusU EvolutionaryGenetics

Join us at Aarhus University to work on basic questions in evolutionary genetics with applied outcomes in the area of antibiotic resistance.

A position as a postdoctoral research associate is available for 12 months (renewable for another 12 months) in the research group of Thomas Bataillon (Bioinformatics Research Center, Aarhus University DK). The work is funded by the project [BH\(BPREPARE\\$B\(I\(B](#) and involves 5 research groups based in Canada (A Wong, Carleton University, R Kassen U of Ottawa), Portugal (C Bank and I Gordo, IGC Portugal) and Denmark (T Bataillon, BiRC, Aarhus University).

The assumption that antimicrobial resistance (AMR) is [BH\(Bcostly\\$B\(I\(B](#) underpins current thinking about the management and stewardship of antibiotic delivery. Evidence suggests, however, that AMR can persist at high levels even in the absence of drug selection implying either that AMR is not as costly as previously thought or that costs are [BH\(Bover rated\\$B\(I\(B](#) because these are labile and can be readily ameliorated through compensatory evolution. We will evaluate these ideas directly, through experiment, and use the data to validate theory aimed at predicting the prevalence of AMR across genetic backgrounds and environments.

The postdoctoral researcher will work on theoretical models for predicting the fitness changes of bacterial strains carrying different types of AMR mutations across

a variety of environments. The work will be primarily theoretical and statistical (to help with the analysis of experimental evolution data from the empirical side of the project).

We expect the post-doctoral researcher to have a background in evolutionary genetics and interest in microbial evolution. Preference will be given to candidates with proven expertise in the area of modelling in evolutionary genetics (either analytical theory and/or computer simulations) and microbial evolution (either experimental evolution or population genetics of naturally occurring populations)

The work will be carried out at the bioinformatics research center (BiRC) in close collaboration with Claudia Bank (leading the Evolutionary Dynamics group at the Gulbenkian Institute, Oeiras Portugal).

BiRC ([www.birc.au.dk](http://www.birc.au.dk)) provides a young, interdisciplinary environment, presently with 45 professors, post docs and PhD-students. There are strong links to Department of Computer Science, Mathematics/statistics and Biology as well as to the Faculty of Health. Within population genomics and evolution, BiRC hosts the integrated research groups of Kasper Munch (recombination, selection in primates, X and Y chromosome evolution), Thomas Bataillon (evolutionary theory, experimental evolution), Asger Hobolth (coalescent methods) and Mikkel H. Schierup (primate population genomics, X and Y), Thomas Mailund (Bioinformatics Algorithmics, Genetics Molecular evolution) and Palle Villesen (Bioinformatics NGS autoimmune disease).

The position is available as early as May 15, 2018 and we will start to review applications immediately.

For applying you should send

- (1) your CV, including a list of publications and the names and email addresses of two potential referees;
- (2) a short cover letter (1 page) describing your research interests and motivations for joining the project.

The position will be filled as soon as a qualified candidate is identified.

Please send inquiries to Thomas Bataillon (tbata@birc.au.dk).

Thomas Bataillon <tbata@birc.au.dk>

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## AarhusU GreatApePopulationGenomics

Post doc in sex chromosome population genomics 971405

A 2-year postdoc position in population genomics is available in the research group of Mikkel H. Schierup at the Bioinformatics Research Centre, Aarhus University. The position is available starting 1 May 2018 or as soon as possible thereafter.

The post doc will develop and apply approaches to study the evolutionary processes affecting sex chromosome evolution with specific focus on human population data sets and new data sets of great apes genomes. The goal is to elucidate the mechanisms underlying the very strong natural selection affecting the X chromosome and its involvement with speciation processes as well as in male fertility. Depending on your interests, focus can be on population genetics methods development, large scale analysis, or both. Data will include RNA expression data from each stage of male meiosis in multiple individuals of both humans and other great apes. Large human cohorts will be investigated in collaboration with DECODE Genetics.

**Required qualifications** We are looking for a highly motivated person trained in population genetics and with some prior experience with analysis of large population genomics data sets. About Bioinformatics Research Centre (BiRC). BiRC ([www.birc.au.dk](http://www.birc.au.dk)) provides a young, interdisciplinary environment, presently with 45 professors, post docs and PhD-students. There are strong links to Department of Computer Science, Mathematics/statistics and Biology as well as to the Faculty of Health. Within population genomics and evolution, BiRC hosts the integrated research groups of Kasper Munch (recombination, selection in primates, X and

Y chromosome evolution), Thomas Bataillon (evolutionary theory, experimental evolution), Asger Hobolth (coalescent methods) and Mikkel H. Schierup (primate population genomics, X and Y).

**Place of Work and area of Employment** The place of work is C. F. Mollers Alle 8, DK-8000 Aarhus C, and the area of employment is Aarhus University with related departments. For further information and discussions of specific ideas please do not hesitate to contact Professor Mikkel Heide Schierup, Ph: +4527782889, email: mheide@birc.au.dk

**Application procedure** Shortlisting is used. This means that after the deadline for applications and with the assistance from the assessment committee chairman, and the appointment committee if necessary, the head of department selects the candidates to be evaluated. All applicants will be notified whether or not their applications have been sent to an expert assessment committee for evaluation. The selected applicants will be informed about the composition of the committee, and each applicant is given the opportunity to comment on the part of the assessment that concerns him/herself. Once the recruitment process is completed a final letter of rejection is sent to the deselected applicants, including the main considerations emphasized during the selection process. Formalities and salary range Science and Technology refers to the Ministerial Order on the Appointment of Academic Staff at Danish Universities under the Danish Ministry of Science, Technology and Innovation. The application must be in English and include a curriculum vitae, degree certificate, a complete list of publications, a statement of future research plans and information about research activities, teaching portfolio and verified information on previous teaching experience (if any). Guidelines for applicants can be found here. Appointment shall be in accordance with the collective labour agreement between the Danish Ministry of Finance and the Danish Confederation of Professional Associations. Further information on qualification requirements and job content may be found in the Memorandum on Job Structure for Academic Staff at Danish Universities. Salary depends on seniority as agreed between the Danish Ministry of Finance and the Confederation of Professional Associations. All interested candidates are encouraged to apply, regardless of their personal background. Research activities will be evaluated in relation to actual research time. Thus, we encourage applicants to specify periods of leave without research activities, in order to be able to subtract these periods from the span of the scientific career during the evaluation of scientific productivity. Aarhus University offers Relocation service to International researchers. You can read more about it here.

Deadline

25.04.2018, apply through this link <http://www.au.dk/-om/stillinger/videnskabelige-stillinger/stillinger/Vacancy/show/971405/5285/>

Mikkel H. Schierup Bioinformatics Research Centre, Aarhus University, CF Mollers Alle Building 1110, 8000 Aarhus C Denmark Ph: +45 8715 6535 Email: mheide@birc.au.dk <http://www.birc.au.dk/~mheide>

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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>

## AhmedabadU DrosophilaAdaptation

Postdoctoral opportunity in seasonal dynamics in tropical *Drosophila* species

Rajpurohit Lab at the division of Biological and Life Sciences, School of Arts and Sciences, Ahmedabad University, Ahmedabad invites potential candidates to write National Postdoctoral Fellowship application. The deadline to apply for this fellowship is April 30<sup>th</sup>, 2018. It is open to Indian nationals only. To explore this opportunity further feel free to me at my email ID: subhash.rajpurohit@ahduni.edu.in

Here is the link to the fellowship guidelines:

<http://www.serb.gov.in/npdf.php> Feel free to ask me additional questions about this fellowship.

Please visit my Lab webpage (<https://www.rajpurohit-lab.org/>) for details about my research programme and ongoing projects. My Lab is currently focusing on three major areas-

1. Cline, seasonality, and rapid adaptations
2. Metabolic ecology
3. Urban evolution

Contact:

Subhash Rajpurohit

Assistant Professor & Ramanujan Fellow

Division of Biological and Life Sciences

School of Arts & Sciences

Ahmedabad University

Ahmedabad 380009, Gujarat

India

Phone: +91-7961911284

Subhash Rajpurohit <subhash.rajpurohit@ahduni.edu.in>

## ArizonaStateU ComputationalPopulationGenomics

\* Postdoctoral position available in Computational Population Genomics \*

A postdoctoral position in computational population genomics is available in the research group of Susanne Pfeifer in the School of Life Sciences at Arizona State University.

Research in the group focuses on computational method development and analysis of large-scale population genomic datasets to characterize evolutionary—processes in primates. We are currently looking for a computational biologist/population geneticist to analyse novel primate genomic datasets in order to elucidate mutation rate evolution across the primate clade. Successful candidates are expected to have a strong computational and statistical background (programming proficiency in R, Perl, or Python, and shell scripting is essential; experience with analysing high throughput sequencing data is highly desired) along with a genuine interest in genetics and evolution. Preference will be given to candidates with a strong publication record, evidence of research productivity, and an ability to successfully communicate scientific information. Funding is available for three years, contingent on annual renewal based on progress. The start date is flexible but anticipated to be in Fall 2018.

The Pfeifer Lab offers a vibrant work environment with excellent opportunities for collaborative efforts as well as independent accomplishments. The Lab is integrated within a diverse evolution and population genetics research community at ASU (ASUpopgen.org), as well as the Center for Evolution and Medicine (evmed.asu.edu), and the Center for Mechanisms of Evolution (biodesign.asu.edu/mechanisms-evolution).

Interested applicants should send a short summary of research interests and motivation to join the group, CV, and contact information for two references to susanne.pfeifer@asu.edu. The review of applications will begin May 1st and will continue until a suitable candi-

date has been found. Informal inquiries are welcome.

— Susanne P. Pfeifer Assistant Professor Arizona State University School of Life Sciences <http://spfeiferlab.org>  
Susanne Pfeifer <spfeife1@asu.edu>

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## AuburnU EvolutionaryGenomics

Postdoctoral Research Associate in Evolutionary Genomics, at Auburn University

The Graze and Stevison Labs at Auburn University are seeking a creative and highly motivated postdoc with research interests in evolutionary genetics and functional genomics. Our labs are in the Biological Sciences Department and we have both heavily computational (dry lab) and experimental (wet lab) aspects of our research programs. In the first 1-2 years, two projects are planned 1) a project in the Graze Lab focused on sex differences in gene expression and hormone signaling and 2) a project co-mentored with Laurie Stevison (Stevison Lab) on the mechanisms underlying environmental variation in recombination.

A strong background in evolutionary genomics and excellent communication, organizational, and leadership skills are required. The applicant should have a strong work ethic, and is expected to develop new ideas that promote current research and her/his own future independence. The post-doc will be expected to assist with training graduate and undergraduate students in the lab, develop synergistic projects, write grants, produce first authored papers, and contribute to co-authored papers.

Ideal applicants will have: -Strong written and oral communication skills -Be a productive member of a research team -Proficiency in computational biology -Ability to code in at least one programming language -Produce high quality research (as evidenced by first authored publications) -Work effectively and collegially with colleagues

Other traits not required, but ideal: -Experience with best practices for analyzing RNA-seq data -Some familiarity with statistical or quantitative genetics -Molecular biology lab skills (e.g. RNA extraction and library preps)

Full support is available for one year, with up to three additional years possible pending satisfactory performance and available funds. Selected applicants will also benefit from funds to travel to national meetings annually,

opportunities for mentoring and career development. Additional lab funds for independent projects are available upon written proposal submission. Anticipated start date is August 2018.

The selected applicant would be joining a strong research community in the Southeastern US. Nearby universities/research facilities (within 2 hours) include UGA, Georgia Tech, Emory, Hudson Alpha, and UAB. The wider SE Community also includes UF, Clemson, UNC, and Duke with local area meetings annually < <http://sepeeg.web.unc.edu/about-sepeeg/> > to network within this community.

Applicants must have a Ph.D. in an appropriate field. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment. Women and minorities are strongly encouraged to apply.

This announcement is informal in nature and candidates of interest will be asked to submit a formal application for complete consideration after initial screening. If interested, please send a cover letter/statement of interest with a list of relevant skills, a CV, including a list of peer-reviewed publications, and contact information for two references by email to Rita Graze at [rmgraze \(at\) auburn \(dot\) edu](mailto:rmgraze@auburn.edu) and/or Laurie Stevison at [lss0021 \(at\) auburn \(dot\) edu](mailto:lss0021@auburn.edu) (please note our mail system is limited to 25Mb messages) with “Evolutionary Genomics Postdoc Position” in the subject line. Receipt of application will be confirmed within 3 days. Review of applications will begin June 1, 2018, and continue until a suitable applicant is found.

—  
Rita M. Graze, Asst. Professor Department of Biological Sciences Auburn University, Auburn AL 36849-5407  
Email: [rmgraze \(at\) auburn \(dot\) edu](mailto:rmgraze@auburn.edu)

Rita Graze <[rmg0022@auburn.edu](mailto:rmg0022@auburn.edu)>

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## BrownU EvoDevo

Brown University Postdoctoral Fellow position for Cell and Developmental Biology

Location: Brown University, Molecular Biology Cell Biology Biochemistry Department (Providence, RI)

We are looking to hire a talented full-time postdoctoral



fellow who conducts her/his independent research under PI's supervision.

In our group, two major projects are currently undertaken:

(1) Cell and Developmental Biology: Identifying how germline factors contribute to cellular functions and development, using sea urchin embryonic cells and human cancer cells.

(2) Evolutionary Developmental Biology: Discovering how the molecular evolution alters the developmental program and contributes to species diversity, using multiple echinoderm embryos.

Both projects require skills in cell biology, embryology or live imaging such as microinjection, optogenetic manipulations of a protein, and 4D-confocal imaging. Experience in Biochemical and bioinformatic approaches is also welcomed: these include Immunoprecipitation followed by proteomic analysis or by RNA-seq to broadly identify the targets.

Although basic training and experience in the above fields is largely appreciated, the PI will provide any other necessary training both in experiments and manuscript/grant writing.

A good accomplishment in her/his Ph.D. work with publications in the above relevant area is highly recommended. The successful individuals are strongly encouraged to apply for postdoctoral fellowships.

We greatly appreciate one's independent thinking, creativity, curiosity, enthusiasm, and hard working. The successful individuals are expected to lead their projects in an independent manner. This is an excellent job opportunity for individuals who seek to develop their own research and eventually to proceed to a next step of their career in next 2-5 years.

Any interested individuals should contact me via e-mail: [mamiko\\_yajima@brown.edu](mailto:mamiko_yajima@brown.edu). Please enclose your CV, reprints of your representative works (if any), name of your thesis advisor. Reviews will begin immediately and continue until position is filled.

Mamiko Yajima <[mamiko\\_yajima@brown.edu](mailto:mamiko_yajima@brown.edu)>

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## ColdSpringHarborLaboratory EvolutionaryGenomics

Postdoctoral Positions in evolutionary genomics are available in Dr. Adam Siepel's research group at Cold Spring Harbor Laboratory. The Siepel Group specializes in the development of probabilistic models, algorithms for inference, prediction methods, and application of these methods in large-scale genomic data analysis. Of particular interest is research relevant to existing, NIH supported projects in: HUMAN POPULATION GENOMICS including demography inference using Bayesian coalescent-based methods, inference of natural selection on regulatory and other noncoding sequences, and prediction of fitness consequences for noncoding mutations; and TRANSCRIPTIONAL REGULATION in mammals and *Drosophila*, including the estimation of rates and patterns of transcriptional elongation from GRO-seq data, prediction of transcription factor binding sites from DNase-seq data, and regulatory network inference based on joint patterns of transcription and binding in inducible systems.

Relevant recent papers include the following:

Danko CG, Choate LA, Marks BA, Rice EJ, Zhong W, Chut T, et al. Dynamic evolution of regulatory element ensembles in primate CD4+ T-cells. *Nat. Ecol. Evol.* 2(3):537-548, 2018.

Huang Y-F, Gulko B, Siepel A. Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. *Nat. Genet.* 49(4):618-624, 2017.

Kuhlwilm M, Gronau I, Hubisz MJ, de Filippo C, Prado J, Kircher M, et al. Ancient gene flow from early modern humans into Eastern Neanderthals. *Nature* 530(7591):429-433, 2016.

Core LJ, Martins AL, Danko CG, Waters CT, Siepel A, Lis JT. Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. *Nat. Genet.* 46(12):1311-1320, 2014.

Rasmussen MD, Hubisz MJ, Gronau I, Siepel A. Genome-wide inference of ancestral recombination graphs. *PLOS Genet.* 10(5):e1004342, 2014.

Required Qualifications:

Ph.D. in bioinformatics, computer science, statistics, genetics, molecular biology, applied mathematics, or

a related field. Fluency in probabilistic modeling and computational statistics. Proficiency in programming, ideally in C or C++, as well as in scripting languages such as Python, Perl, Mat Lab, or R. Should be comfortable in a Linux environment, with large data sets, computer clusters, and databases..

Job location: CSHL, One Bungtown Road, Cold Spring Harbor, NY 11724

TO APPLY: visit the CSHL Careers website at [www.cshl.edu/careers](http://www.cshl.edu/careers) .Position Number:02018-R.

Irene Gill Simons Center for Quantitative Biology

Cold Spring Harbor Laboratory

Office: 516-367-6834 | Fax: 516-367-5501

Email: [gill@cshl.edu](mailto:gill@cshl.edu) | <http://www.cshl.edu/scqb> “Gill, Irene” <[gill@cshl.edu](mailto:gill@cshl.edu)>

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## Colorado ComputationalBiology

Deadline extended to Friday, April 27. (1 week from yesterday!) Apply Now! These are competitive fellowships.

Feel free to contact [David.Pollock@ucdenver.edu](mailto:David.Pollock@ucdenver.edu) for more info about research in evolutionary biology and evolutionary genetics and genomics.

<http://www.ucdenver.edu/computational/Pages/-postdocs.aspx> Postdoctoral Training | Graduate School | University of ... [www.ucdenver.edu](http://www.ucdenver.edu) UC Denver offers more than 115 programs in 13 schools and colleges at the undergraduate, graduate, doctoral and first professional (health) levels.

We seek highly creative and ambitious Postdoctoral Fellows in Computational Biology.

The Computational Bioscience Program at the University of Colorado is looking to fill multiple competitive postdoctoral fellowship positions, fully funded through the program's T15 NIH training grant. Applicants will work with one or more program faculty. The Computational Bioscience Program emphasizes building a strong collaborative community, and successful applicants will interact regularly with program faculty, students, and other postdoctoral researchers. We seek postdoctoral candidates who aim to build an independent research agenda. Successful applicants will be initially appointed for one year, with renewals possible for up to a 3-year training period.

Computational Bioscience Program faculty focus on the development and implementation of novel algorithms and computational models, along with the analysis and interpretation of big data in biomedicine. Accordingly, a successful applicant will be experienced in the development, implementation, and application of computational/statistical models and will have a strong interest in developing new methodologies to solve biological and biomedical challenges. Candidates may also translate computational methods developed into wet laboratory research projects through collaborations across all research campuses.

The Computational Bioscience Program is composed of 18 core faculty members at the CU Anschutz Medical Campus as well as CU Boulder, CU Denver, and National Jewish Hospital. Faculty research interests include Genetics and Genomics, Natural Language Processing, Text Mining, Clinical Research Informatics, Molecular Evolution, Neuroscience, Biostatistics, Personalized Medicine, Computational Pharmacology, Microbiome, Cancer Systems Biology, Metagenomics, Molecular Interaction Networks, and Visual Analytics. Further details are at: <http://www.ucdenver.edu/academics/colleges/Graduate-School/academic-programs/computational-bioscience/Pages/home.aspx> Qualifications

The successful applicant will have completed (or be close to completing) a Ph.D. or M.D./Ph.D. in an applied quantitative discipline. This includes, but is not limited to, Computer Science, Informatics, Biostatistics, Population/Evolutionary Genomics, or Applied Mathematics. The applicant should have a strong interest in either basic or translational research. A track record of applying computational and/or statistical models to solve biological problems is desired. Previous experience in common programming languages is needed (e.g., R, Python, C, Java). Candidates with less than three years of postdoctoral training are preferred. Preference will be given to applicants with strong evidence of productivity, creativity, and self-motivation. A track record of conference poster and/or oral presentations, and first author peer-reviewed publications, is expected. Applications are due by April 27, 2018. For inquiries, or to apply, see <http://www.ucdenver.edu/academics/colleges/-Graduate-School/academic-programs/computational-bioscience/Pages/postdocs.aspx> Eligible candidates must be a U.S. citizen or hold permanent resident status.

How to Apply

Individuals interested in applying for postdoctoral fellowships should send a statement of research in-

terests, the desired research mentor(s), a list of three references, and a complete curriculum vitae to electronically to Elizabeth Wethington (ELIZABETH.WETHINGTON@UCDENVER.EDU). Further questions can be addressed to Elizabeth Wethington via email or directly at 303-724-7280.

We encourage potential applicants to research faculty members and contact them directly regarding research interests and potential openings within individual laboratories.

“Pollock, David” <David.Pollock@ucdenver.edu>

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## DalhousieU MarineGenomics

Postdoctoral Position in Marine Genomics

Dalhousie University

Support is available for a postdoctoral position at Dalhousie University (Halifax, Nova Scotia, Canada) in the laboratory of Daniel Ruzzante (<http://ruzzante.ca/>) for research on genomics of marine and/or freshwater fish. Although ultimately the project will be a function of the successful candidate's interests and skills, a strong background in genomics and bioinformatics is required.

The position is available for 2 years, starting in the fall 2018. Applicants please send a statement of research interests, CV, copies of up to 4 publications and the names and e-mail addresses of two people willing to act as academic references to: Daniel Ruzzante ([daniel.ruzzante@dal.ca](mailto:daniel.ruzzante@dal.ca)).

Informal inquiries are welcome. Review of applications will start June 1, 2018.

Dr Daniel E Ruzzante, Killam Professor Canada Research Chair in Marine Conservation Genetics (2002-2012) Department of Biology, Dalhousie University, Halifax, NS, Canada - B3H 4R2 ph:(902)494-1688 fax:(902)494-3736 <http://ruzzante.ca/> Daniel Ruzzante <Daniel.Ruzzante@Dal.Ca>

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## EarlhamInst UK ColombianBiodiversity

Postdoctoral Research Assistant in Natural Diversity  
RCUK Grow Colombia

Earlham Institute is seeking a highly motivated Postdoctoral Researcher to study genetic and genomic diversity of vertebrates species in Colombia.

About the GROW Colombia Programme:

Earlham Institute (EI) was recently awarded an RCUK-GCRF capacity building grant focused on preserving and managing biodiversity in Colombia. Colombia's biodiversity is not only important for the country's natural heritage and the preservation of unique species in the world, it is also essential for the improvement of human welfare, social equality and economic development.

The programme, led by Professor Federica Di Palma, is a multidisciplinary programme aimed at strengthening Colombian research capability in the biological sciences, computational biology, and socio-economics, and raising general awareness of the importance of biodiversity. The programme brings together an alliance of complementary skills from a wide range of partners to understand the mutual impacts of biodiverse ecosystems and sustainable agricultural productivity. Our goals are to build research capacity, partnerships and knowledge, with the longer-term goals of stimulating economic and social growth around biodiversity.

The funded programme sits alongside the BRIDGE Colombia network ([www.bridgecolombia.org](http://www.bridgecolombia.org)) which is a multidisciplinary network of research organisations in the UK and Colombia founded in March 2017, to develop robust coordinated activities under a shared vision centred on biodiversity as a means to achieve sustainability and peace. The network actively facilitates collaborative and fully integrated research programmes; promotes research excellence and the use of innovation in technologies and approaches to develop resilience in research capabilities; stimulates partnerships; and promotes exchange of knowledge.

Several new academic appointments and operational appointments (postdoctoral and fellowship level) are being made at EI under the GROW Colombia programme.

The role:

EI is seeking a highly motivated Postdoctoral Researcher

to study genetic and genomic diversity of vertebrates species in Colombia. The post holder will be responsible for conducting bioinformatics analyses associated with the project. Part of the project aims at enabling high throughput species identification from Museum and fresh samples sequenced using both traditional approaches (Illumina sequencing) or emerging technologies (Oxford Nanopore).

The post holder will also be responsible for the development of analytical pipelines and the downstream analyses. Including species and population diversity quantification, population parameters and population structuration estimation. Another section of the projects aims at sequencing the genomes of emblematic Colombian Vertebrates species. The post holder will be involved in the assembly, annotation and analysis of the genomes.

The post holder will be required to work with relevant EI staff and with outside collaborators to carry out necessary research to meet key objectives for the project. The post holder may also serve as a key technical resource to clarify issues, participate in analysis, and apply comprehensive knowledge to contribute to the completion of other research projects as part of the RCUK-GCRF funded programme.

The ideal candidate:

The successful applicant will ideally have a PhD in bioinformatics, population genomics, evolutionary biology or a related subject with experience of working on genomics and transcriptomics data and bioinformatics. Experience with NGS analysis (DNA and RNA-Seq) as well as scripting (PERL / Python) are essential. Experience with working on animal genomics or low-input samples is highly desirable.

Additional information:

Salary on appointment will be within the range 31,250 to 38,100 per annum depending on qualifications and experience. This is a full time post for a period of three years.

For further information and details of how to apply, please visit our web site <http://jobs.earlham.ac.uk/> or contact the Human Resources team on 01603 450462 or [nbi.recruitment@nbi.ac.uk](mailto:nbi.recruitment@nbi.ac.uk) quoting reference 1003448.

As a Disability Confident employer, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy.

The closing date for applications will be 2nd May 2018

“Eve Edwards (NBI)” <[Eve.Edwards@nbi.ac.uk](mailto:Eve.Edwards@nbi.ac.uk)>

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## EmoryU Metabarcoding

Post-Doctoral Research Fellow, Quantitative Biology / Bioinformatics

<https://apply.interfolio.com/49652> POSITION DESCRIPTION: The Brosi and Read Labs at Emory University are seeking a post-doctoral research fellow to work on bioinformatic topics related to DNA metabarcoding / amplicon-based metagenomics. The post-doc will specifically work on a project aiming to improve the quantitative reliability of DNA metabarcoding of pollen. The project has strong potential for application to other systems (e.g. microbial systems). We will consider candidates from a wide range of backgrounds, including bioinformatics, biologists with strong quantitative / computational training, as well as applicants from quantitative / computational fields (statistics, applied math, physics, computer science) with strong grounding in biology. The post-doc will be housed in Berry Brosi’s lab at Emory but will be co-advised by Tim Read and will have extensive opportunities to interact with the Read lab, as well as other groups at Emory and other institutions.

The position is available immediately, and we will give preference to applications received before 1-May-2018. While we prefer candidates who are able to begin the position as soon as possible, we have some potential flexibility in start date. The position has an initial duration of one year with the possibility of extending up to three years. The minimum salary for the position is \$48,000 and includes full benefits.

QUALIFICATIONS: REQUIREMENTS: - Ph.D. in a field including bioinformatics; biology with a quantitative or computational focus; or statistics or another quantitative or computational discipline (e.g. physics, applied mathematics, or computer science) with a biological focus - strong quantitative and programming skills - strong publication track record - excellent writing skills - able to work collaboratively in a positive and productive team setting

PREFERRED SKILLS (not required): - experience with using, modifying, and/or developing bioinformatics pipelines for high-throughput sequencing data, particularly amplicon-based - experience with statistical techniques for phylogenetic imputation - experience with matching / assignment optimization algorithms - some basic wet-lab molecular biology skills - interest in and



experience with grant writing

APPLICATION INSTRUCTIONS: Please apply on Interfolio: <https://apply.interfolio.com/49652>. To apply, please submit a cover letter, CV, and 1-3 representative publications on Interfolio (please do not email these materials). Get in touch with PI Berry Brosi, [bbrosi\[at\]emory\(dot\)edu](mailto:bbrosi@emory.edu) if you have any questions regarding the position. While the deadline of the position is set to 22 May, please apply by 1 May 2018 for fullest consideration.

Berry J. Brosi, Ph.D. Winship Distinguished Associate Professor Department of Environmental Sciences Emory University [www.brosilab.org](http://www.brosilab.org) "Brosi, Berry J" <[bbrosi@emory.edu](mailto:bbrosi@emory.edu)>

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## Frankfurt EvolutionOfTEs

Job offer ref. #12-18006 PostDoc - Comparative Genomics of Transposable Elements 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 PostDoc - Comparative Genomics of Transposable Elements (100%)

Your tasks: - Sequencing, assembly, and annotation of metazoan genomes - Comparative genomic analysis of transposable elements in non-model organisms - Evolutionary inference of transposable elements to study their dynamics, phylogeny, and/or mode of transmission

Your profile: - PhD in biology, bioinformatics or related subjects - Experience with genome assembly and scripting - Interest in mobile genetic elements - Experience and solid understanding as well as exceptional interest in comparative genomics and evolutionary biology

research - Teamwork oriented and excellent communication skills in both written and spoken English - Can work independently and meet deadlines

What is awaiting you? - An interesting task in a dynamic team of researchers in an international research group and joining the new LOEWE excellence centre with its 20 new research groups. - Access to unpublished genomes from exotic animal phyla - The opportunity to habilitate at Goethe University or get teaching experience - The possibility to create a network with scientists in interdisciplinary fields in translational biodiversity genomics Salary and benefits are according to a full time public service position in Germany (TV-H E13).

The contract should start on July 1st, 2018 and will initially be limited for two years. The Senckenberg Gesellschaft für Naturforschung support equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application, mentioning the reference of this job offer (ref. #12-18006) before April 30th, 2018 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) Please contact Dr. Maria Nilsson-Janke for more information, [maria.nilsson-janke@senckenberg.de](mailto:maria.nilsson-janke@senckenberg.de)

Dr. Maria Nilsson Janke Biodiversity and Climate Research (BiK-F) Senckenberg Museum Georg-Voigt-Straße 14-16, 3rd floor, room 4.06 D-60325 Frankfurt am Main, Germany Senckenberg Gesellschaft für Naturforschung Rechtsfähiger Verein gemäß Â§22 BGB Senckenberganlage 25 60325 Frankfurt Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr.

Uwe Fritz, Prof. Dr. Ingrid Kröncke Präsidentin: Dr. h.c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt) Vernetzen Sie sich mit uns: [www.senckenberg.de/socialmedia](http://www.senckenberg.de/socialmedia) Die Welt baut ihr Museum - bauen Sie mit! <https://die-welt-baut-ihre-museum.de> Maria Nilsson-Janke <[Maria.Nilsson-Janke@senckenberg.de](mailto:Maria.Nilsson-Janke@senckenberg.de)>



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## GeorgetownU PopulationGenomics

\* Postdoctoral Position in Population Genomics of Range Expansion and Adaptation\*

A postdoctoral position is available in the Armbruster lab (<http://faculty.georgetown.edu/paa9/>) at Georgetown University to study the population genomics of range expansion and climatic adaptation in the invasive mosquito, *Aedes albopictus*. The focus of the project is to: 1) use whole-genome sequence data to determine the evolutionary history of the world-wide range expansion of *Aedes albopictus*, 2) develop genomic tools to rapidly identify the origin of new invasive populations, and 3) identify the genetic basis of life-history adaptation across the species range. The project will leverage historical data and samples to identify allochronic evolutionary changes at both the molecular and phenotypic level. This is a collaborative project with Gisella Caccione's lab at Yale that will involve extensive interaction between the research teams at Georgetown and Yale. The position will also include an opportunity to develop additional research projects. The initial appointment will be for two years, with the possibility of extension based on excellent performance. Starting salary will be \$47,400 per year with benefits. The start date is flexible, but sometime in August or September of 2018 would be ideal.

### QUALIFICATIONS:

Candidates should have completed their PhD in evolutionary biology or a related discipline with a demonstrated record of research productivity and publication. The project will involve substantial insect husbandry, molecular biology and bioinformatics analyses. Candidates with expertise in two of these three areas will be given preference, and a desire to work in all three areas is essential.

### APPLICATION:

Review of applications will begin May 4<sup>th</sup> and continue until the position has been filled. Applicants should submit the following material to Peter Armbruster ([paa9@georgetown.edu](mailto:paa9@georgetown.edu)) with "postdoc application" in the subject line: 1) A CV including names and contact information of three references, and 2) A one-page research statement describing previous accomplishments and long-term goals. Informal inquiries prior to submission of a full application are welcome.

The Biology Department at Georgetown (<https://biology.georgetown.edu/>) is housed in the recently constructed Regents Hall, a state-of-the-art facility. The Biology Department is a vibrant academic community with a diverse set of research groups studying a range of topics in evolutionary ecology. Additionally, Washington D.C. provides exciting opportunities to interact with scientists at other institutions (i.e., NIH, Smithsonian Institution, George Washington University and University of Maryland, etc.). Washington D.C. is also an outstanding place to live with world-class cultural attractions and numerous (sometimes underappreciated) opportunities for outdoor activities. Georgetown University values diversity and is committed to equal opportunity for all persons regardless of age, color, disability, ethnicity, marital status, national origin, race, religion, sex, sexual orientation, veteran status, or any other status protected by law. –

Peter Armbruster, Ph.D. Professor Dept. of Biology, Regents 508 Georgetown University 37th and O Streets NW Washington, DC 20057-1229

Office Phone: 202-687-2567 Lab Phone: 202-687-1741 Fax: 202-687-5662

<http://www9.georgetown.edu/faculty/paa9/> Peter Armbruster <[paa9@georgetown.edu](mailto:paa9@georgetown.edu)>

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## GoetheU EvolutionSpeciesInteractions

The Department for Applied Bioinformatics in the Institute for Cell Biology and Neuroscience, faculty for biosciences, Goethe-university Frankfurt, is offering a PostDoc position (E 13 TV-G-U)

in the project: "Evolution and function of species interaction networks on the example of pioneering species". The position is available from 1st July 2018 for 3 years.

The project is embedded into the newly established LOEWE Centre for Translational Biodiversity Genomics, 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.

The association of organisms in symbiotic communities is an evolutionarily highly successful concept to optimally exploit available resources in a habitat. However,

we are only at the beginning of comprehending nature and extent of the organismic interaction, its molecular basis, as well as its consequences for the evolution of molecular function. In many cases, this is due to the complexity of the ecological niche a symbiotic community is embedded in, which harbors a plethora of species and provides a highly diverse spectrum of resources. A precise delineation of the symbiotic community often hard, preventing a mechanistic understanding of the symbiosis and of the resulting synergies. In this project, we overcome these obstacles by concentrating on pioneering communities, i.e. meta-organisms that are among the first to conquer a new, and often extreme, habitat, such as bare rock or lava fields. On the basis of the newly determined genome sequences of the individual symbionts, we will annotate and analyze the encoded protein interaction networks, and their integration across the symbiotic partners. A comparison to the results obtained from characterizing closely related species without a pioneering status is bound to shed light on the evolutionary trajectory that adapted a species to an extreme environment.

Your profile: - PhD in Bioinformatics, Evolutionary Biology or related subjects

- experience and solid understanding of comparative genomics or evolutionary biology research - experience with de novo assembly of eukaryotic genomes and transcriptomes - programming skills in at least one of the following languages: Python, Perl, Java, C, C++, R.

Please send your application with all necessary documents (CV, Copies of all university degree(s) and school certificates, two letters of reference, a list of publications) latest by 15th may 2018 in electronic format to Prof. Dr. Ingo Ebersberger (haenel@bio.uni-frankfurt.de), Goethe University, Institute for Cell Biology and Neuroscience, Dept. for Applied Bioinformatics, Max-von-Laue Strasse 13, 60438 Frankfurt am Main.

With its around 46,000 students and 4,600 employees, the Goethe University in Frankfurt is the largest university in the state of Hessen and an internationally renowned, important regional employer. Numerous quality and performance oriented internal reforms have been initiated in the recent years. The reorganized campuses for natural sciences and humanities offer an ideal environment for research and education. Since 2008, the Goethe University is a foundation under public law and enjoys full administrative autonomy.

The fixed-term employment of the academic staff is subject to the provisions of the Temporary Science Employment Law (Wissenschaftszeitvertragsgesetz) and the Hessian Higher Education Act (Hessisches Hochschulgesetz).

The University advocates gender equality and therefore strongly encourages women to apply. People with disabilities are given preference if equally qualified.

Koordinationsassistentin LOEWE-TBG Tel: +49 69 7542 1836 Fax: +49 69 7542 1826 andrea.kolb@senckenberg.de Senckenberg Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß §22 BGB) Senckenberganlage 25 60325 Frankfurt [www.senckenberg.de](http://www.senckenberg.de) Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Uwe Fritz, Prof. Dr. Ingrid Kröncke; 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)

Andrea Kolb <Andrea.Kolb@senckenberg.de>

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## Israel InfectiousDiseases

Dear all,

Our research team is interested in supporting candidates applying for The Zuckerman Postdoctoral Scholars Program, who wish to conduct their postdoctoral studies in Israel.

Zuckerman Postdoctoral Scholars receive a scholarship of \$50,000 per academic year for up to two years, with \$36,000 each year for living expenses and \$14,000 each year for research (\$10,000) and travel (\$4,000) expenses. Candidates must be citizens of the United States or Canada, or have a documented status that allows them to study and work in the US.

Successful candidates will be involved in a collaborative project between the University of Michigan (Dr. Luis Zaman), Ben-Gurion University of the Negev (Dr. Hadas Hawlena), the University of Texas at Austin (Dr. Jeffrey Barrick), Michigan State University (Prof. Richard Lenski), and The Hebrew University of Jerusalem (Prof. Shimon Harrus). This project is funded by the Ecology of Infectious Diseases program at the NSF.

The research aims to identify conditions that favor increased parasite evolvability (the evolution of parasite capabilities to produce novel variations) through evolutionary experiments with wild rodents and their bacteria. This study lies at the interface of evolution, ecology, microbiology, immunology, and molecular genetics.

A background in evolutionary biology, community ecology, or disease ecology is desired and skills in molecular biology, bioinformatics, and microbiology are preferred.

More details on the fellowship can be found in the attached files.

Interested candidates are welcome to send an application to Dr. Hawlena: [hadasaw@bgu.ac.il](mailto:hadasaw@bgu.ac.il) ASAP and before April 24.

Thanks, Hadas

Hadas Hawlena, PhD

Mitrani Department of Desert Ecology

Ben Gurion University of the Negev

Midreshet Sde-Boker, Israel

Hawlena Hadas <[hadashaw@bgu.ac.il](mailto:hadashaw@bgu.ac.il)>

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## Liverpool LepResistanceGenomics

We are seeking to recruit a Postdoctoral Research Associate with expertise in computational population genetics, statistics and informatics to join an international research team working to uncover the molecular genetic basis of resistance to Bt-maize in the African maize stemborer moth. You will be based in Liverpool, working closely with Ilik Saccheri (PI) and Al Darby (Co-I). Responsibilities will include: de novo assembly of a reference genome; identifying resistance and tolerance loci; assessing genetic diversity at these loci in natural populations; and analysing resistance allele frequency changes in time. You should have a PhD in population/evolutionary biology, bioinformatics or statistics, and experience of genomic analysis. The post is available until 31 January 2021 (with likely extension to 3yrs from start of contract), ideally starting in October 2018. For additional details and to apply go to <https://recruit.liverpool.ac.uk/> and search for Job Ref 009147 (closing date: 21 May 2018). Informal enquiries to [saccheri@liv.ac.uk](mailto:saccheri@liv.ac.uk).

<[I.J.Saccheri@liverpool.ac.uk](mailto:I.J.Saccheri@liverpool.ac.uk)>

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## LMU Munich 2 MorphoDiversity

2 Post-Doc positions, 100% TV-L

LMU Munich, Faculty of Biology, Zoology

Starting date: 01 October 2018 or earlier

End of application: 15 May 2018

1) Post-Doc position - Morphological diversity of arthropod larvae

We are seeking a highly motivated Post-Doc to take part in the investigation of diversity of arthropod larvae, including extant and fossil representatives. The project is funded by the Volkswagen Foundation.

The project is based on an interdisciplinary approach, in which morphological data of extant and fossil larvae are incorporated into an evolutionary framework. The major data base is provided by morphological investigations of extant and fossil specimens with modern imaging methods. Data are interpreted in a strict phylogenetic framework. The aim of the project is to develop a quantitative approach for comparing the morphological diversity of larval forms, especially between different geological time slices.

Focus groups of research are malacostracan crustaceans and insects. Both groups exhibit a large diversity of morphology and developmental patterns and have a rich fossil record. Specimens will be provided via scientific collections, fieldwork is not considered.

The prospective Post-Doc should have experience in some of the following fields: identification by DNA-barcoding, approaches to handle Big Data, data-banking, statistics in general, programming in R (or equivalent), geometric morphometrics (documentation, image processing, digital measurements, landmarks, Fourier-analysis). Experience with the systematic groups mentioned above is no prerequisite, but the Post-Doc is expected to gain expertise with these groups early in the course of the project.

The Post-Doc is expected to develop own strategies and sub-projects within the larger framework. The results of the project are expected to be presented regularly at national and international conferences by the prospective Post-Doc as well as published in peer-reviewed journals.

The possible candidate is strongly encouraged to participate in teaching and in supervision of bachelor, master

and other projects. The successful candidate will be based in the work group of Zoology at the campus Martinsried south-west of Munich, in close proximity to Munich. Child care facilities as well as schools are nearby.

The position is limited to a maximum duration of five years (60 months). Prospective starting date 01 October 2018 or earlier.

#### 2) Post-Doc position - Microscopic anatomy of Metazoa

We are seeking a highly motivated Post-Doc to participate and support research in microscopic anatomy of metazoans and participate in establishing and expanding an existing image database for virtual microscopy.

The candidate will have the opportunity to develop her/his own research project on a metazoan group of her/his choice. Experience in digital and virtual microscopy is expected. The results of the project are expected to be presented regularly at national and international conferences by the prospective Post-Doc as well as published in peer-reviewed journals.

The Post-Doc will be assigned responsibility in further development of content and didactic perspectives of virtual microscopy, an important tool for teaching and research in our work group.

The possible candidate is strongly encouraged to participate in teaching and in supervision of bachelor, master and other projects. The successful candidate will be based in the work group of Zoology at the campus Martinsried south-west of Munich, in close proximity to Munich. Child care facilities as well as schools are nearby.

The position is limited to a maximum duration of two years (24 months). Prospective starting date 01 October 2018 or earlier.

We offer: 2 Post-Doc positions, one for two years, one for five years; salary according to wage agreement (TV-L); interdisciplinary research project and working environment; modern imaging equipment (macro- and microscopic); histological facilities

We expect: PhD in biology or a closely related field; very good English communication skills (oral and written); ability to work in teams; high motivation; keen interest in zoological evolutionary questions

Applications of women are strongly encouraged. Severely challenged persons will be given preference in case of otherwise equal qualifications.

Please send your application to starck@lmu.de and/or jhaug@bio.lmu.de until May 15, 2018. The application should include CV, letter of motivation, and the names

and contact details of potential referees.

For further information contact:

Prof. Dr. Joachim T. Haug, LMU Munich, Biocenter - Department of Biology II, GroÃhaderner Str. 2, 82152 Planegg-Martinsried, Germany, Phone 1: +49-89-2180-74132 or 74171;

[http://www.zoology.bio.lmu.de/people/joachim\\_haug/-index.html](http://www.zoology.bio.lmu.de/people/joachim_haug/-index.html) Prof. Dr. Joachim T. Haug LMU Munich Biocenter - Department of Biology II and GeoBio-Center

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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>

## MaxPlanckInst Ploen AntibioticResistanceEvolution

### Postdoc Position on Antibiotic Resistance Evolution

The postdoc position will be based in the Schulenburg group, located at both the University of Kiel and the Max-Planck-Institute for Evolutionary Biology, Ploen. The position is for 3 years with the possibility of an extension for another 1 year. It is available from 1.8.2018 onwards or soon afterwards. The salary is at level TV-L E13 or E14 (approx.. euro 51.000 - 58.000 per year before tax reduction).

#### Area of work:

Dissection of antibiotic resistance evolution using experimental evolution, genomics analysis, ideally functional genetics and/or microfluidics. Through several collaborations, we have access to clinical material, for example from cystic fibrosis patients. The postdoc is expected to develop a new project on the dynamics of antibiotic resistance evolution, including the underlying selection processes and/or the involved molecular mechanisms of resistance.

#### Expectations and Requirements:

PhD in the area of evolutionary biology or microbiology. Comprehensive experience in microbiological techniques and statistics. Ideally experience in the performance of evolution experiments, microfluidics, bacterial genome sequence analysis, and/or bacterial functional genetic analysis. High competence in English and writing of



manuscripts. We are looking for someone with creative ideas, enthusiasm for research, and the ability of performing large-scale experiments.

The Max-Planck Institute for Evolutionary Biology and Kiel University aim at a higher proportion of women in research and education, and, therefore, specifically encourage qualified female scientists to apply. Female scientists will be preferentially considered in case of equivalent qualification, competence and achievements. The Max-Planck Institute for Evolutionary Biology and Kiel University specifically support employment of severely handicapped people. Therefore, severely handicapped applicants will be preferentially considered in case of suitable qualification. The Max-Planck Institute for Evolutionary Biology and Kiel University specifically welcome application from people with migration background.

Applications should include a motivation letter (max. 2 pages long), CV, publication list, names and contact details of two referees (who are familiar with the applicant's work), and copies of certificates (only PhD). Deadline for applications is 25.05.2018. Applications should be sent as a single pdf-document by email to:

Prof. Dr. Hinrich Schulenburg,  
hschulenburg@zoologie.uni-kiel.de

Further information can be obtained from Prof. Dr. Hinrich Schulenburg (hschulenburg@zoologie.uni-kiel.de). Please also check: <http://www.uni-kiel.de/zoologie/evoecogen/> Hinrich Schulenburg <hschulenburg@zoologie.uni-kiel.de>

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## MaxPlanck Tuebingen MouseGeneRegulatoryEvolution

### GENETIC MAPPING IN MOUSE INTERSPECIFIC HYBRIDS USING IN VITRO CROSSES

Friedrich Miescher Laboratory, Max Planck Campus,  
Tübingen, Germany

One postdoctoral position and a staff scientist position (both for 2 years in the first instance) are available in the Chan Lab at the Max Planck Institute in Tübingen as part of a prestigious 1.5M EUR European Research Council grant investigating the role of gene regulatory network evolution in mice by studying "in vitro" genetic crosses.

The goal of our research is to adopt cutting-edge tissue

culture techniques for studying evolutionary divergence in gene networks. We have developed a system to use mitotic recombination, as opposed to meiotic recombination through breeding, to generate genetic diversity in F1 interspecific hybrid mouse ES cells under tissue culture conditions (Lazzarano et al., PNAS, 2018). This allows us to create recombinant cell lines of effectively unlimited size at low costs within a matter of weeks. We now aim to use these "in vitro recombinant" panels to obtain phenotypic measurements via tissue engineering, organ-on-a-chip or droplet microfluidic single-cell methods.

We're looking for highly motivated individuals for the following roles:

1) Postdoc: You should be about to earn, or have recently earned your PhD in the areas of genetics, molecular biology or regenerative medicine. You should demonstrate expertise in tissue culture techniques. You should be able to demonstrate promise in early career success in a first author publication or preprint ready for submission. A background in genetic mapping or GWAS will be advantageous. A background in evolutionary biology will be helpful, but not a requirement. We are interested in candidates who are keen to apply and develop new genetic tools and technologies. Passion for research, team spirit and enthusiasm are essential.

2) Staff scientist: You should hold a Bachelors-equivalent degree or higher qualifications in the areas of genetics, molecular biology or regenerative medicine. We are looking for a strong track-record and demonstrated research experience and training, particularly in tissue culture and aseptic techniques. You will be a central team member assigned to work closely with a postdoc in carrying out work mainly using tissue culture, tissue engineering and microfluidics techniques. We will provide training on advanced tissue engineering techniques and microfluidics device fabrication, including but not limited to flow or microfluidics models to assay expression and tissue phenotypes. You will also operate flow cytometry instrument(s) in the context of tissue differentiation and single-cell studies. You will assist in generating DNA and RNAseq libraries to help dissect the genetic architecture of gene expression evolution in mouse or human tissue models.

We are a multidisciplinary team that focuses on the systems biology of development and evolution in mice, combining population and functional genomics with molecular biology and tissue engineering techniques to study the evolution of gene regulatory network in mouse and its close relatives. Our research group is funded by the European Research Council (ERC) and the Max Planck Society and is located on the Max Planck Campus in



Tübingen, Germany. Our campus hosts world-class research groups and operates state-of-the-art sequencing and other core facilities. English is the working language. All seminars and communications are in English.

The position is available for an initial 2 years with the possibility of extension. Salary and benefits are according to the German public service pay scale (TVöD Bund up to and including E13) and are commensurate with training and experience.

The Max Planck Society seeks to increase the number of women in areas where they are underrepresented, and therefore explicitly encourages women to apply. The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. For more information please see: <http://fml.tuebingen.mpg.de/chan-group/-open-positions> Reference Lazzarano et al., Genetic mapping of species differences via in vitro crosses in mouse embryonic stem cells. Proc Nat Acad Sci, 2018. doi: 10.1073/pnas.1717474115

Consideration of applications will begin on 15th April 2018, and will remain open until filled.

Please send your application with:

1. a statement of research interests and why you have applied for this position, 2. your CV, and 3. reference contacts (3 for postdocs and 2 for staff scientists)

to Dr. Frank Chan at [frank.chan@tue.mpg.de](mailto:frank.chan@tue.mpg.de).

Frank Chan Max Planck Research Group Leader  
Friedrich Miescher Laboratory of the Max Planck Society  
Max-Planck-Ring 9 72076 Tübingen Germany

T: +49 (0)7071 601 888 F: +49 (0)7071 601 801 @:  
[frank.chan@tue.mpg.de](mailto:frank.chan@tue.mpg.de)

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

## MichiganStateU PopulationGenetics

The Bradburd Lab at Michigan State is looking for a motivated, independent postdoc to join the lab! The lab is focused on population and evolutionary genetics, and especially on developing statistical methods to learn about evolutionary history of populations over space

and time in a variety of empirical systems, including humans. There are currently two main lines of inquiry in the lab: 1) Spatial population genetics: using population genetic data to study the processes that have generated patterns of genetic variation, with a particular focus on isolation, migration, and local adaptation.

2) Temporal population genetics: studying how population structure changes across space and through time, especially geared toward understanding population replacement and how populations adapt to climate change.

The specifics of the research projects are flexible, but could include methods for inferring spatial population genetic structure and admixture, quantifying the genomic fingerprint of adaptation to climate change, or identifying the genetic basis of traits in admixed populations.

Michigan State is an excellent place to conduct research in population genetics, with numerous research groups focused on similar areas (e.g., Braasch, Boughman, Conner, Edger, Fitzpatrick, Gallant, Huang, Lenski, Liu, Lowry, Meek, Scribner, Shiu). The Bradburd lab is a safe space and is committed to increasing diversity in the scientific community. I therefore strongly encourage applications from diverse candidates with related scientific interests.

Qualifications: Ph.D. in evolutionary biology, computational biology, mathematical biology statistics, or similar field. Strong interest in scripting/programming and statistics is required. Strong background in same is a bonus!

Salary will be competitive and dependent on previous experience. Start date is flexible, but ideally sometime summer/fall 2018.

To apply, please visit [careers.msu.edu](http://careers.msu.edu), respond to Job #498306, and submit a cover letter, current CV, and contact information for 3 referees. Informal inquiries welcome ([bradburd\[at\]msu\[dot\]edu](mailto:bradburd[at]msu[dot]edu)). More information available at the lab website: [genescape.org](http://genescape.org).

-Gideon

Gideon Bradburd Dept. Integrative Biology Michigan State University [genescape.org](http://genescape.org)

“Bradburd, Gideon” <[bradburd@msu.edu](mailto:bradburd@msu.edu)>

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## NewYorkU EvolutionaryGenetics

Postdoctoral position, Rockman Lab, NYU

Join us at NYU to work on fundamental questions in evolutionary genetics as a postdoctoral research associate.

We have an NIH-funded position to study the evolutionary genetics of complex traits, using a neotropical species of obligately-outcrossing *Caenorhabditis* nematode (relatives of *C. elegans*) as an experimental model. The species has convenient attributes for sampling variation from nature and constructing replicable genotypes that vary in autozygosity. The core research question is this: how can we predict the dominance of segregating variants? Directional dominance is ubiquitous but often neglected in evolutionary genetics and genomic prediction. Our powerful experimental system gives us a means to make substantial contributions here. Let's learn new things!

The postdoctoral researcher will have opportunities to approach the work from the perspectives of empirical or theoretical quantitative genetics, empirical or theoretical population genetics, comparative genomics, experimental model-organism genetics, and molecular developmental biology. An ideal candidate will be comfortable in one of these domains and eager to gain experience in one or more of the others. The position includes the option to conduct fieldwork with the worms in Panama, and the postdoc will have substantial autonomy to shape the direction of the research.

The Rockman Lab works on evolutionary genetics and genomics, with a focus on the relationship between developmental mechanisms and population-level phenotypic variation and evolution. Other funded projects in the lab center on developmental variation in a marine annelid populations, causes and consequences of recombination rate variation in nematode genomes, and quantitative genetics of growth patterns in pennate diatoms. NYU and the New York area are home to a broad group of evolutionary biologists and geneticists and an enormous community of exceptionally collaborative nematode researchers. This is a terrific training environment for a postdoc using worms to study evolution. New York City has a lot to offer, and NYU provides subsidized housing for postdocs near our lab in Greenwich Village.

NYU is an Equal Opportunity Employer and is commit-

ted to a policy of equal treatment and opportunity in every aspect of its recruitment and hiring process without regard to age, alienage, caregiver status, childbirth, citizenship status, color, creed, disability, domestic violence victim status, ethnicity, familial status, gender and/or gender identity or expression, marital status, military status, national origin, parental status, partnership status, predisposing genetic characteristics, pregnancy, race, religion, sex, sexual orientation, unemployment status, veteran status, or any other legally protected basis. Women, racial and ethnic minorities, persons of minority sexual orientation or gender identity, individuals with disabilities, and veterans are encouraged to apply for vacant positions at all levels.

Please send informal inquiries to Matt Rockman, mrockman@nyu.edu. An official NYU job application portal will be available shortly. The start date is flexible but the target is summer 2018.

Matthew Rockman <mrockman@nyu.edu>

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## NorthDakotaStateU EvolutionaryPhysiology

Post-doctoral Position: Avian Physiological Evolutionary Ecologist

Position Description: An enthusiastic and highly motivated post-doctoral researcher is sought to join the lab of Dr. Britt Heidinger (britt.heidinger@ndsu.edu) in the Department of Biological Sciences at North Dakota State University (NDSU). This is a 24-month, NSF funded position to study the cross-generational consequences of stress exposure in house sparrows (*Passer domesticus*). This integrative project is being conducted in collaboration with Dr. David Westneat (david.westneat@uky.edu) at the University of Kentucky. The post-doc will primarily reside in Fargo, ND, but will also spend time in Lexington, KY. During this position, the post-doc will gain valuable experience in research design, endocrine and molecular techniques, advanced statistical modeling including the use of animal models, and mentoring graduate and undergraduate students. The post-doc is also encouraged to pursue independent lines of research related to this project, which may include analyses of a unique, long-term database. The start date is somewhat flexible, but ideally will begin before August 1, 2018.

Candidates must 1) have a Ph.D. degree in biological sciences or a related discipline from an accredited insti-

tution; 2) have a demonstrated interest in research in physiological or behavioral ecology; and 3) have strong oral and written communication skills, including an ability to work as part of team and collaborate with others.

Preference will be given to candidates with demonstrated interest in 1) stress physiology; 2) senescence; 3) the long-term effects of early life conditions; and experience with: 4) animal models 5) EIA hormone assays, 6) qPCR and 7) avian systems.

Applicants must submit a cover letter; a curriculum vitae; a description of research experience (2 pages maximum); and contact information (including telephone numbers and e-mail addresses) for three professional references. All application materials must be submitted online at: <http://jobs.ndsu.edu/postings/9055> Review of applications will begin 8 May 2018 and continue until the position is filled.

Questions regarding the search may be sent to [britt.heidinger@ndsu.edu](mailto:britt.heidinger@ndsu.edu) and [david.westneat@uky.edu](mailto:david.westneat@uky.edu)

Britt J. Heidinger, Ph.D.

Assistant Professor

Department of Biological Sciences

NDSU Dept 2715

PO Box 6050

North Dakota State University

Fargo, ND 58108-6050

Email: [britt.heidinger@ndsu.edu](mailto:britt.heidinger@ndsu.edu)

Phone: 701-231-5377

“Heidinger, Britt” <[britt.heidinger@ndsu.edu](mailto:britt.heidinger@ndsu.edu)>

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## Penn Stanford RapidAdaptation

Postdoctoral positions in rapid adaptation

We are seeking to hire postdoctoral associates interested in the genomic, functional and mechanistic basis of rapid adaptation, using *Drosophila* spp. as genetic model systems. Projects include (1) manipulation of identified genes using CRISPR and other methodologies, combined with functional analyses in both the laboratory and field; (2) genomic and phenotypic analysis of natural populations as well as manipulative experiments in our field facility ([https://web.sas.upenn.edu/paul-schmidt-](https://web.sas.upenn.edu/paul-schmidt-lab/orchard/)

[lab/orchard/](https://web.sas.upenn.edu/paul-schmidt-lab/orchard/)). The general context for this work is the ongoing collaboration between the Schmidt laboratory at Penn and the Petrov laboratory at Stanford; there are extensive opportunities for integration across labs as well as development of independent projects.

Inquiries may be addressed to Paul Schmidt ([schmidtp@upenn.edu](mailto:schmidtp@upenn.edu)) or Dmitri Petrov ([dpetrov@stanford.edu](mailto:dpetrov@stanford.edu)), or in person at the *Drosophila* Research Conference, the Population, Evolutionary and Quantitative Genetics Conference, or at Evolution Montpellier 2018.

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## SarsCentre Norway EvolutionOriginSynapsesNeurons

Postdoc position: Evolutionary Origin of Synapses and Neurons

[http://www.sars.no/jobs/2018-](http://www.sars.no/jobs/2018-3862_postdoc_Burkhardt.php)

[3862\\_postdoc\\_Burkhardt.php](http://www.sars.no/jobs/2018-3862_postdoc_Burkhardt.php) There is a vacancy for a postdoctoral research fellow position at the Sars Centre in the research group headed by Dr. Pawel Burkhardt. The position is for a period of 4 years and is funded on the Sars Centre core budget. The Sars Centre belongs to the University of Bergen, and is partner of the European Molecular Biology Laboratory (EMBL).

About the project/work tasks: The Burkhardt group combines comparative biological systems in the laboratory to understand when and how the first synapses and neurons evolved. The group is particularly interested in studying the origin and evolution of synaptic proteins (Burkhardt et al, 2011 PNAS; Burkhardt et al, 2014 MBE; Bhattacharyya et al, 2016 eLife). We are looking for a highly self-motivated and enthusiastic Postdoctoral Research Fellow with interests in evolutionary biology, neurobiology and cell biology. The project will focus on the characterization of synaptic protein homologs in sponges and ctenophores to better understand the evolution of first neuron-like cell types in animals. The successful candidate will undertake research with the possibility to use a variety of techniques, ranging from super resolution immunofluorescence and electron microscopy, biochemical methods (protein purification, co-IPs, and analytical ultracentrifugation), mass spectrometry to X-ray crystallography to study synaptic protein homologs in sponges and ctenophores. The successful candidate will work in close association with the group leader and other lab members with the aim to

eventually contribute to the further development of the project in line with her/his interests.

Qualifications and personal qualities: - The applicant must hold a Norwegian PhD or an equivalent degree or must have submitted his/her doctoral thesis for assessment prior to the application deadline. It is a condition of employment that the PhD has been awarded - Strong motivation/enthusiasm to perform research at an internationally competitive level - Practical experience in biochemical techniques (protein purification, Co-IPs) and with different fluorescence imaging techniques is highly desirable - Specific experience with sponges or ctenophores is beneficial, but not essential - The ability to work both independently and to cooperate with others in a structured manner is essential - Proficiency in both written and oral English

About the position of postdoctoral research fellow: The position of postdoctoral research fellow is a fixed-term appointment with the primary objective of qualifying the appointee for work in top academic positions. The fixed-term period for this position is 4 years. Individuals may not be hired for more than one fixed-term period as a postdoctoral research fellow at the same institution.

Upon appointment, applicants must submit a project proposal for the qualifying work including a work schedule. It is a requirement that the project is completed in the course of the period of employment.

We can offer: - A professional, challenging and international working environment. - Well-equipped, modern laboratories and facilities - Salary at pay grade 57 (code 1352 / pay range 24, alternative 1) according to the state salary scale upon appointment. This constitutes a gross annual salary of NOK 490.900. Further promotions are made according to length of service. For particularly highly qualified applicants, a higher salary may be considered - Enrolment in the Norwegian Public Service Pension Fund (SPK) - A position in an inclusive workplace (IA enterprise) - Good welfare benefits

Your application in English must include: - A brief account of the applicant's research interests and motivation for applying for the position - The names and contact information for at least two reference persons. One of these must be the the main advisor from the PhD programme - CV including most relevant (i.e. first author) published papers and pre-prints - Transcripts and diplomas and official confirmation that the doctoral thesis has been submitted - Relevant certificates/references - List of any works of a scientific nature (publication list)

The application and appendices with certified translations into English or a Scandinavian language must be

uploaded at Jobbnorge.

Send your application electronically via JobbNorge by clicking on the button "Apply for this job" - see here. Please note that applications will be assessed only with the information available in JobbNorge when the deadline expires. It is the applicant's responsibility to ensure that all relevant attachments are submitted by the deadline.

Applications by e-mail only will not be considered.

Application deadline: 02 May 2018.

General: For further information about the position please contact Group Leader

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## ScandinavianResearchSchool Biosystematics

Considering a postdoc in systematic biology in Scandinavia?

ForBio - the Scandinavian Research School in Biosystematics is organising a training program for outgoing and incoming postdoctoral fellows to apply for European Commission H2020 MSCA Individual Fellowships.

The training program is open to potential incoming fellows to, and outgoing fellows from, research groups in systematic biology in Scandinavia, including systematics, taxonomy, phylogenetics, biogeography, etc. The target group are academically-engaged senior PhD students, postdocs and junior researchers. This covers the IF programs ER-ST (Standard European), ER-CAR (Career Restart Grant), ER-SE (Society and Enterprise), ER-RI (Reintegration), and GF (Global). We aim to have a mixed group of incoming and outgoing fellows.

The program runs from June 1st to the submission deadline of the H2020 MSCA-IF call on September 12th 2018. The training includes match-making between fellows and hosts, coaching, an intensive 3-day workshop at the University of Oslo, writing support, peer review, and liaison with EU coordination offices.

For more information about teachers, target group, course plan, costs and registration, see: <http://->

[www.forbio.uio.no/events/courses/2018/MSCAIF.html](http://www.forbio.uio.no/events/courses/2018/MSCAIF.html)

For potential hosts for incoming fellows see here (<http://www.forbio.uio.no/events/courses/2017/mscaif-hosts.html>), but also consider any relevant host at the University of Oslo, NTNU Trondheim, University of Bergen, University of Tromsø, Gothenburg University, Uppsala University, Stockholm University, The Natural History Museum of Denmark, University of Copenhagen, Swedish Museum of Natural History, University of Aarhus, etc etc. SE (Society and Enterprise) fellowships can include mobility to research agencies, SMEs and NGOs.

Registration: Fellows should register online and provide contact information of their host before May 15th. Registered fellows will be evaluated and notified by May 21st regarding acceptance and participation in the training program. Make sure the reserve the dates 18-20 June for the workshop.

If you have any questions, contact Hugo de Boer ([hugo.deboer@nhm.uio.no](mailto:hugo.deboer@nhm.uio.no)) for more information.

Hugo de Boer

Natural History Museum University of Oslo P.O. Box 1172 Blindern 0318 Oslo, Norway Phone: +47 22851875

Leader of ForBio - the Scandinavian Research School in Biosystematics [www.nhm.uio.no/english/about/organization/research-collections/people/-hugode/](http://www.nhm.uio.no/english/about/organization/research-collections/people/-hugode/) [www.forbio.uio.no/](http://www.forbio.uio.no/) Hugo de Boer <[h.d.boer@nhm.uio.no](mailto:h.d.boer@nhm.uio.no)>

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## StirlingU HostPathogenEvolGenetics

Post Details Post Doctoral Research Assistant in host-pathogen evolutionary genetics for sustainable insect pest control Fixed Term Contract - 10months Grade 6 -25,728- 31,604 p.a. The closing date for this post is midnight on Monday 30th April 2018. Interviews are being held on Friday 11th May 2018.

A 10-month, full-time postdoctoral position is available to work with Drs Luc Bussière (Stirling), Matthew Tinsley (Stirling) and Ricardo Polanczyk (UNESP, Brazil) on a BBSRC-FAPESP Newton funded grant “Overcoming insecticide resistance using diverse fungal pathogens and heterogeneous agricultural landscapes”. The project studies the interactions between lepidopteran crop pests and fungal pathogens that can be deployed as biopesticides.

The Post Despite extensive research on insecticide application regimes, insecticidal compounds and genetically modified crops, insects continue to evolve resistance against control agents with predictable regularity. In an effort to develop more sustainable approaches to pest control, our project borrows insights from evolutionary science and the particular features of host-pathogen interactions. Insecticide resistance evolution occurs when a single control agent is applied over a broad area, then consistent evolutionary pressures drive previously-rare resistance genes to spread rapidly through the pest population. To prevent this, we will study how multiple fungal pathogen biopesticide strains can be used in a spatial matrix across agricultural landscapes, so that selection for resistance varies in different locations, preventing a uniform evolutionary response.

This post is based in Stirling, but joins a project that combines research in Stirling and Jaboticabal, Brazil to study the genetic architecture of host resistance to several entomopathogenic fungi when insects are reared on several different host plants. The project studies lepidopteran crop pests and investigates the power of genotype by environment interactions to prevent resistance evolution to fungal pathogens used in biocontrol. Collaboration and joint training with other researchers involved in the project will be encouraged and facilitated

The research will be conducted using the Stirling University’s state-of-the-art Controlled Environment Facility and University Gardens. The appointee will be part of a thriving research environment within Biological and Environmental Sciences (BES) with more than 40 principal investigators, alongside postdoctoral researchers and 60 PhD students.

Equality and diversity are central to our activities at the University of Stirling. We believe everyone should be treated with respect and we deal with people as equals. We promote equality and celebrate diversity through a variety of initiatives. The University has been awarded the Athena SWAN Bronze award, the national charter for women in science, which recognises and promotes good practice in advancing women’s careers in STEMM academia (Science, Technology, Engineering, Mathematics and Medicine). In addition, Biological & Environmental Sciences holds a departmental Athena Swan bronze award. Further details can be found here:

<http://www.stir.ac.uk/equalityanddiversity/-athenaswan/> <https://www.stir.ac.uk/news/2015/-10/athena-swan-awards/>

We welcome applications from everyone irrespective of gender and ethnic group, but as women and members of ethnic minority groups are currently under-represented at this level of post, we would encourage applications



from members of these groups. Appointment will be based on merit alone.

**Description of Duties** The appointee will be expected to contribute to the intellectual development of the project, including participating in analysis and write-up of papers describing the work. In addition, the appointed researcher will participate in project meetings, and help supervise undergraduate and MSc students working on related research.

The appointed researcher will manage a large quantitative genetics experiment: manipulating infection status and diet for many half-sibling families of lepidopteran larvae, then monitoring responses to infection. The researcher will also oversee the day-to-day husbandry of insect cultures and manage the growth of larval food plants. The ability to travel to Brazil in late May to assist in field collections is desirable, but not essential.

**Essential Criteria** - BSc in a relevant discipline, such as evolutionary biology, parasitology, infection biology, entomology or quantitative genetics. Experience in working with insects. Strong organisation and communication skills. - The appointed candidate must be organised and independent, able to communicate well, work collaboratively in a team, and

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## UAlabama EvolutionaryBiology

Comparative Cryptobiosis University of Alabama, Tuscaloosa

A postdoctoral research position in the field of evolutionary biology is available in the laboratory of Dr. Jason Pienaar in the Department of Biological Sciences at the University of Alabama (<https://bsc.ua.edu/profiles/-jason-pienaar/>)

This position will entail developing communities of tardigrades, nematodes, and rotifers typically associated with bryophytes into an experimental microcosm for studying cryptobiosis (the ability to suspend metabolic activity and enact morphological and physiological changes to survive complete desiccation). The applicant will in addition interact with the laboratory of Dr. Janna Fierst

(<https://bsc.ua.edu/profiles/janna-fierst/>) to decipher the genomics and transcriptomics underlying cryptobiosis.

This position is available for a highly enthusiastic post-doctoral research associate whose primary career interest is to develop expertise in integrative approaches to addressing mechanistic and evolutionary questions of the evolution of enigmatic traits such as cryptobiosis. Depending on academic experience, the primary responsibilities of the post doc could be any combination of: genomic and transcriptomic assembly and analyses; molecular phylogeny development; development of culture techniques to establish lab populations and managing field collections and/or; experimental induction of cryptobiotic states and data collection for phylogenetic comparative method analyses. Other duties will consist of gathering and managing preliminary data from the field, participating in experimental design, aiding in grant writing, collaborating with undergraduate, graduate students and other faculty as appropriate and outreach. The expectation is that findings will be published in peer reviewed journals and presented at relevant conferences.

Applicants with diverse research backgrounds are encouraged to apply. Candidates must have received a Ph.D. in a relevant field by the start date.

Funding is available for 2 years with annual renewal dependent on performance evaluation, and will include a competitive salary, full benefits, and conference travel allowance. The University of Alabama offers a range of professional development opportunities. Application review will begin July 1st, 2018 and will continue until the position is filled. Start date is negotiable, but the successful applicant should preferably be able to start in the Fall 2018 or Spring 2019 semester.

Applicants interested in the position should contact Dr. Jason Pienaar ([jpienaar@ua.edu](mailto:jpienaar@ua.edu))

Applicants must apply by submitting an application to the Fall 2018 Biological Sciences Departmental post-doctoral pool at [facultyjobs.ua.edu](http://facultyjobs.ua.edu) (requisition number 0811250): <http://facultyjobs.ua.edu/postings/42653> Materials should include:

1. Cover letter stating your application for the “Comparative cryptobiosis” position, a brief description of research accomplishments and interests, and career goals.
2. The names and contact information for 3 references.
3. Curriculum vitae.
4. Two representative publications.

About the University of Alabama:

The University of Alabama is the flagship campus of the University System of Alabama, with an enrollment of over 35,000 students. The University is committed to achieving excellence as one of the country's primary centers of research and education. It is located in the vibrant college town of Tuscaloosa, AL, which boasts many cultural and athletic activities. The campus also benefits from the close proximity to the Birmingham metropolitan community.

The University of Alabama is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

"Pienaar, Jason" <jason.pienaar@ua.edu>

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## UBologna MarineBiodiversity

### POST-DOCTORAL RESEARCH POSITION

Dear all,

In the context of an European Project on Marine Metabarcoding Benthic Biodiversity, we are seeking to recruit an enthusiastic and highly motivated Postdoctoral researcher to work at the laboratory of Ecological and Environmental Genetics in Ravenna Campus (University of Bologna, Italy).

The successful applicant will be involved in a research project aiming to use barcoding and metabarcoding (DNA based identification and high-throughput DNA sequencing) to unlock the barriers that prevented the development of marine monitoring networks for hard bottoms benthic habitats, in particular by: (1) establishing rationale rules based on connectivity patterns to determine the network of sites to be monitored, (2) standardizing the sampling procedures for hard bottom assemblages, and (3) finding solutions to automatize and standardize species composition assessment. The project includes partners from France, Italy and Spain and will assess the communities established on natural substrates and which type of systems for standardized sampling of hard substrates (e.g. ARMS, ASU) better represents them. Species composition will be assessed using, and improving, innovative automatized methods (e.g. metabarcoding) calibrated with traditional identifications based on morphology.

The candidates must have a PhD degree in an area that includes the use of modern molecular biological methods to answering environmental or ecological questions, and with enough publications and experience in the

corresponding themes.

The candidate will be primarily responsible for fieldwork, metabarcoding libraries, analyses of data, and shall contribute to manuscript writing.

The candidates should have experience in: 1. Experimental planning and fieldwork, organisation of sample collection (at least second level dive certification).

2. DNA extraction, barcoding and preparation of library for metabarcoding; Statistical analyses; scripting in R; bioinformatic methods for analysis of high throughput DNA sequencing in DNA metabarcoding applications; and high quality data presentation for publication.

3. Morphological taxonomy of benthic species (invertebrates, algae).

4. Working knowledge of English, good communication, teamwork and organisational skills as well as to be able to work independently.

The work will be mainly conducted at the Ravenna Campus (University of Bologna). However, the candidates may be required to do some fieldwork and spend some time in other labs, both in France and in Spain.

Moreover, there will be opportunities for training, conference attendance and networking.

The position is a full time contract available immediately (September 2018) for one year in the first instance, with the possibility after review to extend the contract for further two years.

For more information, and for consideration, please email a complete CV, your motivations and two reference letters) to federica.costantini@unibo.it Federica Costantini, Laboratory of Experimental Ecology University of Bologna Via S. Alberto 163 I-48100 - Ravenna Italy

– Federica Costantini, PhD

Laboratorio di Ecologia sperimentale Universite di Bologna, Dipartimento di Scienze Biologiche, Geologiche ed Ambientali BIGEA, sede di Ravenna Via S. Alberto 163, 48123 Ravenna, Italy

tel: +39 0544 937401 fax: +39 0544 937411 e-mail: federica.costantini@unibo.it skype username: fedalpha

Pagina WWW: <http://www.ecology.unibo.it> <http://www.ecology.unibo.it/page/federica.htm> federica costantini <federica.costantini@unibo.it>

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## UBuffalo FunctionalGenomics

Two postdoctoral fellowships are available in the lab of Dr. Trevor Krabbenhoft in the Department of Biological Sciences and the RENEW Institute ([www.buffalo.edu/-renew](http://www.buffalo.edu/-renew)) at the University at Buffalo.

One position will focus on using functional genomics to understand morphological and ecological variation in coregonid fishes of the Great Lakes. The project will involve a combination of genome sequencing, sequence capture, and experimental approaches to identify and understand how genetic variation produces the extensive phenotypic diversity in a species flock of the genus *Coregonus*.

The second position is more open in research focus. Funding is available to support projects in several potential research areas, depending on the interests and expertise of the successful applicant. Possible areas, building off ongoing projects in the lab include:

1. Fish genome sequencing and assembly using long read technology
2. Genome evolution following WGD (gene silencing, diploidization, etc.)
3. Integration of ecology and genomics/evolutionary biology
4. Epigenetics and its role in adaptation
5. Genetic and environmental control of sex determination

The Krabbenhoft Lab strongly encourages creativity and is open to new research directions. A PhD in biology, computer science, bioinformatics, or related field is required. Candidates with strong bioinformatics skills are especially encouraged to apply. Salary and benefits are highly competitive. Both positions are available initially for one year and renewable for up to three years.

University at Buffalo is a comprehensive research university and member of the Association of American Universities. Buffalo was recently ranked the #1 most affordable place to live in the U.S. by Forbes Magazine, the city with the 6th best quality of life by NerdWallet, and was among the eight most underrated cities in America by Jetsetter. The city is large enough to have urban amenities, arts and culture, but with easy access to nature, including two Great Lakes, Niagara Falls, the Finger Lakes region, and Adirondacks.

Review of applications will begin at the end of April 2018 and will continue until positions have been filled. The start dates are flexible but we hope to fill at least one position by mid-May 2018. Please contact Trevor

Krabbenhoft ([tkrabben@buffalo.edu](mailto:tkrabben@buffalo.edu)) for more information or to discuss potential research directions. Job details may be found at the following links:

<https://www.ubjobs.buffalo.edu/postings/13852>

<https://www.ubjobs.buffalo.edu/postings/13853> “The Research Foundation for SUNY is an Equal Opportunity Employer, and welcomes all to apply including females, minorities, individuals with a disability, protected veterans. The RF does not discriminate against employees or applicants based on sexual orientation, gender identity, or any other characteristics protected by applicable law.”

“Krabbenhoft, Trevor” <[tkrabben@buffalo.edu](mailto:tkrabben@buffalo.edu)>

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## UCalgary ConvergentAdaptation

The Yeaman lab at the University of Calgary is looking to hire a postdoctoral fellow to work on a meta-analysis studying the repeatability of adaptation at the genome scale. The basic idea of the project is to apply some methods we recently developed (<https://www.biorxiv.org/content/early/2018/03/09/279661>) to quantify the repeatability of adaptation in a range of published datasets and test hypotheses about potential causal factors. We expect that this will include datasets from experimental evolution in microbes and genome scans of local adaptation in natural populations, but may extend to data on QTLs. There is a particular interest in applying these methods to medically relevant traits. Depending upon the interests of the applicant, it would also be possible to work on some individual-based simulations exploring a range of questions related to the genetic and genomic architecture of adaptation. This position will require advanced R skills and familiarity with GWAS and other genome scan methods.

The position will run for 2+ years (CAD \$50k salary + benefits).

TO APPLY: Please send a CV and a short description of your interest in the position and any relevant research experience to [samuel.yeaman@ucalgary.ca](mailto:samuel.yeaman@ucalgary.ca), along with the names and emails of three people I could contact for reference letters. I will begin reviewing applications on May 1st, 2018, but please contact me to check in if you need to make a quick decision.

[https://yeamanlab.weebly.com/uploads/5/7/-9/5/57959825/postdoctoral\\_position.pdf](https://yeamanlab.weebly.com/uploads/5/7/-9/5/57959825/postdoctoral_position.pdf)

“yeaman@zoology.ubc.ca” <[yeaman@zoology.ubc.ca](mailto:yeaman@zoology.ubc.ca)>

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## UCalifornia Berkeley PopulationGenetics

Recruitment Period Open date: April 16th, 2018 Next review date: May 1st, 2018 Apply by this date to ensure full consideration by the committee. Final date: May 17th, 2018 Applications will continue to be accepted until this date, but those received after the review date will only be considered if the position has not yet been filled.

Description Description: The Moorjani Lab (<https://moorjanilab.org/>) at University of California, Berkeley has a post-doctoral position available for motivated candidates with background in statistical population genetics and/or data science.

Our lab focuses on using statistical and computational approaches to study questions in human genetics and evolutionary biology. A central aim in the lab is to understand the impact of evolutionary history on genetic variation and to apply this knowledge to learn about human history and biology. To this end, we use genetic data from ancient specimens and present-day species to learn about: (1) when key events (such as introgression and adaptations) occurred in human history, (2) how different evolutionary processes such as mutation rate evolve across primates, and (3) how we can leverage these patterns to identify genetic variants related to human adaptation and disease. The research in the lab involves both development of new methods and large-scale genomic data analysis.

Responsibilities: A successful candidate will develop and apply computational approaches to large genomic datasets to characterize patterns of population history and evolution. The main responsibilities include conducting research, attending regular lab meetings and journal clubs, and preparing research results for publication and presentations at scientific meetings. Opportunities may also exist for mentoring graduate and undergraduate students.

Minimum/Basic Qualifications required at the time of application: - Completion of all doctoral degree requirements except the dissertation in genetics, computational biology, biostatistics, population genetics or related fields.

Additional Qualifications (required by start date): - PhD or equivalent degree in genetics, computational

biology, biostatistics, population genetics or a related field.

- Knowledge of statistics and population genetics theory.
- Demonstrated record of research productivity and publications.
- Programming experience (e.g. C/C++, Python/ Perl, R or other programming languages)

Preferred Qualifications: Experience with large-scale genomic data analysis.

Salary: This is a full-time position. Salary is commensurate with qualifications and experience.

How to apply: To apply, please go to the following link: <http://apptrkr.com/1205272> Applicants should submit the following materials: - A cover letter - A curriculum vitae - Statement of Research (One-page summary of research interests) - Contact information for 3 references Letters of reference are not required at this time. We will seek your permission before contacting your references. All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are provided via a third party (i.e., dossier service or career center), to the UC Berkeley statement of confidentiality: <http://apo.berkeley.edu/evalltr.html> . This position will be open until filled. The anticipated start date is May 2018. The appointment is for a duration of one year with the possibility of annual renewal up to three years. Please address inquiries to Maria Ruiz, [maruiz@berkeley.edu](mailto:maruiz@berkeley.edu).

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: <http://policy.ucop.edu/doc/4000376/-NondiscrimAffirmAct> . Job location Berkeley, CA Requirements Documents - Curriculum Vitae - Your most recently updated C.V.

- Cover Letter - Statement of Research - One-page summary of research interests References 3 references required (contact information only)

Jessica Godoy <[jessica@jobelephant.com](mailto:jessica@jobelephant.com)>



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## UCCork Ireland ConservationBiology

Post-Doctoral Researcher Job Posted: 06 Apr 2018 Closing Date for Applications: 01 May 2018 Environmental Research Institute, University College Cork, Ireland, School of Biological, Earth and Environmental Sciences College of Science, Engineering and Food Science Contract Type: Fixed Term Whole-Time Job Type: Research Salary: pounds 36,853-pounds 43,828 p.a. (IUA Salary Scale)

**Position Summary** The School of Biological, Earth & Environmental Science, University College Cork, Ireland is seeking a Post-Doctoral Researcher to support an important new research project in the area of conservation biology: Horizon 2020 AMBER project - Adaptive Management of Barriers in European Rivers (<https://amber.international/>). The position will be based at the Marine Institute's research facility in Newport Co. Mayo, but the successful candidate will be expected to travel and liaise with a large network of 20 partners from 11 countries. Essential requirements 'V A PhD in life sciences or equivalent disciplines with experience in conservation assessment of vertebrate taxa. Knowledge of Population Viability Analysis, IUCN Red List classification and relevant software (e.g. RAMAS; VORTEX; MARXAM; InVEST), and Geographical Information Systems is required. A publication record commensurate with career stage is expected.

**Background to project** There are a conservatively c. 5,000 unique Atlantic salmon populations in the North-east Atlantic, whose existence is important for maintaining the resilience of the species (portfolio effect). The species is currently classified as 'ÅYVulnerable'Å in the IUCN Red List of Threatened Species. Unfortunately, the IUCN assessment did not take into account differences in the conservation status of individual stocks (including sub-populations within individual river basins), some of which (particularly in S. Europe) may be near extinction. The species has gone extinct in Belgium, Czech Republic, Germany, Netherlands, Poland, Slovakia, and Switzerland, and many populations have been lost from the Iberian Peninsula, Denmark, Sweden, Norway, Ireland, France, England, Wales, Scotland, and European Russia. Although local extirpations have been attributed to a number of factors, the damming of rivers and subsequent loss of connectivity has been signalled

as the principal and most widespread cause for salmon declines.

This project will use the Barrier Inventory being developed in the AMBER project to undertake a trans-European, river by river assessment of the status of Atlantic salmon within a Geographical Information System (GIS) based framework. We will be focussing specifically on the impact of barriers on river connectivity and the distribution of the species within individual watersheds. We will apply AMBER tools to provide the first quantitative, river by river assessment of the conservation of A. salmon across Europe, and determine barrier effect thresholds. These models will be validated with spatially explicit national juvenile salmon stock assessment datasets collated by various national agencies within the EU.

A key deliverable of this task will be to provide accurate estimates of the global extent of river habitats lost to Atlantic salmon (and other migratory fish) across Europe at four spatial scales: 1. Individual river systems; 2. Genetically explicit regionally river groups; 3. Politically explicit regional groups; 4. Trans-European level.

Furthermore, we will seek to identify, locate and target barriers whose removal or modification will result in the greatest benefit for the restoration of self-sustaining populations and highest economic and social return.

A second important deliverable will be the production of the EU Salmon Atlas and associated database which will be overlaid with the European Barrier Inventory. For this we will work closely with European Joint Research Centre and Swansea University (Prof Carlos Garcia de Leaniz, [c.garciadeleaniz@swansea.ac.uk](mailto:c.garciadeleaniz@swansea.ac.uk)).

Post duration: 24 months Salary: pounds 36,853-pounds 43,828 p.a. (IUA Salary Scale) Project: Assessing The Conservation Status of Atlantic Salmon in Europe.

**Key Duties and Responsibilities** Post-Doctoral Researcher (PDR): This title will apply to newly qualified Post-Doctoral Researchers and will be considered as a period of training as the researcher will have dual goals in terms of the research project and their own career development.

The researcher will be mentored by a Principal Investigator (PI). It is expected that a researcher would spend not more than 3 years at the Post Doctoral level, subject to the term of the project and would then be eligible to compete for a Senior Post Doctoral post advertised by the University.

The primary focus of the Postdoctoral Researcher will be research however a particular emphasis during this



stage should include;

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## UExeter TreePhylogenetics

Two year Post-doctoral position working with a project building research partnerships and techniques that can deliver more productive agroforestry and silvopastoral systems in Brazil using native, nitrogen fixing Inga (Leguminosae-Mimosoideae) tree species. This BBSRC Global Challenges Research Fund (GCRF) funded post is available from May 2018 - April 2020 on a full-time basis.

You will apply next-generation, hybrid-capture sequencing techniques and phylogenetic analyses to identify relatives of Inga species already utilised in agroforestry systems. Because Inga is highly species-rich and ecologically important in Latin American rain forests, your results will also have direct relevance to big questions in tropical evolution and ecology.

The post will include: (i) Establishment of next-generation, hybrid-capture sequencing techniques for Inga (using existing protocols). (ii) Bioinformatic analysis of data for subsequent phylogenetic and population genetic analysis. (iii) Phylogenetic analysis of hybrid-capture DNA sequence data. (iv) Development of markers based on transcriptome and hyb- seq data for interpreting genetic diversity within Inga species. (v) Mentoring of technical staff and students (vi) Leading paper-writing and presentation of results at international meetings

The successful applicant will be able to present information on research progress and outcomes, communicate complex information, orally, in writing and electronically and prepare proposals and applications to external bodies.

Applicants will possess a relevant PhD (or be nearing completion) or possess an equivalent qualification/experience in a related field of study and be able to demonstrate sufficient knowledge in the discipline and of research methods and techniques to work within established research programmes. Applicants will have

experience in working with library preparation for next-generation sequencing and good general molecular biology laboratory skills. In addition, they will be familiar with bioinformatics for managing and analysing next generation DNA sequence data and have experience with phylogenetic and population genetic analysis. The successful applicant will also be able to work collaboratively and to supervise the work of others as required.

For further information please contact Toby Pennington on e-mail [t.pennington@ex.ac.uk](mailto:t.pennington@ex.ac.uk) or telephone 01392 723342.

Relevant papers: Porro, R. et al. 2012. *Advances in Agroforestry* 9: 391-428; Pennington, T.D & Fernandes, E.C.M. 1998. *The Genus Inga: Utilization*. RBG Kew, UK. Nicholls et al. 2015. *Frontiers in Plant Science* <http://dx.doi.org/10.3389/fpls.2015.00710> Richardson, J.E. et al. 2001. *Science* 293: 2242-2245. Dawson, I.K. et al. 2008. *Conservation Genetics* 9: 361-372.

Job title: Postdoctoral Research Associate Job reference: P62137 Application closing date: 17/05/2018 Location: Exeter Salary: The starting salary will be from pounds 28,936 up to pounds 33,518 pa on Grade E, depending on qualifications and experience.

[https://jobs.exeter.ac.uk/hrpr\\_webrecruitment/-wrd/run/ETREC107GF.open?VACANCY\\_ID=-975311LS9O&WVID=3817591jNg&LANG=USA](https://jobs.exeter.ac.uk/hrpr_webrecruitment/-wrd/run/ETREC107GF.open?VACANCY_ID=-975311LS9O&WVID=3817591jNg&LANG=USA)  
KIDNER Catherine <[Catherine.Kidner@ed.ac.uk](mailto:Catherine.Kidner@ed.ac.uk)>

## UFlorida Biodiversity

Starting immediately, I have 2 years of funding for a postdoc to work on an NSF Dimensions of Biodiversity project. This phase of the project is aimed at understanding the feedbacks between moss genotypic variation (mostly RADseq data), epiphytic microbial community assembly, N-fixation, and the abiotic environment. The postdoc has the opportunity to conduct fieldwork in Alaska if they are interested. The team also includes Michele Mack (NAU), Noah Fierer (CU), and Jose-Miguel Ponciano (UF) - it's a dynamic and fun group.

The main short term duties are to analyze RADseq / GBS data, and mentor undergraduate researchers. There will be opportunities to develop and pursue independent research, both in the context of the Dimensions project as well as with the ongoing *Ceratodon* genome project.

The University of Florida has a strong postdoc community with a numerous laboratories working in genetics, genomics, and plant biology. The Biology Department has a collegial and intellectually stimulating environment.

Please get in touch if you are interested in the position, or feel free to pass this ad along to qualified candidates.

Thanks much,

Stuart

Stuart McDaniel

Associate Professor Department of Biology PO Box 118525 University of Florida Gainesville FL 32611

ph: 352 273 0123

fax: 352 392 3704 <http://mcdaniellab.biology.ufl.edu/>

Twitter: @mcdaniellab

“McDaniel, Stuart” <stuartmcdaniel@ufl.edu>

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## UFlorida HumanEvolutionaryGenetics

Post-doctoral position in Human Evolutionary Genetics and Epigenetics, Laboratory of Connie Mulligan, Genetics Institute, University of Florida, Gainesville, FL, USA

Post-doctoral position to work on two ongoing NSF and internally funded projects:

1) Investigation of genetic, epigenetic, and biological signatures of war trauma exposures in Syrian refugees. This is a collaboration with Catherine Panter-Brick (Yale University) and Rana Dajani (Hashemite University, Jordan) to integrate genetic and epigenetic analyses into an ongoing study to measure the effects of violence and trauma in Syrian refugees. The first project is an intergenerational study to investigate the epigenetic impacts in offspring of mothers and grandmothers who were exposed to war trauma while pregnant. The overarching question is to determine if trauma-induced methylation changes are heritable across two generations in humans. In the second project, genetic variants are being assayed to predict the impact of past trauma exposures and the effects of a program intervention on self-reported measures of mental health in Syrian refugee youth. Epigenetic variants will be tested as possible mediators of the effect of stress on mental health outcomes. See project website at <http://www.elrha.org/map-location/>

[yale-psychosocial-call2/](http://www.elrha.org/map-location/yale-psychosocial-call2/) .

2) Investigation of an epigenetic mechanism to mediate the effects of maternal stress on maternal and infant health in the Democratic Republic of Congo (DRC). We are testing for associations between maternal stress exposures, newborn health outcomes and changes in DNA methylation and gene expression in mothers and their infants. More broadly, we are interested in the idea that mechanisms may have evolved to allow the genome to respond to psychosocial stressors and that complex phenotypes may be shaped by early life experiences that alter gene expression through epigenetic alterations. Samples and data have already been collected and research is funded by NSF. See <http://www.tandfonline.com/doi/pdf/10.4161/epi.21180> and <http://onlinelibrary.wiley.com/doi/10.1111/cdev.12487/epdf> .

Qualifications: A PhD, good publication record, and strong background in the generation of genetic data (microarray, gene expression, NGS, SNP detection) and data analysis (gene association analysis, regression analysis, genetic ancestry estimation, linkage analysis, etc) are essential. A background in evolutionary genetics and experience with methylation data (Illumina chips, pyrosequencing, etc), RNA sequence or gene expression array data, and/or additional computational or bioinformatics experience is a plus. Candidates who speak French or Swahili are encouraged to apply. In addition to the projects listed above, there are excellent opportunities for the successful candidate to develop new lines of research as well as productive collaborations outside the lab.

The University of Florida is a top 10 public university with a university-wide commitment to genetic research. The Department of Anthropology ([www.anthro.ufl.edu](http://www.anthro.ufl.edu)) has 30 full-time faculty with diverse interests and is one of the top rated programs in the country (6th among public institutions, 11th overall). The University of Florida Genetics Institute ([www.ufgi.ufl.edu](http://www.ufgi.ufl.edu)), where the Mulligan lab is located, is an inter-college institute with a dedicated research building intended to enhance opportunities for collaboration. Gainesville is located in north central Florida (away from the hurricanes!), with average temperatures ranging from 45F to 90F. Beaches on the gulf and Atlantic coast are ~ 1½ hours away.

To apply: via email, send a CV, statement of research interests, and names and contact information for three references. Applications and inquiries should be addressed to Connie Mulligan at [cmulligan@ufl.edu](mailto:cmulligan@ufl.edu). Send an email to set up a meeting if you will be at the AAPA meetings in Austin.

Review of materials will begin April 30 and will continue

until the position is filled. Start date is flexible and the successful candidate can begin as early as May, 2018. Salary is commensurate with experience. Position may be extended for a total of three years. Informal inquiries prior to submitting a formal application are welcome. AA/EOE

— Connie J. Mulligan, PhD Professor, Department of Anthropology 2033—Mowry Rd, PO Box 103610 | University of Florida | Gainesville, FL 32610-3610 Office: 409 Genetics Institute | Telephone: 352-273-8092 | Fax: 352-273-8284 Website: <http://www.clas.ufl.edu/users/-mulligan/Webpage/index.html>

“Connie J. Mulligan” <cmulligan@ad.ufl.edu>

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## UHaifa EvolutionaryBiol

\* Postdoctoral positions available in ecology and evolution \*

Postdoctoral scholarships are available for North American scientists of US or Canadian citizenship. Candidates are invited to apply for a position in any of the research groups in the Department of Evolutionary and Environmental Biology and the Institute of Evolution at the University of Haifa: <http://sciences.haifa.ac.il/-newsci/main/index.php/en/faculty-orig> The Department of Evolutionary and Environmental Biology and the Institute of Evolution offer a diverse, interdisciplinary, international, and multilingual work environment. The various research groups offer a diverse range of projects involving lab experiments and field studies, behavioral, developmental, cellular, molecular, and genetic essays, genomic/transcriptomic/microbiome analyses, and bioinformatics. Postdocs will have opportunities for collaboration with research groups working in various fields, with organisms ranging from bacteria to mammals and agricultural crops, and employing complementary techniques from tracking animal flight to evolutionary genomics.

Candidates should hold a Ph.D. in biology and have experience in advanced techniques in their respective field. Candidates from adjacent or complementary fields will also be considered (for example, conservation ecology or evolutionary modelling). Preference will be given to candidates with a strong publication record and research productivity. The Department and the Institute aim at a higher proportion of women in science. Qualified female scientists are encouraged to apply. Female

scientists will be preferentially considered in case of equivalent qualification, competence and achievements. Candidates must hold a Ph.D. degree, or must submit their Ph.D. thesis by October 1, 2018. To apply, candidates must obtain the support of a potential supervisor. The start date is flexible but anticipated to be in Fall 2018.

Funding is available for two years, with an optional extension, including an annual scholarship of \$36,000US (not taxable), \$10,000 for research expenses, and \$4,000 for travel.

Candidates should first obtain the support of a potential supervisor (PI) and then submit an application to Ms. Gali Levy: [glevy3@univ.haifa.ac.il](mailto:glevy3@univ.haifa.ac.il) \*\*\* Application deadline: May 26, 2018 \*\*\*

The application should include the following: 1) Curriculum vitae 2) List of publications 3) Research proposal (maximum 3 pages) 4) Three letters of recommendation 5) Letter of support from the potential hosting supervisor

Informal inquiries are welcome.

Eyal Privman <[eprivman@univ.haifa.ac.il](mailto:eprivman@univ.haifa.ac.il)>

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## UIceland Bioinformatics

The University of Iceland is seeking a Post doctoral researcher in bioinformatics to work on research and to build up bioinformatic services. The university has established Mimir, a computer cluster for bioinformatic analyses. The researcher will have dual responsibilities, one as a bioinformatics manager working with different research groups, many of which take part in the Biomedical center, University of Iceland (<http://lifvisindi.hi.is/>) and the other as a researcher working with the Melsted bioinformatics group (<https://melstedlab.github.io>).

Field of work The managerial duties are, installing and maintaining selected bioinformatic programs and libraries, establish analysis workflows, assist groups with specific projects and analyses, train graduate students and other researchers. The research project with the Melsted group will focus on development of algorithms for high throughput sequencing and programs for analyses of DNA/RNA assembly or RNA quantification. The candidate will have an opportunity to take part in ongoing research projects, earn co-authorship on scientific manuscripts, and perform independent research.

Qualification requirements Doctoral degree in bioinformatics, computational biology, biostatistics, or equivalent. Extensive experience working in bioinformatics, computational biology, biostatistics, or equivalent is required. Practical experience with linux and bioinformatics, for example installing programs, scripts, libraries and handling updates, programming and scripting in Python, R/Bioconductor and bash and run next-generation genome data analyses programs is essential. Direct experience and interest in developing bioinformatic software and develop accessible tools and workflows for the scientific community is desired.

How to apply The position is available for two years with a possibility of an extension should the project be continued. The applicant is expected to start the position as soon as possible.

Please include the following with the application: Description of how the applicant meets the requirements, interests in the project and how they can contribute to the project (max 2 pages). CV. Certificates of education (BSc, MSc, PhD) and distribution of grades. The name, telephone number and e-mail address of two referrals (with a statement of their connection to the applicant). Overview of publications if applicable. Applicants are also invited to send PDF of MS and/or PhD thesis (in any language) and any other relevant publications if available (max 5 documents).

Salary will be according to the current collective wage and salary agreement between the Union of University Teachers and the Minister of Finance.

All applicants will receive a reply and they will be informed as to the selection of a successful applicant when the decision has been made. Applications may be valid for up to 6 months after the closing of the application deadline.

Appointments to positions at the University of Iceland are made in consideration of the Equal Rights Policy of the University of Iceland.

The University of Iceland has a special Language Policy.

The School of Engineering and Natural Sciences employs ca. 360 people in academic positions. The School offers an international working environment, with the number of international employees and students increasing each year. Currently about quarter of all employees and graduate students are international. There are around 2900 students at the School, divided into six faculties, including approximately 350 MS students and 150 doctoral students. Research institutes at the School are the Science Institute that divides into the Institute of Earth Sciences and Institute of Physical Sciences, Institute of Life and Environmental Sciences, Engineering Research

Institute and the Institute for Sustainability Studies which is an interdisciplinary institute and belongs to the five schools of the University of Iceland.

The University of Iceland is the largest teaching, research and science institute in Iceland.

For further information contact Professor Pall Melsted (pmelsted@hi.is) or Associate Professor Arnar Palsson (apalsson@hi.is). Deadline

The application deadline is through April 17, 2018

<https://ugla.hi.is/radningar/index.php?sid=-2448&starf=295> – Arnar Palsson - Associate

Professor in Bioinformatics Faculty of Life and Environmental Sciences University of Iceland Sturlugata 7, 101 Reykjavik, Iceland Tel: +(354) 525 4265 Fax: +(354) 525 4632 E-mail: apalsson@hi.is uni.hi.is/apalsson/en/apalsson@hi.is

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## UInnsbruck Bioinformatics

MOLECULAR ECOLOGY, DEPARTMENT OF ECOLOGY, UNIVERSITY OF INNSBRUCK PostDoc position

We seek to hire a PostDoc with training in bioinformatics. This is a 31-months position at the Molecular Ecology group of the Department of Ecology, starting from 2 July 2018. Centering on the Alpine Space, the group's mission is interdisciplinary research, embedded in international collaboration networks. A list of research topics can be found at: < [http://www.uibk.ac.at/ecology/-forschung/molecular\\_ecology.html.en](http://www.uibk.ac.at/ecology/-forschung/molecular_ecology.html.en) >. The successful candidate will participate in resequencing individual transcriptomes and genomes of the ant *Tetramorium alpestre* to identify signatures of aggressiveness vs. nonaggressiveness.

\*\*\*Responsibilities\*\*\*

1. SNP calling in individual genomes using Illumina data and the reference genome
2. searching for genomic signatures by genome-wide association study and by searching for genomic footprints of selective sweeps
3. searching for signatures in individual transcriptomes using Illumina data and the annotated genome
4. editome analyses
5. provision of advice / training to other group members in analysing high-throughput sequencing data and participation in other bioinformatics tasks as need arises in the group
6. participation in manuscript writing
7. contact and collaboration with scientists and laboratory technicians at



the Faculty of Biology in Innsbruck and internationally  
 \*\*\*Selection criteria\*\*\* A. PhD degree in bioinformatics or a related field B. published research experience in bioinformatics, preferentially in identifying genomic and transcriptomic signatures of phenotypic traits C. excellent skills in the maintenance of Linux systems for bioinformatic purposes D. proficiency in Python, R, scripting languages E. experience in the use of relevant software packages for genome and transcriptome analysis (e.g. Bowtie2, Trinity) and genealogy reconstruction (e.g. BEAST, RevBayes) F. ability to work as part of a multi-disciplinary team G. ability to work independently H. very good knowledge of English

\*\*\*Salary\*\*\* The annual gross salary is Euro 51,955.40 for a 40 h/week employment for 31 months. Extension to 37 months and corresponding reduction of the weekly working hours are possible and welcome. The contract includes health insurance and 5 weeks of holidays annually.

\*\*\*How to apply\*\*\* To apply, please submit by E-mail to <florian.m.steiner@uibk.ac.at>: a cover letter, systematic point-by-point replies as to your readiness for the responsibilities and how you meet the selection criteria, a brief statement of research interests, your curriculum vitae, and your complete list of publications. Also, arrange for at least one letter of recommendation to be sent to <florian.m.steiner@uibk.ac.at> Applications must be written in English. Review of applications will begin immediately and continue until a suitable candidate has been found. The University of Innsbruck is striving to increase the percentage of female employees and therefore invites qualified women to apply. In the case of equivalent qualifications, women will be given preference. An offer of employment is contingent on a satisfactory pre-employment background check.

\*\*\*The research institution and its environment\*\*\* Detailed information about the Molecular Ecology group can be found at < [https://www.uibk.ac.at/ecology/forschung/molecular\\_ecology.html.en](https://www.uibk.ac.at/ecology/forschung/molecular_ecology.html.en) >. The University of Innsbruck has a long-standing and internationally renowned tradition in life sciences and offers a vibrant research atmosphere. It has close to 30,000 students and 4,500 staff members. Innsbruck is situated in the Alps and very close to Switzerland, Germany, and Italy; scenery and outdoor recreation are fantastic.

\*\*\*More information needed?\*\*\* For more information, please contact: Florian M. Steiner <florian.m.steiner@uibk.ac.at>

Assoc.-Prof. Dr. Florian M. Steiner

Department of Ecology University of Innsbruck Technikerstr. 25 6020 Innsbruck, Austria

Phone: +43 512 507-51752 Fax: +43 512 507-51799 [http://www.uibk.ac.at/ecology/forschung/molecular\\_ecology.html.en](http://www.uibk.ac.at/ecology/forschung/molecular_ecology.html.en)

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## UKentucky Phylogenomics

A post-doctoral position is available in the lab of David Weisrock in the Department of Biology at the University of Kentucky (weisrocklab.com). We are recruiting an evolutionary biologist with interests in the analysis of phylogenomic data who will contribute to ongoing research in the lab on difficult-to-reconstruct areas of the tree of life. Current research involves comparative study systems in salamanders and lemurs and the use of genome-scale data to resolve rapid species radiations. This research provides the opportunity to interact and collaborate with a number of researchers with similar interests, including Dr. Anne Yoder and her lab at Duke University. Ideal candidates for this position will have a strong background in phylogenetic analysis, and while prior genomic experience is not required, the candidate should have computational skills (e.g., experience with python, perl, R, etc.) that can be applied to the analysis of large data sets.

The Weisrock Lab is one half of a dual-PI lab shared with Dr. Catherine Linnen (linnenlab.com) in the T.H. Morgan Building at UK. We offer a vibrant atmosphere in the study of evolution with an opportunity to interact with faculty, postdocs, graduate students, and undergraduate students, all with an interest in the study of speciation, genetics, and evolution.

Review of applications will begin April 23rd and will continue until the position has been filled. Candidates will have completed their Ph.D. prior to starting the position, but need not have defended their dissertation prior to applying for the position. Applicants must submit the following: 1) CV which includes names and contact information of three references and 2) a one-page research statement (upload as Specific Request 1).

The University of Kentucky is home to a diverse set of research groups that use laboratory, field, computational, and mathematical tools to study questions in population and evolutionary genetics and genomics, ecological genetics, phylogenetics, evolutionary ecology, physiological ecology, conservation biology, behavioral ecology, plant ecology, and other fields in evolution and ecology. UK is located in Lexington, KY, known for the



many bucolic horse farms that surround the city, thoroughbred racing at Keeneland, and equestrian events at Kentucky Horse Park. Lexington and the surrounding area is home to many bourbon distilleries and micro-breweries and numerous outdoor activities including hiking and world-class climbing at the nearby Red River Gorge. The cost of living in Lexington is modest and many UK students, faculty, and staff live close to the University and commute by walking or biking.

The University of Kentucky is committed to a diverse and inclusive workforce by ensuring all our students, faculty, and staff work in an environment of openness and acceptance. We strive to foster a community where people of all backgrounds, identities, and perspectives can feel secure and welcome. We also value the well-being of each of our employees and are dedicated to creating a healthy place to work, learn and live. In the interest of maintaining a safe and healthy environment for our students, employees, patients and visitors the University of Kentucky is a Tobacco & Drug Free campus.

As an Equal Opportunity Employer, we strongly encourage veterans, individuals with disabilities, women, and all minorities to consider our employment opportunities.

More details regarding this position and complete application instructions can be found at <http://ukjobs.uky.edu/postings/180770> Dave Weisrock

David Weisrock Department of Biology University of Kentucky [dweis2@uky.edu](mailto:dweis2@uky.edu) [weisrocklab.com](http://weisrocklab.com)

“Weisrock, David” <[david.weisrock@uky.edu](mailto:david.weisrock@uky.edu)>

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## ULausanne FungalSymbiont

Postdoctoral position 'V Epigenetic versus Genetic and Variation in Fungal Symbionts and How it Affects Plant Growth (Uni. Lausanne, Switzerland)

**Job Description:** A postdoctoral position is available in the Sanders' group to study the role of epigenetic versus genetic variation in mycorrhizal fungi on plant growth. Our research indicates that variation in mycorrhizal fungi is associated with large differences in plant growth. We will study this in more detail to find out which aspects of genetic or epigenetic variation in these fungi causes high growth rates in plants (especially cassava).

It is intended that the results of this project will be combined with research in the field where our work is

leading to real solutions to increase production of food in areas of the world where starvation is a major problem. More information about our work can be found at <http://people.unil.ch/iansanders/> The project is part of a wider collaboration between the University of Lausanne, Dr Marco Pagni at the Vital-IT center of the SIB Swiss Institute of Bioinformatics and Prof. Alia Rodriguez at the National University of Colombia.

**Your skills and qualifications:** Candidates must be highly motivated, have a PhD (or expect to have very soon), and have knowledge in one or more of the following fields: genetics; plant or fungal molecular biology; epigenetics; quantitative or population genetics. Sound knowledge of bioinformatics would be an advantage and an interest in solving problems in an analytical way. The successful candidate should also have good interpersonal skills and an ability to work well in a team.

**Job information:** The position is available as soon as possible and is initially for 1 year (100% contract), renewable for a maximum of 4 more years (depending on the number of years since your PhD). Preference will be given to someone who recently obtained a PhD.

Most of the postdoc's time will be dedicated to research, but a contribution to teaching is expected, including the possibility of supervising master students. Formally, the contract stipulates : 70% Personal research 25% Participation to teaching activities 5% Maintenance of lab equipment or other institutional tasks

**Applications:** To apply you must upload a CV and motivation letter in English, including the names of 2-3 referees, to the University of Lausanne job portal at:

<https://bit.ly/2HbCjzV> Applications must be received not later than 5th May 2018. Informal enquiries may be made by email to [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch)

**NOTE:** We are currently seeking a PhD student with the same profile but the hiring of the two people should be complementary, i.e. one more laboratory-based and one more computational/bioinformatics based.

Ian Sanders <[ian.sanders@unil.ch](mailto:ian.sanders@unil.ch)>

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## ULeuven MicrobialEvolution

A six year postdoc position is available in the research group of Prof. Tom Wenseleers (University of Leuven, Belgium) to work on an interdisciplinary research project entitled “Heterogeneity and speed of gene regulation

in model microbes". The project will make use of deterministic differential equation-type as well as stochastic Monte Carlo simulations and systems biology-type models to look at the evolution of optimal speed and heterogeneity of gene regulatory responses in fluctuating environments. The developed models will be tailored to two model systems, namely maltose gene regulation in yeast and stochastic switching to antibiotic-tolerant persister states in \*E. coli\*. Empirical data to validate all models will be obtained using various state-of-the-art techniques (microfluidics, single-cell RNA-seq, Bar-seq & Tn-seq) in collaboration with the partner groups of Profs. Kevin Verstrepen and Jan Michiels. Depending on experience the candidate can be involved of part of this wet-lab work as well if desired, or in specific bioinformatics analyses, although the bulk of the project would be focused on theoretical modelling.

Key words: theoretical modelling, dynamic models, systems biology, bioinformatics

Key references:

Van den Bergh B.\*, Michiels J.\*, Wenseleers T.\*, Windels E., Vanden Boer P., Kestemont D., De Meester L., Verstrepen K., Verstraeten N., Fauvart M., Michiels J. (2016) Frequency of antibiotic application drives rapid evolutionary adaptation of \*Escherichia coli\* persistence. \*Nature Microbiology\*, art.nr. 16020.

Verstraeten N., Knapen W., Kint C., Liebens V., Van den Bergh B., Dewachter L., Michiels J., Fu Q., David C., Fierro Gutiérrez A., Marchal K., Beirlant J., Versées W., Hofkens J., Jansen M., Fauvart M., Michiels J. (2015) Obg and membrane depolarization are part of a microbial bet-hedging strategy that leads to antibiotic tolerance. \*Molecular Cell\* 59: 9-21.

A.M. New, B. Cerulus, S.K. Govers, G. Perez-Samper, B. Zhu, S. Boogmans, J. Xavier, K.J. Verstrepen (2014) Different levels of catabolite repression optimize growth in stable and variable environments. \*PLoS Biology\* 12: e1001764

Start: Negotiable, but ideally September-October 2018, funding guaranteed for six years, but trial contract of one year would be offered to start with, salary on post-doc scale

Required:

- PhD in Biology, Systems Biology, Bioengineering or Physics.
- Proven track record in theoretical modelling or systems biology.
- Good publication record.
- Good ability to work in a team.

- Ready to present for a Skype interview.

Application: send your CV and a brief motivation letter to Prof. Tom Wenseleers (tom.wenseleers@kuleuven.be) and Dr. Pieter van den Berg (pvdberg1@gmail.com) before 1st of June 2018. Position will stay open until filled.

General information on the research groups involved:

<https://bio.kuleuven.be/ento/wenseleers/-twenseleers.htm> <https://www.kuleuven.be/verstrep/en> <https://www.biw.kuleuven.be/dtp/cmpg/spi/> Piet van den Berg <pvdberg1@gmail.com>

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## UMassachusetts Amherst MicrobiomeEvolution VisitingProf

The Biology Department at the University of Massachusetts Amherst seeks candidates with exceptional promise in research, commitment to outstanding teaching and the ability to work with people of diverse perspectives, experiences, and backgrounds for a 3-Year Visiting Assistant Professor (VAP) position starting in September 2018. This is an unusual position that requires sponsorship of a faculty member with an active research laboratory and requires teaching an experiential research course for undergraduate students.

My laboratory is sponsoring candidates with interests in microbiome research. The VAP will join an active research group that includes external collaborators associated with the Harvard Forest, the DOE Joint Genome Institute (JGI), the DOE Environmental Molecular Sciences Laboratories (EMSL), and New England BioLabs (NEB). With funding from DOE, NSF and NEB we are developing a genetic scaffold for soil community research at Harvard Forest through phylotype, metagenome, metatranscriptome and single cell sequencing of forest soil organisms in our experimental warming plots. The VAP will leverage these emerging data sets to discovery novel taxonomic groups, determine how long-term warming has changed population structure of soil microorganisms and to detect evidence of selection in response to warming.

Our recent project with the JGI using flow cytometry to separate out single cells resulted over 2,000 genomes and identification of novel viral and bacterial groups, some that are likely associated in the soil with eukarotic hosts. I am willing to sponsor candidates from diverse scientific backgrounds including entymology, mycology,

protistology, virology and bacteriology that will bring new perspectives to the project and that are motivated to develop genomic methods for sequencing organisms directly from the environment. We will work with the VAP to write grants, including large scale sequencing projects that will provide the VAP support in setting up an independent research program.

For 20 years I have been teaching genomics and bioinformatics courses, including hands-on Perl, Python and R sessions often capped with student designed research projects. The Visiting Assistant Professor (VAP), with my assistance, will develop a new genomics and bioinformatics laboratory course to provide an inquiry-based research experience for a maximum of 20 undergraduate students per semester. In the first semester the VAP and faculty mentor will plan the development of the new lab course (with a bent towards the interests and experiences of the VAP). In the second semester, the VAP and faculty mentor teach the course together as a pilot. In semesters 3-6 the VAP leads the course, with guidance and participation from the faculty mentor. The VAP is expected to continue research throughout the academic year and summer.

This position requires the ability to work with diverse populations/students. Our research group has an extensive history of working with underrepresented undergraduate and graduate students at UMass. We are especially interested in candidates whose accomplishments reflect engagement with varied perspectives and constituencies.

More information on the position can be found at <https://umass.interviewexchange.com/jobofferdetails.jsp;jsessionid=-4E5A791C8DAAF86C428665779263A8D3?JOBID=-95724&CNTRNO=0&TSTMP=1522680291803>. While the official deadline for the position is May 7, I am asking that candidates contact me through email (jeffb@bio.umass.edu) with a cover letter and CV no later than Friday, April 27th for guidance on putting together a competitive application.

Regards,— Jeff Blanchard

Associate Professor, Biology Co-Director, Center for Microbiome Research Graduate Program in Organismal and Evolutionary Biology University of Massachusetts Amherst, MA 01003 Morrill Science Center II Office 409; Lab 411 413-577-2130 <http://www.bio.umass.edu/micro/blanchard/> jeffb@bio.umass.edu

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## UMassBoston PhylogeneticComparativeMethods

\*Postdoctoral fellowship in phylogenetic comparative method development (in R)\*

Applications are invited for a postdoctoral fellowship in the Revell lab at the University of Massachusetts Boston to work on phylogenetic comparative method development in R. Qualifications should include experience developing new theoretical approaches and/or applying methods in software.

This is a re-advertisement of a postdoc that I posted last year (but didn't fill), with two important updates:

1. The position is for a \*minimum of 2 years\* (given satisfactory progress, etc.) rather than for one year as previously advertised.
2. The postdoc is for \*phylogenetic comparative method development in particular\*, rather than phylogeny methods more broadly.

I consider phylogenetic comparative methods to include anything related to the use of phylogenies to make evolutionary inferences (rather than the estimation of phylogenetic trees) - but please contact me if you'd like clarification (liam.revell@umb.edu).

More information along with a link to apply is available on my blog: <https://goo.gl/h97tKV>. Note that the application deadline is May 11, 2018.

– Liam J. Revell, Associate Professor of Biology University of Massachusetts Boston & Profesor Asociado, Programa de Biología Universidad del Rosario web: <http://faculty.umb.edu/liam.revell/>

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## UMunich SexDetermination

Research: See ResearchGate or Google Scholar (<https://scholar.google.com/citations?user=-uzOGmTgAAAAJ&hl=de>)

Postdoc position to work on floral-development genes and plant sex determination at the Ludwig-Maximilians University in Munich, Germany, and in Gif-sur-Yvette,

France

We are seeking to recruit a scientist at the post-doctoral level ('Wissenschaftlicher Mitarbeiter'; salary TV-L 13 = DFG postdoc E 13 Level 3) to work on sex determination in the economically important Cucurbitaceae family, specifically on the assembly of a genome of a dioecious species in the Cucumis/Citrullus clade. The project centers on bioinformatics and involves collaboration between the labs of Abdel Bendahmane (Institut of Plant Sciences Paris-Saclay) and Susanne Renner (University of Munich). The postdoc will spend time in both labs, with Munich being the main location. The data come from third-generation sequencing platforms using single-molecule sequencing, namely Oxford Nanopore Technology (MinION) and Pacific Biosciences (PacBio). The assembly will focus on three gene families known to be involved in floral sex determination; functional characterization of X- and Y-linked sex genes will be carried out in the Bendahmane lab.

The position is from 1 June 2018 until 31 May 2020, with the option of a prolongation. Candidates must have a doctoral degree in the area of plant genomics and experience in bioinformatics. Knowledge of German or French is not required, but obviously helpful for enjoying life in Munich and Paris.

Candidates should submit their CV, including a list of publications and a statement of research interests, along with the contact information of two referees to Professor Susanne Renner ([renner@lmu.de](mailto:renner@lmu.de)). Deadline: 30 April 2018 or when position is filled.

Recent and ongoing work in the Bendahmane lab: <http://www.versailles.inra.fr/urgv/analysis-cropFunctionalGen.htm> Work in the Renner lab: <https://scholar.google.de/citations?user=uzOGmTgAAAAJ&hl=en> Susanne Renner <[renner@lmu.de](mailto:renner@lmu.de)>

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## UNeuchatel EvolutionPlants

Two Postdoc positions, Institute of Biology, University of Neuchatel, Switzerland

Two postdoctoral positions in plant-animal-microbe interaction are available in the research group of Sergio Rasmann at the Institute of Biology, University of Neuchatel. The postdocs will join a team of other postdocs and PhD students working on aspects of plant ecology, with a current emphasis on the causes and conse-

quences of phytochemical diversity within communities along steep ecological gradients.

Research scope and skills sought - The postdocs' research direction and projects can be tailored to her or his interests and expertise. However, apart from having a strong interest (and PhD) in plant ecology and/or chemical ecology, we are ideally seeking someone with a skill set that includes at least one of the following: generation and analysis of metabolomics data; field-based experimental design, entomology, plant-microbe interaction. Experience and an interest in working with plants and associated arthropod community is a priority (e.g., including managing glasshouse, climate chambers, common garden and/or field experiments). The successful candidate should also have good communication and interpersonal skills, and an ability to work in a team. Although not a requirement, some knowledge of French would be an asset.

Host Department and University - The Institute of Biology, hosts a broad range of research groups, and its members enjoy a lively intellectual and social life. Although the University of Neuchatel is francophone and of small size, the department is highly international, and all its research activity and seminars are conducted in English. The University of Neuchatel has four faculties and approximately 4'200 students. It is situated on a beautiful campus on the shores of Lake Neuchatel, between Zurich, Geneva and Bern, and is close to the Swiss Alps.

Contract details - The position is envisaged at 80% for an initial period of one year, with a possible renewal of one or two years, depending on funding. Most of the postdoc's time will be dedicated to research, but a contribution to teaching is expected, including the possibility of supervising master students. The starting date is flexible, but funding is available immediately.

Applications - Informal enquiries for further details of the aims of the project should be sent to Sergio Rasmann ([sergio.rasmann@unine.ch](mailto:sergio.rasmann@unine.ch)). Formal applications should include a cover letter detailing your research interests, experience and motivation for applying, a CV, and the names of two or three referees. Applications should be sent as a single PDF to [sergio.rasmann@unine.ch](mailto:sergio.rasmann@unine.ch). Applications received by July 01 will receive full consideration.

University equality policy - The University of Neuchatel promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

Sergio Rasmann Institute of Biology University of Neuchatel Rue Emile-Argand 11 CH - 2000 Neucha-



tel Office - D225 P +41 32 718 23 37 F +41 32 718 30 00  
E sergio.rasmann@unine.ch W laboratory of functional  
ecology (LEF)

RASMANN Sergio <sergio.rasmann@unine.ch>

experience to Andrew Kern (adkern@uoregon.edu)  
“adkern@uoregon.edu” <adkern@uoregon.edu>

## UOregon PopulationGenomics

Postdoctoral position in Population Genomics at University of Oregon

Seeking qualified applicants for a NIH funded post-doctoral position with Andrew Kern in the Department of Biology and the Institute of Ecology and Evolution at the University of Oregon. I'm looking for a colleague who will work with me on the development and application of machine learning methods for inferring population genetic parameters from genome-scale datasets. Planned projects will exploit cutting-edge Deep Learning techniques to elucidate the contributions of selection, migration, and demographic history to patterns of genetic variation in humans and mosquitos.

The ideal candidate would hold a Ph.D. and have a record of research achievement in population genetics, evolutionary biology, phylogenetics/phylogeography, computational biology, computer science, statistics, or a related field. Indeed your exact field of research to date is less important to me than your demonstrated record of publication and tenacity. The ideal candidate would have experience programming in python or R (but any scripting language is fine), have experience with cluster computing environments, and have some familiarity with C/C++ (although this is negotiable). No prior experience with machine learning or deep learning is necessary I will train you. Your job is to bring your enthusiasm and a desire to learn.

More information about the Kern lab can be found here: <http://kernlab.org> . More information about the Institute for Ecology and Evolution can be found here: <https://ie2.uoregon.edu/> . The lab is located on the gorgeous University of Oregon campus. Eugene is wonderful small city with an affordable quality of life, that affords abundant outdoor opportunities in the nearby Cascade mountains and Oregon coast.

Review of applications will begin immediately and continue until the position is filled. The position could begin as early as August, 2018. Interested candidates should submit an electronic version of their CV along with a cover letter describing their qualifications and relevant

## UOttawa FungalPlantGenomics

“Three year Postdoctoral position in Fungal/Plant genome analysis

A Postdoctoral Fellow position is available in the laboratory of Dr. Nicolas Corradi (<https://-corradiilab.weebly.com/>) at the University of Ottawa (ON, Canada). The position is initially available for one year, and is renewable for up to 3 years.

The position is partially funded by Mitacs (<https://www.mitacs.ca/en>). The successful applicant will spend most of his/her research time in the Corradi lab, and the PDF research is expected to improve knowledge of important bio-fertilizers and natural products using genome analyses. Throughout the research, the PDF will also acquire important professional skills in data management and participate in an industry-relevant R&D product with high translational potential through collaborations with the industry. In particular, the successful PDF will acquire unique experience in the domain of organic agriculture, natural health product research, regulation, and industry practices.

Projects:

The applicant is expected to work on these two projects in collaboration with PhD students.

1) Assembly, annotation and analysis of dikaryotic arbuscular mycorrhizal genomes:

Recent studies from our lab (see Ropars et al. 2016 Nature Microbiology; Corradi and Brachmann, 2017, Trends in Plant Science) have shown that model AMF strains are either homokaryotic - i.e. contain multiple co-existing nuclei with one MAT-locus and one dominant genome - or ”dikaryotic“ - i.e. all nuclei harbor one of two co-existing and diverging MAT-loci.

Recent studies in our lab have revealed the existence of many additional dikaryotic AMF strains, providing new and exciting opportunities to investigate the genome evolution and biology of this unique cellular condition.

The applicant will be involved in the acquisition of optimal - ideally chromosome level - assemblies for all dikaryotic strains found to date. This will be done by combining Illumina sequencing approaches with long-



read technologies (PacBio, Nanopore). New genome assemblies will be annotated and compared to investigate the degree, nature and function of genome diversity that is present within and among AMF dikaryons. In parallel, the newly assembled genomes will be used to detect the relative contribution of each nucleotide to the AMF development and establishment of mycorrhizal symbiosis using RNA-seq approaches.

2) Assembly, annotation and analysis of the *Echinaea purpurea* genome.

*Echinacea* species are widely used for medicinal purposes, with a global market of \$1 billion, yet high-quality genome data from this group is lacking. This project aims to distinguish unique *Echinacea* genetic resources by identifying new and improved traits related to both agriculture and natural health product through genome analyses.

In collaboration with other plant genome experts, the PDF will identify putative new genes and biochemical pathways to guide development of new products with improved medicinal properties. The PDF will also benefit from interdisciplinary research skills provided by this collaboration (i.e. in-house laboratory work, bioinformatics) and the R&D experience with the industrial collaborator, which builds industry-relevant knowledge relating to natural products and agriculture.

Applicants and Desired Skills:

Applicants are expected to have strong background in "Genome Analysis", and in handling large amounts of sequence data. Evidence of prior success with assembly of large and complex genomes using long-read technologies is desired. Past practical knowledge of Plant Genomics, or evidence of work on highly heterozygous diploid and/or polyploid organisms, will be seen as an asset for this position.

Starting date and Application:

The position is available starting August 2018, with the application process closing as soon as a suitable candidate is found. A complete application package will include: 1) a CV; 2) a short description of past research accomplishments and future goals; and, 3) the names and e-mail addresses of at least 2 references.

Complete applications can be sent to Dr. Nicolas Corradi: [ncorradi@uottawa.ca](mailto:ncorradi@uottawa.ca)

Location:

The University of Ottawa is a large, research-intensive university, hosting over 40,000 students and located in the downtown core area of Canada's capital city (<http://www.science.uottawa.ca/fac/welcome.html>). Ottawa is a vibrant, multicultural city with a very high quality of

life (<http://www.ottawatourism.ca/fr/>)"

Nicolas Corradi

Associate professor - Professeur Associe

Department of biology - Departement de biologie

Universite de Ottawa - University of Ottawa

Bureau/Office: GNN257 - Tel : 613 5625800 - ext 6563

Website: <http://corradilab.weebly.com/>

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## UOttawa StatisticalGenetics

Postdoctoral Research Fellow Position in Statistical Genetics University of Ottawa School of Epidemiology and Public Health and Department of Mathematics and Statistics

A Postdoctoral research fellow position in statistical genetics is available at the University of Ottawa School of Epidemiology and Public Health in the context of an ongoing collaborative project under a cosupervision by Dr. Marie-Hélène Roy-Gagnon from the School of Epidemiology and Public Health and Dr. Kelly Burkett from the Department of Mathematics and Statistics.

The position involves the development and application of statistical and computational methods with the overall goal to combine large-scale genealogical and genomic data in genetic association studies. The successful candidate will also be expected to maintain and further develop existing R packages implementing the methods, and collaborate on other ongoing projects involving graduate students. Basic qualifications: Ph.D. in a quantitative field (e.g., statistics or biostatistics, bioinformatics or computer sciences) strong quantitative research background, statistical and programming proficiency (including R, perl or python, and C/C++), strong genetic knowledge, as well as good written and oral communication skills.

Additional qualifications include strong knowledge of population genetics and coalescence models, and previous experience developing and maintaining R packages.

Please submit a brief statement of interest, your CV, including contact information for at least 3 references,

and one sample publication by email to Marie-Hélène Roy- Gagnon, mroygagn@uottawa.ca

Kelly Burkett Assistant Professor | Professeure adjointe Department of Mathematics and Statistics | Département de mathématiques et de statistique University of Ottawa | Université d'Ottawa

Kelly Burkett <kburkett@uottawa.ca>

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## UppsalaU EvolutionaryGenomics

Dear colleagues,

A 2-year postdoc position is available in my group to work on evolutionary genomics of filarial nematodes. More information here: <https://www.uu.se/en/about-uu/join-us/details/?positionId=198726> Please forward this ad to anyone who might be interested. Application deadline is April 15.

Thanks and cheers, Alex

“alexander.suh@ebc.uu.se” <alexander.suh@ebc.uu.se>

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## UQueensland EvolQuantGenetics

<http://jobs.uq.edu.au/caw/en/job/504146/-postdoctoral-research-fellow> Postdoctoral Fellow in Evolutionary Quantitative Genetics.

The position will be based in the School of Biological Sciences at the University of Queensland. The school is one of the largest most productive Biology Departments in Australia with strengths in ecology, evolution, genetics, and conservation biology. Information about the School may be accessed: <http://www.biology.uq.edu.au/>. This position is associated with Prof. Mark Blows' and Dr Katrina McGuigan's research groups, which have a strong focus on the evolution of genetic variation of complex traits, using *Drosophila serrata* as a model.

**\*The role\*** The successful applicant will conduct research into how selection acts on mutations to determine standing genetic variance of complex traits. The core project involves analyses of both large genomic datasets and classical observational pedigrees in conjunction with phenotypic data. The successful applicant will have the opportunity to contribute substantially to the project

through data analysis and writing papers. There are opportunities within the position for the successful candidate to develop their own independent research projects.

**\*The person\*** Applicants should possess a PhD qualification in evolutionary quantitative genetics or a similar discipline, with postdoctoral experience in statistical analyses of complex pedigrees and /or multivariate phenotypes and/or GWAS. Applicant will be required to have a strong background in experimental quantitative genetics, excellent communication and analytic skills, and strong interpersonal skills. They should demonstrate strong organisational skills and an ability to be work independently to meet collaborative project goals. The University of Queensland values diversity and inclusion. Applications are particularly encouraged from Aboriginal and Torres Strait Islander peoples. For further information please contact our Australian Indigenous Employment Coordinator at: [atsi\\_recruitment@uq.edu.au](mailto:atsi_recruitment@uq.edu.au) Applications are also encouraged from women. This role is a full-time position; however flexible working arrangements may be negotiated.

**\*Remuneration\*** This is a full-time, fixed term appointment for two years at Academic level A. The remuneration package will be in the range \$64,533.50 - \$87,535.13p.a., plus employer superannuation contributions of up to 17% (total package will be in the range \$75,504.20- \$102,416.10p.a.).

**\*Position Description\*** is available at <http://-jobs.uq.edu.au/caw/en/job/504146/postdoctoral-research-fellow> **\*Enquiries\*** To discuss this role please contact Dr Katrina McGuigan at [k.mcguigan1@uq.edu.au](mailto:k.mcguigan1@uq.edu.au). To submit an application for this role, use the Apply button at the bottom of the page at <http://jobs.uq.edu.au/caw/en/job/-504146/postdoctoral-research-fellow>. All applicants must supply the following documents: Cover letter Resume Responses to Selection Criteria in the Position Description (available at: <http://jobs.uq.edu.au/caw/en/job/504146/postdoctoral-research-fellow>).

Applications close: 24 Apr 2018 (11:55 PM) E. Australia Standard Time

Katrina McGuigan <[k.mcguigan1@uq.edu.au](mailto:k.mcguigan1@uq.edu.au)>

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## USydney Vertebrate Viviparity Evolution

Postdoctoral Research Associate - The University of Sydney School of Life and Environmental Sciences, Faculty of Science Reference no. 579/0318F

Research position focused on evolutionary biology, genomics, and physiology at the University of Sydney Full-time, 2 Years Fixed-Term.

Academic Level A, Base Salary: \$90,276 p.a. plus leave loading and a generous employer's contribution to superannuation. Visa sponsorship is available if required.

Closing date: 11:30pm 2 May 2018 (Sydney Time)

About the opportunity

Applications are invited for a Postdoctoral Research Associate to join our research team working on a project investigating the evolution of viviparity and the placenta across vertebrates. We are a friendly, supportive, and hardworking research group. We encourage lab members to get involved in our collaborative research projects with scientists from across Australia, Europe, South America, and the USA. We also encourage active involvement in lab and departmental activities, and attendance at conferences.

About you

We are looking for a highly motivated Postdoctoral Research Associate with a PhD in genetics and genomics, physiology, evolutionary biology, bioinformatics, or related disciplines. In addition, evidence of publication of research in high quality, peer-reviewed journals is required. The Postdoctoral Research Associate will be responsible for:

- Contributing to our research programme investigating the evolution of viviparity and the placenta across vertebrates;
- Planning and executing experiments, including developing new research methods, preparing applications for animal ethics approval, and occasionally carrying out field work within Australia as required to meet the aims of the research programme;
- Generating, managing and analysing large sets of genomic, transcriptomic and proteomic data;
- Co-supervising and training undergraduate and higher degree by research students in areas related to the research programme;
- Preparing the results of the research for publication in high quality journals.

To apply:

Please visit the University of Sydney recruitment website at <https://sydney.nga.net.au/cp/index.cfm?event=jobs.checkJobDetailsNewApplicationToEvent=jobs.processJobSearch&jobid50D7C1-3BC2-420C-99EB-A8B200C7959B&CurATC=EXT&CurBID=9319bc%8504&jobsListKey<a9d9c7%2Db328%2D4ba2%2D9d12%2D325a039307riables=CurATC,CurBID,jobsListKey&lid!558900008>

For further information about this position, contact Dr Camilla Whittington (+61 2 9351 8621 or [camilla.whittington@sydney.edu.au](mailto:camilla.whittington@sydney.edu.au)). Applications must be made via the online portal at the link above.

"[camilla.whittington@sydney.edu.au](mailto:camilla.whittington@sydney.edu.au)"

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## UTexas Evolutionary Genomics

The Havird Lab at the University of Texas at Austin is looking for an enthusiastic and motivated postdoctoral researcher. Our group is generally focused on the processes and implications of cytonuclear coevolution. Ongoing projects in the lab examine coevolution between mitochondrial and nuclear genomes, the roles of cytoplasmic genomes at species boundaries, and ecophysiology/environmental adaptation. Multiple organismal systems are used in the lab, including plants and animals, as we often make use of existing publicly available genomic datasets.

Desirable experience/interests include:

- Identifying signatures of selection using sequence and protein-structure based approaches
- Biochemical assays of mitochondrial function and metabolism (e.g., OXPHOS)
- Examining environmental adaptation via molecular and physiological approaches
- Broad intellectual interests and enthusiasm for addressing evolutionary questions
- Motivation and ideas for seeking independent postdoctoral funding
- Mentoring of undergraduate researchers
- A desire to foster a positive, fun, and collaborative research environment

Our lab uses large sequencing datasets in many projects, so previous experience in bioinformatics or motivation to learn such techniques is also strongly desired.

We are part of the growing Integrative Biology Department at the University of Texas, which has strengths in evolution, genomics, and ecology, including a community of researchers with expertise in cytonuclear interactions. Postdocs should therefore be able to establish a large network of colleagues and collaborators across campus.

The University of Texas is located in Austin, TX, which is known for its high quality of life, environmental awareness, outdoor culture, and eccentricity.

If you are interested in joining the lab or learning more, please email Justin Havird ([justin.havird@colostate.edu](mailto:justin.havird@colostate.edu)) and provide a brief cover letter describing your research interests, career goals, and how you would complement the interests of the lab, along with a current CV (\$B!H(BBoilerplate\$B!!(B correspondence reminiscent of spam will likely be ignored).

Timing is flexible, with an anticipated start date sometime in Fall 2018 or Spring 2019.

Justin Havird Assistant Professor Integrative Biology Dept. (<https://integrativebio.utexas.edu/>) University of Texas <http://jchavird.wixsite.com/jchavird/> Justin Havird <[Justin.Havird@colostate.edu](mailto:Justin.Havird@colostate.edu)>

## UToronto PopulationGenomics

Postdoctoral Position in Population and Medical Genomics

A Postdoctoral position is available in the population and medical genomics laboratory of Philip Awadalla in Toronto at the University of Toronto and Ontario Institute for Cancer Research (<https://pawadallalab.org>). The lab focuses on analysis, development of methods and sequencing experiments studying the evolutionary genomics of aging processes (including mutation and recombination), disease and cancer evolution using data from large longitudinal population cohorts that we oversee, including the Canadian national population cohort (CPTP, <https://portal.partnershipfortomorrow.ca> and its regional partners).

The researcher can develop research questions of their choosing but possible projects can include: 1) Next-generation approaches (whole genome, RNA-seq, epigenomic, long-read and single-cell) integrating population genetic approaches for genomic studies of large population cohorts. Our lab is directing the longitudinal collection of genomic material in Canada's national populations cohort, the Canadian Partnership for To-

morrow Project, which has enlisted 315,000 participants across Canada with administrative health data (EHRs) and physical measures. 2) Capturing de novo tissue and cell-specific mutation and recombination events from normal or malignant tissue including single cell applications. Fitness consequences of mutations from genome-wide collections of empirical population and comparative data. 3) Understand evolutionary genetic histories and molecular control points associated with simple and complex disorders oncological/hematological phenotypes or diseases including immunodeficiencies, childhood cancer, and age-related clonal hematopoiesis (ARCH).

Our lab also works in close collaboration with a number of research laboratories in Toronto and internationally, including new programs within the Ontario Institute of Cancer Research and Princess Margaret Hospital. Our Genome Canada platform for genomics and bioinformatics (the Genome Canada Canadian Data Integration Centre <http://genome-cdic.ca>) supports much of our initiatives.

The successful candidate will be nearing the completion/having a PhD or equivalent postdoctoral training in genomics or population/ statistical genetics. Postdoctoral research scientists can work on projects of their choosing related to the labs current projects. Some recent publications from the lab are listed below.

Projects are well supported by a number of external grants and institutional resources for next generation sequencing and bioinformatics. Interested individuals should please write to Philip Awadalla ([philip.awadalla@oicr.on.ca](mailto:philip.awadalla@oicr.on.ca)).

Sincerely, Philip Gene-by-environment interactions in urban populations modulate risk phenotypes. < <https://www.ncbi.nlm.nih.gov/pubmed/29511166> > Favé MJ, Lamaze FC, Soave D, Hodgkinson A, Gauvin H, Bruat V, Grenier JC, Gbeha E, Skead K, Smargiassi A, Johnson M, Idaghdour Y, Awadalla P.

Nature Communications. 2018 Mar 6;9(1):827.

The impact of recombination on human mutation load and disease. < <https://www.ncbi.nlm.nih.gov/pubmed/29109227> > Alves I, Houle AA, Hussin JG, Awadalla P.

Philos Trans R Soc Lond B Biol Sci. 2017 Dec 19;372(1736). pii: 20160465. doi: 10.1098/rstb.2016.0465. Review.

Recombination affects accumulation of damaging and disease-associated mutations in human populations. < <https://www.ncbi.nlm.nih.gov/pubmed/25685891> > Hussin JG, Hodgkinson A, Idaghdour Y, Grenier JC,



Goulet JP, Gbeha E, Hip-Ki E, Awadalla P.

Nature Genetics. 2015 Apr;47(4):400-4.

High-resolution genomic analysis of human mitochondrial RNA sequence variation. < <https://www.ncbi.nlm.nih.gov/pubmed/24763589> > Hodgkinson A, Idaghdour Y, Gbeha E, Grenier JC, Hip-Ki E, Bruat V, Goulet JP, de Malliard T, Awadalla P.

Science. 2014 Apr 25;344(6182):413-5.

Philip Awadalla <Philip.Awadalla@oicr.on.ca>

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### UTuebingen AdaptiveFunctionsFluorescence

6-year Postdoctoral Academic Associate in marine visual ecology

The Animal Evolutionary Ecology unit investigates adaptive functions of fluorescence or light redirection through reflective structures in marine fish, focusing on prey-predator coevolutionary interactions. We use selected model systems as well as phylogenetically corrected comparative analyses (e.g. Anthes et al. 2016, Front. Evol. Ecol.). We use state-of-the-art spectroradiometry and behavioural experiments in the lab and in the field. In addition to carrying out experiments in 150 saltwater tanks rooms with controlled light conditions for individual performance assessment in Tübingen, we also spend up to two months per year in the field for in situ experiments, light measurements, and documentation (Mediterranean, Red Sea, Indopacific).

The successful candidate has a PhD in any or several of the following: Visual ecology, physics, neurobiology, bio-optics, (3D) eye anatomy or neuroanatomy. She/he is expected to develop a high-profile research program. This position is institution-funded and comes with a teaching obligation for a total of 120 h/year. This includes supervision and co-supervision of students at the BSc, MSc and PhD level. Teaching is in English. Experience with SCUBA diving in a scientific context is an asset.

Formal employment procedures will be carried out by the University's Central Administration. The position is fulltime and limited to six years. The pay grade classification E13 refers to the German federal public service scale (TV-L). Disabled candidates will be given preference over other equally qualified applicants. The University seeks to raise the number of women in re-

search and teaching and therefore urges qualified women to apply.

Please send a single PDF to office.michiels@biologie.uni-tuebingen.de that including (1) a motivation letter, (2) a full CV and (3) max. three most relevant publications or manuscripts. Include details on research interests and accomplishments, teaching experience and email addresses of at least two referees in the motivation letter. Screening will commence on 15 July 2018, and will continue until suitable candidates have been identified. Earliest appointment is 1 September 2018.

Prof. Dr. N. Michiels, University of Tübingen, Department of Biology, Institute of Evolution and Ecology, Auf der Morgenstelle 28, 72076 Tübingen, Germany

More info from nico.michiels@uni-tuebingen.de

Nico Michiels, Prof. Dr. Animal Evolutionary Ecology Department of Biology Auf der Morgenstelle 28 72076 Tuebingen Germany

Tel. +49 7071 29-74649 Fax +49 7071 29-5634 Mobile +49 170 4758003

nico.michiels@uni-tuebingen.de

office.michiels@biologie.uni-tuebingen.de

[www.evoeco.uni-tuebingen.de](http://www.evoeco.uni-tuebingen.de)

Nico Michiels

<n.k.michiels@uni-tuebingen.de>

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### UUtah EvolutionaryGenomics

POSTDOCTORAL FELLOW POSITION:

EVOLUTIONARY GENOMICS AT THE UNIVERSITY OF UTAH

Postdoctoral position available in the laboratories of Dr. Mike Shapiro and Dr. Denise Dearing in the Department of Biology, University of Utah. We seek a highly motivated colleague to identify the genetic and physiological mechanisms that facilitate the ingestion of dietary toxins by herbivorous vertebrates. Our current research focuses on identifying and understanding the genomic changes associated with creosote feeding in herbivorous woodrats (*Neotoma*).

Please visit our websites for more information about the labs: <http://www.biology.utah.edu/shapiro> <http://biologylabs.utah.edu/dearing> Requirements:

1. Ph.D. in genetics, genomics, evolutionary biology, or a closely related field



2. Track record of productivity
3. Demonstrated ability and willingness to work both independently and collaboratively
4. Excellent written and oral communication skills

A strong background in genomics and transcriptomic analyses of vertebrates is preferred.

To apply, please submit the following materials:

1. CV, including a list of publications
2. Statement that includes your research experience and interests, as well as your preferred start date on or after July 15, 2018.
3. Names of three referees who will be willing to submit letters of reference upon request

For full consideration, please submit application materials by May 15, 2018.

Please email application materials in PDF format to Mike Shapiro: shapiro@biology.utah.edu

Informal inquiries are welcome prior to formal application.

Recent publications from our labs relevant to this position include:

Malenke JR, Skopec MM, Dearing MD. (2014) Evidence for functional convergence in genes upregulated by herbivores ingesting plant secondary compounds. *BMC Ecology*. 14:23.

Magnanou E, Malenke J, Dearing MD. (2013) Hepatic gene expression in herbivores on diets with natural and novel plant secondary compounds. *Physiological Genomics*. 45:774-785. DOI: 10.1152/physgen.00033.2013.

E.T. Domyan, Z. Kronenberg, C. Infante, A.I. Vickrey, S.A. Stringham, R. Bruders, M.W. Guernsey, S. Park, J. Payne, R. Beckstead, G. Kardon, D.B. Menke, M. Yandell, M.D. Shapiro. (2017) Molecular shifts in limb identity underlie development of feathered feet in two domestic avian species. *eLife* 5:e12115.

A.I. Vickrey, E.T. Domyan, M.P. Horvath, M.D. Shapiro. (2015) Convergent evolution of head crests in two domesticated columbids is associated with different missense mutations in EphB2. *Molecular Biology and Evolution* 32: 2657-2664. doi: 10.1093/molbev/msv140.

M. D. Shapiro, Z. Kronenberg, C. Li, E.T. Domyan, H. Pan, M. Campbell, H. Tan, C.D. Huff, Haofu Hu, A.I. Vickrey, S.A. Nielsen, S.A. Stringham, Hao Hu, E. Willerslev, M. T. P. Gilbert, M. Yandell, G. Zhang, J. Wang. (2013) Genomic diversity and evolution of the head crest in the rock pigeon. *Science* 339: 1063-1067.

## SCIENTIFIC AND CULTURAL ENVIRONMENT

The Department of Biology comprises a diverse and vibrant group of laboratories, with research interests ranging from environmental biology to biochemistry. The genetics and genomics biology communities are strong on the University of Utah main campus and medical school and offer numerous opportunities for collaboration. The evolutionary genetics and genomics community on campus is especially strong. Both PIs have a strong record of mentoring and success in placing trainees.

The University of Utah is located in beautiful (and affordable) Salt Lake City, with easy access to world-class entertainment and recreation. Salt Lake City and nearby Park City are home to the annual Sundance Film Festival and a vibrant year-round cinema scene, as well as outstanding restaurants and brewpubs. Several national parks are located within a just few hours' drive, and the university is within a 40-minute drive of at least six major alpine skiing and snowboarding resorts, including venues of the 2002 Olympics. Hiking and mountain biking trails begin essentially on campus. Outside Magazine recently called Salt Lake City "one of the nation's most underrated outdoor meccas." The city is also a major airline hub, with non-stop flights throughout North America and Europe.

Denise Dearing <denise.dearing@utah.edu> Denise Dearing <denise.dearing@utah.edu>

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## UWisconsin Milwaukee FeatherGenomics

Postdoctoral Research Associate in Functional Genomics of Birds, University of Wisconsin-Milwaukee

We are recruiting a Postdoctoral Research Associate to study the Functional Genomics of bird feathers. The position is part of a NSF funded study of sexual selection and ornamentation in common yellowthroats led by Peter Dunn and Linda Whittingham at UW-Milwaukee and Corey Freeman-Gallant at Skidmore College. This study will use genomic analyses to test hypotheses for the genetic basis of ornament expression both within and between populations that have different sexually selected ornaments. The Postdoctoral Research Associate will primarily conduct genomic analyses to understand the functional basis of variation in the size and color of feather ornaments. The post-doc will also participate in some short-term fieldwork in New York, Arizona or

Belize.

Applicants are required to have a Ph.D. in evolutionary ecology, genomics or genetics. Familiarity with genomics software is essential, preferably for transcriptome analysis in non-model species, as well as a high-level of motivation to publish results, as evidenced by the candidate's publication record.

The position is funded for up to two years at a starting salary of \$47,500/ yr. The position may begin as early as June 2018 and will remain open until filled.

To apply, please submit a brief cover letter, a one-page description of your research experience/interests, and a CV with the names and contact information for three references to Peter Dunn (pdunn@uwm.edu). Please also send any questions or informal inquiries regarding the position to Peter Dunn, and see <http://people.uwm.edu/pdunn/> to learn more about our research. UWM has an active group of researchers studying evolutionary ecology and behavior:

<https://uwm.edu/biology/research/ecology-evolution-and-behavior/> UW-Milwaukee is an equal opportunity/equal access/affirmative action employer fully committed to achieving a diverse workforce. Applicants from groups traditionally underrepresented in science are especially encouraged to apply.

Peter Dunn Dist. Professor Univ. of Wisconsin-Milwaukee Dept. of Biological Sciences 3209 N. Maryland Ave. Milwaukee, WI 53211 414-229-2253 <http://people.uwm.edu/pdunn/> pdunn@uwm.edu

Peter O Dunn <pdunn@uwm.edu>

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## UWisconsin Milwaukee KelpGenomics

Post-Doctoral Research Associate

The Department of Biological Sciences at the University of Wisconsin-Milwaukee (UWM) is currently accepting application submissions for a postdoctoral appointment in Dr. Filipe Alberto's laboratory, studying genetic improvement for aquaculture of the giant kelp *Macrocystis pyrifera*. This is part of a grant funded by the Department of Energy, Arpa.e agency, program Mariner. You can read more about this program here <https://arpa-e.energy.gov/?q=arpa-e-programs/mariner>. And learn about some of the funded projects here (<https://arpa-e.energy.gov/?q=news->

[item/departement-energy-announces-18-new-projects-accelerate-development-macroalgae-production](#)).

The postdoc will be conducting the development of a germplasm collection of haploid strains of kelp (brown algae). The collection will be the basis for a genetic improvement program aimed at faster growth; and temperature and low nutrient tolerance in aquaculture. The postdoc will contribute to routine culture tasks, but mostly through supervision of a research assistant and undergraduate students. Experience in growing kelp cultures in the laboratory conditions is preferable but not essential, training can be provided.

Preferred skills: Experience with genomic analysis, both wet and dry lab, including the analysis of high-throughput sequencing data, coding experience in R, Python or other languages and excellent organizational skills and capacity to work under strict deadlines.

Requirements: Applicants are required to have a Ph.D. in evolutionary ecology, plant breeding, population genetics/genomics or genetics. Familiarity with population genetics/genomics software is essential, as well as high-level of motivation to publish results, as evidenced by the candidate's publication record.

During the first year, most project tasks will involve cultivation of individual haploid strains to provide sufficient biomass to extract DNA in quantity and quality required for genomic analysis. Microsatellite marker analysis will also be used to monitor strain identify and purity at different stages of growth. The germplasm collection will be the basis for a Marker Assisted Selection program developed with partner institutions (UC Santa Barbara, U Southern California and JCVI) involving genome sequencing and annotation, phenotype typing of outplanted sporophytes in Southern California, capture sequencing of genetic variants (SNP) and the estimation of a predictive model linking genotype and phenotype for traits of interest.

Other broad research interests in the Alberto lab are population genetics and evolutionary ecology of seaweeds and marine plants. Our focus is both on empirical research through the acquisition of population genetics data, using molecular marker techniques, and simulation-based hypothesis testing.

Informal inquiries about the project are encouraged. Please apply by sending a pdf document including 1) CV, 2) a declaration of research interests, 3) previous experience and fit for the position and 4) the email address and telephone number of potential contacts for reference letters.

Applications should be emailed to Dr. Filipe Alberto, albertof(at)uwm(dot)edu. The initial contract will be for

one year with possible extension to three years. Benefits information can be found at <http://www.wisconsin.edu/hr/benefits/gradben.pdf>. The position is expected to start as soon as possible and it will remain open until a suitable candidate is found.

UWM is an AA/EEO employer.

For more information about the lab see <http://alberto-lab.blogspot.com/>. UWM has an active group of re-

searchers studying evolutionary ecology and behavior:

<https://uwm.edu/biology/research/ecology-evolution-and-behavior/> Filipe Alberto Associate Professor Dept. of Biological Sciences University of Wisconsin - Milwaukee 3209 N. Maryland Ave. Milwaukee, WI 53211 URL: <http://alberto-lab.blogspot.com/> Email: [albertof@uwm.edu](mailto:albertof@uwm.edu) Tel: 414-229-6343

Filipe AOs Alberto <[albertof@uwm.edu](mailto:albertof@uwm.edu)>

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### ACoruna Spain Metabarcoding Jun27-28

Dear colleagues,

We would like to invite you to the “A Coruña DNA metabarcoding workshop”. Organised by AllGenetics, the Universidade da Coruña, and the Instituto de Investigación Biomédica de A Coruña, the workshop will

take place June 27th - 28th, 2018 in A Coruña, Spain.

We are expecting to hold between 15 and 18 talks given by researchers from different European institutions. Talks will be focused on examples on the use of DNA metabarcoding (industrial applications, soil biology, human microbiome, diet analysis, analysis of bulk meta-zoan/plant samples, bioreactor microbiome...). Other talks will cover technical aspects such as the impact of reference databases, primer design, high-throughput sequencing platforms, bioinformatic pipelines, mistagging / tag jumping / index hopping, as well as the need for biological and technical replicates, quantitative estimates from DNA metabarcoding data, and statistics of DNA metabarcoding.

Confirmed speakers:

Antón Vizcaíno (AllGenetics & Biology SL). Arjen de Groot (Wageningen University and Research). Carola Gómez-Rodríguez (Universidade de Santiago de Compostela). Daniel Marquina (Stockholms universitet - Naturhistoriska Riksmuseet). Felix Heeger (Leibniz-Institut für Gewässerökologie und Binnenfischerei). Fernando Ángel Fernández-Álvarez (Consejo Superior de Investigaciones Científicas - Institut de Ciències del Mar). Hugo de Boer (Universitetet i Oslo - Naturhistorisk museum). Joaquín Vierna (AllGenetics & Biology SL). Jorge Doña (Consejo Superior de Investigaciones Científicas - Estación Biológica de Doñana and University of Illinois at Urbana-Champaign - Illinois Natural History Survey). Marta Vila (Universidade da Coruña). Neus Marí-Mena (AllGenetics & Biology SL). Sarah Siu Tze Mak (Københavns Universitet - Statens Naturhistoriske Museum). Silvia Matesanz (Universidad Rey Juan Carlos). Vanessa Álvarez-López (Consejo Superior de Investigaciones Científicas - Instituto de Investigaciones Agrobiológicas de Galicia). Verónica Rojo (AllGenetics & Biology SL).

The workshop is free but registration is required. Registration will be open until April 30th at <http://www.allgenetics.eu/index.php/a-coruna-dna-metabarcoding-workshop.html>. Kind regards, Joaquín

Joaquín Vierna <jvierna@udc.es>

## Bangkok Agricultural Metagenomics Jun18

Dear colleague

I wanted to bring your attention to a 4-day workshop on agricultural microbiomes and their ecological/evolutionary interactions we are organising in Thailand this June.

Run by Hawkesbury Institute for the Environment in collaboration with UTS (Prof Aaron Darling), and Kasetsart University, the workshop aims to up-skill and empower a small number of participants (of any level, Student, Post-doc or Faculty) to run microbiome experiments.

Specifically:

- \* learning about the state of the art in microbiome genomics (for biodiversity and functional analyses)
- \* how to design a microbiome experiment and undertake quality control (because as we say in genomics: well-designed samples in -> well designed papers out)
- \* create a 16S library (a wet lab component where you will see that making your own libraries is not that hard!)
- \* analyse it using the QIIME 2 package (focusing on the ecological theory and what it actually means rather than just copying commands)

The expertise of the group comes from a number of sources (medical, marine, insects, plants) and even though the science will be broad, we will keep the techniques species agnostic :)

Beyond teaching core skills, the workshop aims to also explain the state of the art in the genomics of agricultural microbiomes, lighting talks from selected participants, and significant time for research networking. We think this will be an awesome experience for researchers who want to expand their skill set and interact with like-minded people.

The schedule and further information are available here: <http://stressedfruitfly.com/bangkok2018/> The deadline for registration is approaching rapidly (7th of May) and we may have to cap registration to ensure the correct student-teacher ratio.

We have tried to keep the costs to minimum but if you have/are student from a non-biomedical laboratory with limited funding, we're happy to negotiate a discount

after the 7th of May (if there are still open positions).

Please feel free to forward this email to anyone who might be interested.

If you have any queries, please feel free to contact me. Alexie Papanicolaou

–

Dr. Alexie Papanicolaou <http://stressedfruitfly.com>  
Senior Lecturer / Assistant Professor in Bioinformatics < [http://www.westernsydney.edu.au/hie/people/-researchers/doctor\\_alexie\\_papanicolaou](http://www.westernsydney.edu.au/hie/people/-researchers/doctor_alexie_papanicolaou) > Hawkesbury  
Institute for the Environment

“A.Papanicolaou@westernsydney.edu.au”

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## Barcelona EcoEvolutionOmics Jul8-13

Course Announcement: ‘Ecology through the omics lens’

Dear colleagues,

The 6th edition of the Ramon Margalef Summer Colloquia: ‘Ecology through the omics lens’ organized by the Marine Sciences Institute (ICM-CSIC) will take place from July 8th- 13th in Barcelona, Spain.

Course Overview: The use of omics techniques has spread rapidly across the field of Ecology and Evolution during the last decade, but there is substantial work ahead to link the obtained results with the existent ecological theory. The course aims to move from “what” to “why” when using omics approaches to study the ecosystem, as well as to frame their omics-based research in a theoretical ecological framework. The course will cover different environments (marine, terrestrial, host associated) as well as organismal sizes (from microbes to plants and animals), thus becoming an excellent opportunity to bring together researchers with similar questions, but working in fields that seldom communicate between each other.

The Colloquium will be structured in 4 sessions. Each session consist of a combination of lectures, and group discussion.

Advanced doctoral students and early post-docs are encouraged to apply.

More information and registrations: <http://www.acoio.org/margalef-summer-colloquia> or write us

to: [margalefcolloquia@acoio.org](mailto:margalefcolloquia@acoio.org)

Registration is open until 30th April.

Fellowships to students from developing countries are available.

Best regards,

Dr. Javier del Campo, Dr. Ramiro Logares and Dr. CÀlia Marrasé Ramon Margalef Summer Colloquium 2018 Organizers

Margalef Colloquia <[margalefcolloquia@acoio.org](mailto:margalefcolloquia@acoio.org)>

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## Berlin DataVisualisationPython Oct15-19

Course: Data Manipulation and Visualization with Python

Berlin, 15th-19th October 2018

( <https://www.physalia-courses.org/courses-workshops/-course38/> )

INSTRUCTOR:

DR. Martin Jones (founder, Python for biologists: ( <https://www.physalia-courses.org/instructors/t1/> ) )

Overview One of the strengths of the Python language is the availability of mature, high- quality libraries for working with scientific data. Integration between the most popular libraries has lead to the concept of a “scientific Python stack”: a collection of packages which are designed to work well together. In this workshop we will see how to leverage these libraries to efficiently work with and visualize large volumes of data.

Format The workshop is delivered over ten half- day sessions. Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer’s discretion. Each session uses examples and exercises that build on material from the previous one, so it’s important that students attend all sessions. The last two sessions will be kept free for students to work on their own datasets with the assistance of the instructor. A description of the sessions can be found at the bottom of this page.

Assumed Background This workshop is aimed at researchers and technical workers with a background in biology and a basic knowledge of Python (if you’ve taken the Introductory Python course then you have the Python knowledge; if you’re not sure whether you



know enough Python to benefit from this course then just drop us an email).

Requirements Students should have enough biological/bioinformatics background to appreciate the example datasets. They should also have some basic Python experience (the Introduction to Python course will fulfill these requirements). Students should be familiar with the use of lists, loops, functions and conditions in Python and have written at least a few small programs from scratch. Students will require the scientific Python stack to be installed on their laptops before attending; instructions for this will be sent out prior to the course.

Please visit our website to have more information about the course content: ( <https://www.physalia-courses.org/courses-workshops/course38/> )

Here is the full list of our courses and Workshops: <https://www.physalia-courses.org/courses-workshops/> Carlo Pecoraro, Ph.D

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## Berlin Epigenomics May28-Jun1 Last Call

Dear all,

we still have a few places available for the course “Epigenomic Data Analysis” which will be held in Berlin from the 28th of May to the 01st of June 2018.

Registration deadline: 26th April 2018.

( <https://www.physalia-courses.org/courses-workshops/-course31/> )

Instructors:

Dr. Federico Comoglio (Cambridge Institute for Medical Research (UK))

Dr. Iros Barozzi (Imperial College London (UK))

Overview

This course will introduce researchers and technical workers to the bioinformatic analysis of large epigenomic data sets obtained using Next-Generation Sequencing (NGS) technologies, with a focus on ChIP-seq, RNA-seq and DNase-seq / ATAC-seq. The course will cover the theoretical foundations of the most widely adopted algorithms and analysis pipelines, a targeted introduction to scripting in bash and R/BioConductor, and extensive hands-on tutorials using publicly available NGS data sets. At the end of this course, the students should be able to efficiently analyze their own data and identify common pitfalls of genomics data analyses.

### TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at researchers moving the first steps in epigenomic data analysis and / or interested in learning more about this subject. The course will offer a balanced mixture of lectures and hands-on practical tutorials using popular tools and R/BioConductor packages. Previous knowledge of genomics data formats from Illumina sequencers and exposure to bioinformatics is beneficial but not a necessary prerequisite.

#### Assumed Background

The participants should have some basic background in biology and understand the central role of DNA for biodiversity studies. No programming or scripting expertise is required and some basic introduction to UNIX-based command line applications will be provided on the first day. However, some basic experience with using command line and/or R is clearly an advantage as not all the basics can be thoroughly covered in that short amount of time. All hands-on exercises will be run in UNIX-environments (Linux, Mac) on remote servers. Statistical analyses will be run in R using RStudio.

For more information about the course, please visit our website: <https://www.physalia-courses.org/courses-workshops/course31/> Here is the full list of our courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops/> )

Best regards,

Carlo

Carlo Pecoraro, Ph.D

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## Berlin LandscapeGenomics Nov26-30

Course: LANDSCAPE GENOMICS

Berlin, 26-30 November 2018

Botanischer Garten und Botanisches Museum  
Berlin/Freie Universität Berlin Königin-Luise-Straße  
6-8

<https://www.physalia-courses.org/courses-workshops/-course17/> INSTRUCTORS:

Dr. Stéphane Joost (Lab of Geographic Information Systems (LASIG), EPFL, Lausanne, Switzerland)

Oliver Selmoni, MSc (Lab of Geographic Information Systems (LASIG), EPFL, Lausanne, Switzerland)

Workshop overview Landscape genomics is an emerging research field that studies how genetic diversity distributes across space and how environmental features can modify this structure through local adaptation. In this workshop, students will learn the basics of this approach and train using state of the art methods. The course will provide an overview of the type of dataset that can be used for a landscape genomics analysis. Firstly, students will learn how to obtain environmental data from publicly available databases, how to process it with Geographic Information Systems (GIS) and how to use the latter to produce indicators able to describe the characteristics of the landscape. Next, the course will discuss the different approaches to obtain genetic data and subsequently show how to study genetic variation and population structure across space in the R environment. Students will be given an overview of the different statistical approaches to study local adaptation, and will be trained in using two of them, Sambada and LFMM. The course will also cover the critical task of the interpretation and validation of the results. Finally, the workshop will consider the crucial aspects and good habits to account for when planning a landscape genomics experiment (e.g. sampling design).

Targeted Audience & Assumed Background This workshop is aimed at all biologists, ecologists, geneticists, veterinarians that want to implement the landscape genomics approach in their own studies of evolutionary biology and conservation. Even though the course is not intended for a specialized audience, basic knowledge in evolutionary biology and population genetics would help.

Students will learn how to use GIS, but basic computer skills are desirable (e.g. in the R environment). A basic understanding of statistics is also necessary.

Teaching Format The course is organized in ten learning sessions. During the first two sessions, the course will provide a contextualization of the research field. Then, students will be guided through a landscape genomics experiment with sessions that couple brief theoretical introductions with practical work.

Please visit our website to have more information about the course content: ( <https://www.physalia-courses.org/courses-workshops/course17/> )

Here is the full list of our courses and Workshops: ( <https://www.physalia-courses.org/courses-workshops/> )

Carlo Pecoraro, Ph.D

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## Berlin Phylogenomics Jun4-8

Course: Phylogenomics 4-8 June 201

( <https://www.physalia-courses.org/courses-workshops/-course21/> )

WHERE

BGBM, Königin-Luise-Straße 6-8, 14195 Berlin

Instructor: Dr. Michael Matschiner (University of Basel (Switzerland)); [ [www.evoinformatics.eu](http://www.evoinformatics.eu) ] ( <http://www.evoinformatics.eu> )

overview Recent advances in sequencing technology, and the rapid increase in the availability of genetic data, have revolutionized the field of phylogenetics. While genomic data promise unprecedented insights into the evolution of the tree of life, they also pose new challenges that must be addressed to avoid misleading results and to fully leverage the potential of the genome-scale data sets. These challenges include the identification of orthologous sequences that are suitable as phylogenetic markers, the selection of appropriate models of sequence

evolution, and the detection of gene-tree discordance due to incomplete lineage sorting and introgression. In this workshop I will present theory and exercises to infer time-calibrated phylogenies from multi-locus, RADseq, and whole-genome data sets while accounting for these confounding factors.

**Workshop Format** The workshop will be delivered over the course of five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group. Computing will be done using tools installed on the attendees laptop computer.

**Who Should Attend** This workshop is aimed at researchers, PhD or postdoc level planning to infer phylogenetic relationships and divergence times from multi-locus, RADseq, or whole-genome data.

**Requirements** Attendents should have basic knowledge of UNIX and will need to use the command line on their laptops. Familiarity with a scripting language such as Ruby, Python, or Perl will be helpful but is not required.

**Session content:** ( <https://www.physalia-courses.org/courses-workshops/course21/curriculum-21/> )

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## Berlin Phylogenomics Jun4-8 LastCall

Dear all, we still have a few places available for the course on “Phylogenomics” which will be held in Berlin from the 4th to the 8th of June (BGBM/ FU University, Konigin-Luise-Str. 6-8, 14195 Berlin)

<https://www.physalia-courses.org/courses-workshops/->

[course21/](#) Instructor:

Dr. Michael Matschiner (University of Basel (Switzerland); [www.evoinformatics.eu](http://www.evoinformatics.eu))

Overview

Recent advances in sequencing technology, and the rapid increase in the availability of genetic data, have revolutionized the field of phylogenetics. While genomic data promise unprecedented insights into the evolution of the tree of life, they also pose new challenges that must be addressed to avoid misleading results and to fully leverage the potential of the genome-scale data sets. These challenges include the identification of orthologous sequences that are suitable as phylogenetic markers, the selection of appropriate models of sequence evolution, and the detection of gene-tree discordance due to incomplete lineage sorting and introgression. In this workshop we will present theory and exercises to infer time-calibrated phylogenies from multi-locus, RADseq, and whole-genome data sets while accounting for these confounding factors.

**Workshop Format**

The course will be delivered over the course of five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group. Computing will be done using tools installed on the attendees laptop computer.

**Who Should Attend**

This course is aimed at researchers, PhD or postdoc level planning to infer phylogenetic relationships and divergence times from multi-locus, RADseq, or whole-genome data.

**Requirements**

Attendents should have basic knowledge of UNIX and will need to use the command line on their laptops. Familiarity with a scripting language such as Ruby, Python, or Perl will be helpful but is not required.

**Session content:** <https://www.physalia-courses.org/courses-workshops/course21/curriculum-21/>

Here is the full list of our courses and Workshops: <https://www.physalia-courses.org/courses-workshops/>  
Best regards,

Carlo

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## Berlin RADseq Jul2-6

Course: RAD-seq data analysis

Berlin, 2nd-6th July 2018

INSTRUCTOR:

Dr. Julian Catchen (University of Illinois, Urbana-Champaign; <http://catchenlab.life.illinois.edu/>)

Dr. Josie Paris (University of Sussex, UK)

Overview

Reduced representation genome sequencing methods are revolutionizing evolutionary analyses of non-model organisms. Several data generation and data analysis protocols have been developed to generate thousands of sequence variants in hundreds of individuals at relative low cost and speed. In this course, we will introduce the different approaches for obtaining reduced representation genome sequencing data and will specially focus on the data analysis. We will cover all necessary steps to obtain genome variants from short read data that are informative for population genetics, phylogenetic and association studies.

**TARGETED AUDIENCE & ASSUMED BACKGROUND**

This course is aimed at researchers and technical workers who are generating and/or analyzing reduced representation genome sequencing data (RAD-seq, ddRAD, 2bRAD, GBS, BDI(B)). Examples demonstrated in this course will involve primarily non-model organisms and examples of applications of this data type for different purposes will be covered. Attendees should have a background in biology. We will dedicate one session to some basic and advanced Linux concepts. Attendees should have also some familiarity with genomic data such as that arising from NGS sequencers.

Please visit our website to have more information about the course content: ( <https://www.physalia-courses.org/courses-workshops/course16/> )

Here is the full list of our courses and Workshops: (

<https://www.physalia-courses.org/courses-workshops/> )

Best regards,

Carlo

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## CatalinaIsland Genomics Aug10-26

Hi Colleagues,

This summer our team is offering two workshops on the use of high-throughput sequencing to study gene expression and genetic variation. For more details, see this link or the description that follows. <http://people.oregonstate.edu/~meyere/workshops.html> We aim to train biologists with little or no NGS experience to prepare sequencing libraries and analyze the millions of DNA sequences that result. Participants are expected to provide DNA or RNA samples from their own study systems, and we will prepare sequencing libraries together from those samples as well as a shared set of samples for a group project.

Participants will learn to analyze these data themselves using simple command line tools on a high-performance computing cluster. We'll cover each step of the process from DNA or RNA in a tube, to millions of DNA sequences, to biological data on gene expression or genetic variation.

Registration for these workshops includes room and board (three meals a day including plenty of coffee and snacks) throughout the workshop, and reagents/sequencing such that each participant can sequence and analyze a set of their own samples, generating pilot data for their species of interest.

Our Tag-Seq workshop will run from Aug 10-18, and the 2bRAD workshop from Aug 18-26. Registration for either workshop alone costs \$1,900. Participants enrolling in both workshops will pay a discounted rate of \$3,700 altogether.

For more details, including information from previous years' workshops, please see the full posting at the following website: <http://people.oregonstate.edu/~meyere/workshops.html> Contact us with questions, with "Workshops 2018" in the subject line. To reserve your spot, please contact Demian Willette ([demian.willette@lmu.edu](mailto:demian.willette@lmu.edu)). For specific questions about 2bRAD, contact Eli Meyer ([eli.meyer@oregonstate.edu](mailto:eli.meyer@oregonstate.edu)), and for specific questions about TagSeq, contact Carly Kenkel ([ckenkel@usc.edu](mailto:ckenkel@usc.edu)).

Space is limited! To reserve your spot, please confirm your participation no later than May 15th and pay registration fee by June 15th. Thanks, hope to see some of you on Catalina this August!

Eli Meyer, Oregon State University. [eli.meyer@oregonstate.edu](mailto:eli.meyer@oregonstate.edu) Demian Willette, Loyola Marymount University. [demian.willette@lmu.edu](mailto:demian.willette@lmu.edu) Carly Kenkel, University of Southern California. [carly.kenkel@gmail.com](mailto:carly.kenkel@gmail.com)

– Eli Meyer Assistant Professor, Integrative Biology Oregon State University Cell: (310) 618-4483 Office: (541) 737-3751 Lab: (541) 737-3752 <http://people.oregonstate.edu/~meyere> –

Eli Meyer <[meyere@oregonstate.edu](mailto:meyere@oregonstate.edu)>

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### cE3c Portugal Measuring Biodiversity Jun25-29

Subject: Portugal-cE3c-Course Measuring Biodiversity-June 25th-29th 2018

cE3c 'V Centre for Ecology, Evolution and Environmental Changes is organizing the Advanced Course Measuring Biodiversity by Joaquin Hortal - June 25th-29th 2018@ Lisbon, Portugal

Measuring Biodiversity: How to get data, assess its quality and measure different aspects of diversity

**OBJECTIVES:** This five-days intensive course offers an overview of the different ways to measure biodiversity, and provides tips for the stratification of primary biodiversity data and the construction of variables that describe its various facets. It also includes an in-depth review of the different types of data used to measure biodiversity and their problems and limitations.

See the PROGRAMME at: <http://ce3c.ciencias.ulisboa.pt/training/?cat> Course INSTRUCTOR: Joaquin Hortal (Senior Research

Scientist, Museo Nacional de Ciencias Naturales 'V CSIC, Madrid, Spain)(<http://jhortal.com/>)

**INTENDED AUDIENCE** This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD or MSc students in Ecology, Geography or related areas, and postdocs and other professionals working in related topics. The course is free for 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: June 1st, 2018

For additional details about the course and to know how to register, go to: <http://ce3c.ciencias.ulisboa.pt/-training/?cat> For more information about the course, please contact: [jhortal@mncn.csic.es](mailto:jhortal@mncn.csic.es)

Margarida Matos <[mmmatos@fc.ul.pt](mailto:mmmatos@fc.ul.pt)>

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### CIBIO-InBIO Portugal BiodiversityBiogeography Jul2-6

The diversity of life on Earth (biodiversity) exhibits temporal and spatial patterns calling for theoretical interpretations. This five-day course reviews several theoretical approaches describing patterns of species richness and relative abundance. The objective of this course is to make participants familiar with these theories' rationales, assumptions and limitations.

A major goal of this course is to demystify the use of mathematics in ecology. To this end, the course emphasizes the development and interpretation of mathematical formulae and their relationship with the biological phenomena they describe. The course has a hands-on approach, and participants will be engaged in computer exercises using R that aim to illustrate and implement the mathematical methods discussed. After the course the attendants should have a newfound appreciation for the role of theoretical models, with a view to being able to follow (and contribute to) advancements in theoretical ecology.

Click < <https://cibio.up.pt/workshops-courses/details/advanced-course-theoretical-perspectives-on-biodiversity-and-biogeography-2018> > here to see the programme for the course.

COURSE INSTRUCTORS



< <https://cibio.up.pt/people/details/lbordadeagua> >  
 LuÃ's Borda-de-Ãgua - CIBIO-InBIO | THEOECO  
 < <https://cibio.up.pt/people/details/alirezazadeh> >  
 Saeid Alirezazadeh â euro " CIBIO-InBIO | THEOECO

INTENDED AUDIENCE Minimum: 6

Maximum: 25

Priority will be given to:

- 1st year and other PhD students attending the BIODIV Doctoral Program;
- PhD students attending other courses;
- Other post-graduate students and researchers.

REGISTRATION Registration deadline: May 9, 2018.

Participation is free of charge for BIODIV students | 95 (students) / 200 (other participants). CIBIO-InBIO members will have an additional discount of 20%. Does not include lunch nor coffee breaks.

To apply, please send an e-mail accompanied by your short CV (max. two A4 pages) to <mailto:post.graduation@cibio.up.pt> post.graduation@cibio.up.pt. Please refer your academic status (PhD student, MSc Student, Other) and the institution to which you are affiliated.

For more information about the course, please contact: post.graduation@cibio.up.pt.

CIBIO - Centro de InvestigaÃem Biodiversidade e Recursos Geneticos/ InBIO Laboratorio Associado, Universidade do Porto

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f: <https://www.facebook.com/cibio.inbio> CIBIO-InBIO Divulgaçã

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**Crete**  
**EvolutionGeometricMorphometrics**  
**Sep10-14**

Dear evolDir members,

Transmitting Science is offering the 3rd edition of the course 'STUDYING EVOLUTION WITH GEOMETRIC MORPHOMETRICS'.

Instructor: Chris Klingenberg (University of Manchester, UK).

Dates: September 10th-14th, 2018.

Location: Heraklion, Crete (Greece)

Course overview

Morphometric approaches are used increasingly to study a wide range of questions concerning the evolution of organismal shape and its developmental and genetic basis. The standard techniques of the 'morphometric synthesis' of the mid-1990s have been supplemented by a set of new methods that address specific biological questions in specific contexts such as morphological integration, modularity, phylogenetic comparative analyses, and studies of symmetry and asymmetry. This course will introduce these recent approaches to an audience of researchers who are familiar with the fundamentals of geometric morphometrics. Lectures will present the theoretical basis of the methods, and software demonstrations and practical exercises will provide participants with the opportunity to try out the methods themselves. Practical work, as far as possible with the participants' own data or with data provided as examples, and discussions of the participants' research questions are intended to help them to apply the new methods to their own projects. The course will be taught using the software MorphoJ.

For more information and registration: <https://-www.transmittingscience.org/courses/geometric-morphometrics/evolution-geometric-morphometrics/>

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@transmittingscience.org](mailto:haris.saslis@transmittingscience.org)

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## Faro Portugal Phylogenetics Sep24-29 DeadlineApr30

\*\*\*\*\* REGISTRATION DEADLINE 30th APRIL \*\*\*\*\*

EMBO Practical Course: <http://meetings.embo.org/event/18-phylogenetics> Tree building: Advanced concepts and practice of phylogenetic analysis

24 - 29 September 2018, Faro, Portugal

\*About the practical course\*

The use of phylogenetic methods to reconstruct the evolutionary history of molecular sequences is a vital part of biological research. These methods underpin studies on the evolution and epidemiology of plant and animal parasites and disease-causing organisms, and more generally they allow an objective analysis of the patterns and processes generating biological diversity. To carry out phylogenetic analysis properly, it is necessary to have a good understanding of the strengths and weaknesses of the key methods and approaches. This EMBO Practical Course has been designed to provide the theoretical and practical skills needed to carry out state-of-the-art phylogenetic analyses.

The past few years have seen have an explosion in new methods of analysis including the application of Bayesian analysis methods in phylogeny reconstruction, the development of improved non-homogeneous models that much better represent the dynamics of sequence evolution, and the development of methods for high-throughput genome-wide analyses. This EMBO Practical Course has been designed to cater for these newest of methods and for understanding how they relate to the more traditional methods. Our goal is to teach technical sophistication without losing sight of the need for a critical attitude to data and analyses.

\*Speakers\*

Martin Embley - University of Newcastle, UK Tal Dagan - University of Kiel, Germany Tom Williams - University of Bristol, UK Peter Foster - Natural History Museum (London), UK Rachel Warnock - ETH Zurich, Switzerland Mark Wilkinson - Natural History Museum (London), UK

\*Selection criteria\*

Participants will be early-career postdoctoral researchers and advanced PhD students who will be chosen on merit,

as judged from a motivational letter, CV, and abstract for a 10 minute oral presentation. The selection procedure will also consider the need to balance numbers of participants representing different nationalities, to avoid over-representation from the host country (Portugal), to include a majority of participants resident in EMBO countries, and to maintain a reasonable gender balance.

\*Abstract guidelines\*

Abstract (200 words) for a 10 minute PowerPoint presentation that each participant will present to introduce their work and open-up discussion of their use of phylogenetic methods.

\*Registration fees\*

Student/postdocs 300 euros Academic 400 euros Industry 400 euros

\*Registration includes\*

Accommodation 23rd - 29th September 2018, inclusive (7 nights) Lunch and coffee each day Dinner each day, including Welcome Dinner and Gala Transport to and from UALG campus (Gambelas) Registration administration Course materials

(All participants and speakers will be accommodated in a hotel in central Faro. We will try to accommodate all participants in single rooms but due to availability we are likely to ask for some participants to share.)

\*Payment\*

Payment of the registration fees will be made by inter-bank transfer after notification of acceptance.

\*Travel grants\*

A limited number of travel grants are available for participants. Applicants do not need to apply separately for travel grants for this event but should indicate on the registration form if they wish to be considered for a travel grant.

More information is available at EMBO Travel Grants' page < <http://www.embo.org/funding-awards/travel-grants> >.

\*Registration deadline\*

30 April 2018

\*Selected participants will be notified by\*

18 May 2018

<http://meetings.embo.org/event/18-phylogenetics>  
<http://events.embo.org/enews/index.php?EventID=pc18-16> For informal enquires contact: Cymon J. Cox: [ccmaratt@ualg.pt](mailto:ccmaratt@ualg.pt)

Cymon Cox <[cymon.cox@googlemail.com](mailto:cymon.cox@googlemail.com)>

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**Greiswald DZG2018**  
**CRISPRCas9Applications Sep11**

Dear colleagues,

during evolution, animals have conquered the most extreme habitats and have evolved astonishing capabilities and a fascinating diversity of forms. However, it has remained a challenge to understand the genetic mechanisms underlying many evolutionary phenomena because functional genetic work has been restricted to a selected number of well-established model organisms.

With modern molecular methods, many organisms are now amenable to functional genetics: next generation sequencing can reveal genome sequences and expression profiles and CRISPR/Cas9 genome editing tools allow the targeted precise modification of genomes.

When used together, these techniques allow for a plethora of evolutionary questions to be addressed at the genetic level. This workshop aims to foster the use of CRISPR/Cas9 mediated genome editing in various animal models.

In this workshop we want to bring together scientists with experience in genome editing with those that wish to apply this technique to study different evolutionary and zoological questions. After some talks on the application of the method you will have the opportunity to discuss your project idea with our invited experts.

This meeting is a Satellite Symposium of the 111th Annual Meeting of the German Zoological Society (DZG) organized by the "Fachgruppe Entwicklungsbiologie" of the DZG.

For more information and registration

<https://dzg-meeting.de/de/satellite-symposia-workshops/crispcas9-applications-in-zoology/>

Invited experts

Lennart Randau (Marburg, Germany)

Wiebke Herzog (Münster, Germany)

Sebastian Fraune (Kiel, Germany)

Jörg Bantin (BioRad, Germany)

Max Farnworth (Göttingen, Germany)

Patricio Ferrer Murguia (Vienna, Austria)

Deadline for Abstract Submission

May 31, 2018

Date/Time

September 11, 2018; 9 am to 5 pm

Venue

Lecture Hall Complex (Ernst-Lohmeyer-Platz 6), Greifswald, Germany

Fees

Early Bird (April 1 to May 31, 2018): euro 65 (Regular Participants), euro 45 (Students)

Late (June 1 to September 10, 2018): euro 75 (Regular Participants), euro 50 (Students)

Please note that the fees will be lower for members of the DZG and attendees of the 111th Annual Meeting of the German Zoological Society.

Organizers/Contact

Susanne Änel

Gregor Bucher

Nico Posnien

–

Nico Posnien

Georg-August-University Göttingen

Johann-Friedrich-Blumenbach Institute for Zoology and Anthropology

Department of Developmental Biology

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NEW WEBSITE: <http://www.posnien-lab.net> Twitter: @PosnienLab

Nico Posnien <[nico.posnien@gmail.com](mailto:nico.posnien@gmail.com)>

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## Hannover SNPdata Jun11-14

Dear All

for those working with SNP data, I would like to draw your attention to a four day workshop from June 11–14,2018 on:

“SNP data management with TheSNPpit software package”

organized at the Institute of Farm Animal Genetics (FLI) in Mariensee near Hannover/Germany and run by Helmut Lichtenberg, Hermann Schwarzenbacher and myself. The workshop will start on Monday afternoon and finish on Thursday at noon.

TheSNPpit is a high performance database system for managing large scale SNP data. (for detailed information see: <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0164043> )

The course is targeted at people needing to manage and handle SNP data from whatever sources, be it plants or mammals from any SNP array. Thus it is for research institutions needing to keep track of many sets of project SNP data, or breeding programs with large scale genotyping with high density SNP chips and millions of samples.

The course will cover everything from software installation to hands on use of TheSNPpit. Furthermore, will shall deal with TheSNPpit integration into existing pipelines. This will include programmatically querying the SNP database as is, for instance, required when doing parentage control for which running code will be provided.

Other topics are user support, software maintenance and further development of TheSNPpit also as user group contributed software.

Course participants bring their Linux laptops together with their own SNP data. After the workshop they will be able to setup and manage their own SNP databases be they limited in size or very large.

Accommodation will be available locally. There is no course fee, but participants will have to pay for their travel, accommodation and meals.

Registration deadline is April 19th (FCFS).

Greetings

Eildert – Eildert Groeneveld

Institute of Farm Animal Genetics (FLI) Mariensee  
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Eildert Groeneveld <eildert.groeneveld@gmx.de>

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## Kaunas Lithuania ForestTreeGenomics Jun4-7

Training course 'From genotypes to phenotypes: assessing forest tree diversity in the wild' 4-7 June 2018  
Kaunas, Lithuania

Assessing how genetic diversity at potentially adaptive loci is structured in natural forest tree populations is a complex matter. Demographic processes and natural selection interact to produce genomic signatures that need to be disentangled. Single nucleotide polymorphisms, SNPs, are the most common type of genetic variation among living organisms. Studies based on SNP genotyping in trees, in particular on variation underlying adaptive traits, is an expanding research field which will help understand how trees adapt to climate change.

The course will show how genomic data sets can be analyzed to yield information on how environmental factors shape local adaptation and how genomic variation affect phenotypic diversity and how this can be used in breeding programs.

Main topics of the course include: - Genomics: from theory to practice - SNP genotyping - Statistical analysis of molecular data (methods and software) - High throughput phenotyping for association studies - Measuring and analyzing variability at potentially adaptive genes.

The lectures are based on datasets, analyses and preliminary results from research conducted within GenTree project. The last day of the course will be spent in the field to acquire experience with drone-based phenotyping. Nice weather, beautiful forests and good atmosphere are guaranteed!

Venue: Faculty of Forest Science and Ecology, Aleksandras Stulginskis University, Student str. 11, LT-53361 Akademija, Kaunas reg., Lithuania

Lecturers: Santiago Gonzalez-Martinez (INRA, France), Tanja Pyhajarvi (University of Oulu, Finland) ), Sebastian Richter (University of Marburg, Germany), Leopoldo Sanchez-Rodriguez (INRA, France), Ivan

Scotti (INRA, France).

The course is intended for PhD students and early-stage researchers in forestry, ecology and forest genetics. The content will be tailored to the background and experience of applicants.

To participate: The course is designed for a maximum of 20 participants, who will be selected based on their background and motivation. Lectures, food and accommodation are free of charge. Travel expenses are the responsibility of the attendees.

The course is organized by the EU H2020 project GenTree (<http://www.gentree-h2020.eu/>). Evoltree (<http://www.evoltree.eu/>) members can ask for financial help.

Details for registration (before April 23, 2018): <http://www.gentree-h2020.eu/events/event/from-genotypes-to-phenotypes-assessing-forest-tree-diversity-in-the-wild-training-course/>

Bruno Fady <bruno.fady@inra.fr>

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### MaxPlanck-Ploen TalkingEvolution Sep26-28

Register now for the workshop 'Talking Evolution - On Principles and Advances in Evolutionary Thinking'!

<https://workshops.evolbio.mpg.de/event/8/> This workshop will take place from September 26th-September 28th 2018 at the Max Plank Institute for Evolutionary Biology in Plön, Germany.

It aims to clarify, update and expand on traditional evolutionary thinking by providing a platform for discussion. Critics have argued evolutionary studies to be very gene-centric and dismissive of other mechanisms contributing to evolutionary change. In particular, they call for a wider recognition of topics such as:

- Niche construction theory - Extra-genetic inheritance - Developmental bias - Phenotypic plasticity

While the importance of these fields is backed by empirical evidence, wider recognition is trailing behind. We would like to change that. If this interests you, please join us and let's talk evolution!

Keynote talks will be given by: - Paul M. Brakefield (Trinity College, UK) - Luis-Miguel Chevin (CEFE, France) - Troy Day (Queen's University, Canada) - Ilkka Kronholm (University of Jyväskylä, Finland) - Kevin

Laland (University of St. Andrews, UK) - Sonia E. Sultan (Wesleyan University, USA)

All the accepted participants will be able to present their research either in the form of a talk or a poster.

Scientific Organizers: Noémie Erin, Alice Feurtey, Dominik W. Schmid, Vandana R. Venkateswaran

Workshop coordination: Maren Lehmann

"erin@evolbio.mpg.de" <erin@evolbio.mpg.de>

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### Montpellier TeachingEvolution Aug18

Looking for ways to share your excitement about evolution with your students? Would you like to learn about effective resources and methods for teaching evolution?

Join us at the Undergraduate Evolution Education Workshop (before the Joint Congress) on the 18th of August in Montpellier, France.

Register at <https://goo.gl/forms/u4P7KaljboOdgYps1> until April 9th. Space is limited.

More information can be found on the website: <https://qubeshub.org/groups/evoteachworkshop2018> "awarwick@msu.edu" <awarwick@msu.edu>

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### Developmental bias - Phenotypic plasticity

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Workshop coordination: Maren Lehmann

Noémie Erin <erin@evolbio.mpg.de>

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### NewHaven SoftwareCarpentry May3-4

Dear All:

The Biology Department at Southern Connecticut State University will be hosting a Software Carpentry workshop May 3-4, 2018 in New Haven, CT. Topics covered will include data management and basic analysis in R, Git, and Unix. Although the content of the workshop is not specific to evolutionary biology, the skills covered are widely utilized for conducting analyses and managing data in evolutionary biology.

No previous experience is required. Registration is \$30 and will remain open through April 27th. Space is limited. Full details and registration information can be found here: <https://bpteague.github.io/2018-05-03-scsu/> Feel free to contact me with questions.

Cheers, Steve Brady

Steven P. Brady Assistant Professor | Southern Connecticut State University Lab: Jennings 214 | Office: Jennings 215A Web: [stevenbrady.weebly.com](http://stevenbrady.weebly.com) | Phone: 203-392-7206

"Brady, Steven P." <bradys4@southernct.edu>

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### NorthCarolingMichigan Avida-ED Summer

We are currently soliciting applications for participants in a training workshop to teach faculty how to use Avida-ED, a free, web-based program designed to teach both principles of evolution and the nature of science, based on the research platform Avida.— This summer, we are holding two such workshops, \*\*one at Michigan State University (in East Lansing) from August 1-3\*, and\* one at the North Carolina A&T (in Greensboro) June 14-16\*\*\*.— Workshop participants will learn how to use this program, and incorporate it into courses that they teach.— We will give priority to applications submitted as teams of two, though \*in a change from last year, we are also accepting applications from single individuals\*.— Full details on the workshops, and information on how to apply, can be found at <https://avida-ed.msu.edu/active-lens-train-the-trainers-workshop-2018-edition> ; \*please note that the original application deadline has passed, but we are still considering applications on a rolling basis until full\*.— If you have any questions about this, please don't hesitate to contact me at [mwiser@msu.edu](mailto:mwiser@msu.edu)

Mike Wisner Postdoc in Evolution Education  
[mwiser@msu.edu](mailto:mwiser@msu.edu)

"mwiser@msu.edu" <[mwiser@msu.edu](mailto:mwiser@msu.edu)>

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### OakSpring eFLOWERSummerSchool Sep18-27

Oak Spring eFLOWER Summer School Oak Spring Garden Foundation, Upperville, Virginia, USA; 18-27 September 2018

Full information available here: <http://eflower.myspecies.info/oakspringsummerschool>

We invite applications for the Oak Spring eFLOWER Summer School to be held at the Oak Spring Garden Foundation in Upperville, Virginia (USA) from 18 to 27 September 2018. The goal of the Summer School is to deliver high-quality training in the modern comparative methods used to study plant macroevolution. While the methods are general and applicable to any group

of organisms, all of our empirical datasets will be drawn from our recent work on flowering plants. A unique feature of this School will be that the students themselves will participate in the creation of the datasets (floral traits and fossil calibrations) in our collaborative database PROTEUS, thereby gaining hands-on experience of the problems and questions associated with compiling data and building real-life datasets for comparative analyses. In doing so, we hope to further promote the rapidly evolving field of macroevolution among graduate students in plant sciences, while also conveying our experience in building high-quality datasets.

Topics addressed in the Summer School will include: divergence time estimation using molecular dating methods (relaxed clock methods, fossil calibration), ancestral state reconstruction and correlation of morphological traits (using maximum likelihood and Bayesian methods), and diversification rates and state-dependent diversification. All of these approaches start with phylogenetic trees obtained from molecular or genomic data and thus prior understanding of and experience with phylogenetic reconstruction based on such data is an essential prerequisite for participants, because this topic will not be taught in the Summer School. We also plan to include an outreach component in the form of a short video made by the participants during the course, explaining in simple terms what they have learned and why these methods are important to understand plant evolution.

The Oak Spring eFLOWER Summer School is free (no registration fee), including food and accommodation on site. All participants will also receive up to US\$ 1000 on a reimbursement basis for their economy flights to Dulles Airport (IAD), Washington D.C. Participants are entirely responsible for arranging their own travel insurance and visas. The School is ideally suited to graduate students (enrolled in a master's or PhD program) who already have some botanical and phylogenetic background, but who lack training in current macroevolutionary methods. International applicants are welcome (but fluency in English is a requirement of the course) and we will attempt to achieve a good balance in terms of gender and origin in the final Summer School group selected.

To apply, please send a one-page letter of motivation and a CV, as a single PDF file with your name, to [herve.sauquet@gmail.com](mailto:herve.sauquet@gmail.com). Deadline for applications: 1st June, 2018. Decisions will be made by 18th June. Please include the names and contact details of two referees (e.g., current or previous supervisor), but no letter of support (we will contact referees if necessary). Applications that do not meet these requirements may

be automatically rejected. The total number of participants will be limited to 15.

Organizers: Hervé Sauquet (Royal Botanic Gardens and Domain Trust, Australia) Susana Magallón (Universidad Nacional Autónoma de México, Mexico) Jürg Schönenberger (University of Vienna, Austria) Peter Crane (Oak Spring Garden Foundation, USA)

Confirmed Guest Lecturers: Else Marie Friis (Swedish Museum of Natural History, Sweden) Laura Lagomarsino (Louisiana State University, USA) Stacey Smith (University of Colorado-Boulder, USA)

Links to learn more: Oak Spring Garden Foundation < <https://www.osgf.org/> > eFLOWER project < <http://www.eflower.org/> > First eFLOWER Summer School < <http://eflower.myspecies.info/node/45> >

– Dr. Hervé Sauquet

Systematic Botanist, Royal Botanic Gardens and Domain Trust Mrs Macquaries Rd Sydney, NSW 2000, Australia E-mail: [herve.sauquet@rbgsyd.nsw.gov.au](mailto:herve.sauquet@rbgsyd.nsw.gov.au) or [herve.sauquet@gmail.com](mailto:herve.sauquet@gmail.com) Tel: +61 292 318 316 (office) or +61 412 331 062 (mobile)

Associate Professor, Université Paris-Sud Lab. Écologie, Systématique, Évolution (ESE) CNRS UMR 8079, bât. 360 91405 Orsay, France

[www.eflower.org](http://www.eflower.org) [www.sauquetlab.org](http://www.sauquetlab.org) Hervé Sauquet <[herve.sauquet@gmail.com](mailto:herve.sauquet@gmail.com)>

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## Portugal ComparativeMethods Jul23-25

Phylogenetic comparative methods are commonly used nowadays to investigate how species diversification occurs and test hypotheses about the mechanisms that drive phenotypic evolution, e.g. to model speciation and extinction, to understand why some groups are more diverse than others, to test whether phenotypic traits have evolved under neutral, directional or diversifying selection, to investigate how evolutionary rates are modified across the evolutionary history of a group etc. In all these cases, a phylogenetic hypothesis for the group of interest is combined to phenotypic and ecological data at the species level to understand the tempo and mode of evolutionary change.

The objective of this course is to provide an overview of these methods and of the tools available for their implementation in the R statistical language. During

theoretical sessions, we will review the main concepts and statistical tools necessary for testing hypotheses about species diversification and phenotypic evolution. These will then be implemented in practical lab sessions through worked examples to provide the participants with hands-on experience on data management and the implementation of these methods to real biological data.

A good knowledge of basic operations in R (file import, handling objects, using functions, getting help) is required and assumed to be able to adequately follow this course. BIODIV students are encouraged to take the Introduction to R course first.

Click < <https://cibio.up.pt/workshops-courses/details/advanced-course-phylogenetic-comparative-methods-for-studying-diversification-and-phenotypic-evolution> > here to see the programme for the course.

#### COURSE INSTRUCTORS

< <http://cibio.up.pt/people/details/akaliont> >  
Antigoni Kaliontzopoulou, AP, CIBIO-InBIO

< <http://cibio.up.pt/people/details/ajpajares> > Jess Muoz, PLANTBIO, CIBIO-InBIO

**INTENDED AUDIENCE** The course will be open to a maximum number of 20 participants.

Priority will be given to:

§1st year and other PhD students attending the BIODIV Doctoral Program;

§PhD students attending other courses;

§Other post-graduate students and researchers.

**REGISTRATION** Registration deadline: May 23, 2018

Participation is free of charge for BIODIV students | 65 euro (students) / 125 euro (other participants). CIBIO-InBIO members will have an additional discount of 20%. Does not include lunch nor coffee breaks.

To apply, please send an e-mail accompanied by your short CV (max. two A4 pages) to [post.graduation@cibio.up.pt](mailto:post.graduation@cibio.up.pt). Please refer your academic status (PhD student, MSc Student, Other) and the institution to which you are affiliated. BIODIV students should also mention which year of their PhD they are in. If you are interested in more than one course, you need to send a separate application for each of them. All applicants will be notified about whether they are accepted a month prior to the course starting date.

Please note that new rules apply for all BIODIV students.

For more information about the course, please contact: [post.graduation@cibio.up.pt](mailto:post.graduation@cibio.up.pt).

CIBIO - Centro de Investigao em Biodiversidade e Recursos Geneticos

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

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

CIBIO-InBIO Divulgao

## Portugal PopGenetics May14-18

Course Announcement / Reminder PGDH18 Population Genetics and Demographic History: model-based approaches

with Mark Beaumont, Louns Chikhi, Willy Rodriguez and Vitor Sousa

Key terms: Model-based Population Genetics

**IMPORTANT DATES** for this Course Deadline for applications: May 4th 2018 Course date: May 14th - May 18th 2018

The GTPB is proud to announce that the above referenced hands-on training course is open for applications

**Admission:** Candidates with adequate profile will be accepted in the next 72 hours after the application until we reach 20 participants.

**Course description:** Genetic and genomic data are increasingly used by ecologists and evolutionary biologists in general. It has thus become important for many biologists with different levels of experience to produce and analyse genetic (and genomic) data. In this course we will take a practical approach to the analysis of genetic and genomic data, but we will also provide some of the theoretical background required to understand the outputs of the software used. This course will be organised so as to mix lectures where important notions are introduced with practicals where freely available software will be used. While this will not be the focus of

the course, we will also introduce and discuss genealogical (coalescent-based) simulation methods and those based on forward-in-time simulations. Altogether this will allow to discuss the potentialities and limitations of the tools available to the community.

In this five-day course we will introduce the main concepts that underlie many of the models that are frequently used in population genetics. We will focus on the importance of demographic history (e.g. effective sizes and migration patterns) in shaping genetic data. We will go through the basic notions that are central to population genetics, insisting particularly on the statistics used to measure genetic diversity and population differentiation. The course will also cover a short introduction to coalescent theory, Bayesian inference in population genetics and data simulation. We will also introduce methods that have been recently developed to analyse genomic data such as the PSMC method of Li and Durbin that reconstructs the demographic history of a species or population with the genome of a single individual.

Most theory will be put into practice in practical sessions, analyzing real and/or simulated datasets. In these sessions, we will look at measures of genetic diversity and differentiation and use methods to infer demographic history. We will learn how to perform coalescent simulations of genetic/genomic data (using mainly Richard Hudson's ms program). We will also show how to simulate data for PSMC analyses. This will allow users to compare the PSMC obtained with real data to those obtained for the models they used. We will also look at how habitat fragmentation can be simulated using an in-house program. Some exercises will make use of R scripts (R being a freely available statistical program). Basic R knowledge is a pre-requisite but we will provide a short introduction to R. The R statistical package is a very powerful tool to analyse data outputs from many population genetics software, and can also be used to simulate genetic data under simple demographic scenarios.

More information at the GTPB website, <http://gtpb.igc.gulbenkian.pt/bicourses/2018/PGDH18/> Hoping that this course meets your interests,

Pedro Fernandes – Pedro L Fernandes Bioinformatics Training Coordinator Instituto Gulbenkian de Ciência Apartado 14 2781-901 OEIRAS PORTUGAL Tel +351 21 4407912 <http://gtpb.igc.gulbenkian.pt> – The Gulbenkian Training Programme in Bioinformatics General Office Rua da Quinta Grande, 6 2780-156 OEIRAS Portugal

“Pedro L. Fernandes” <pfern@igc.gulbenkian.pt>

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## UCalifornia LA Computational Genomics Jul30-Aug3

Dear Colleagues,

We're organizing a summer course in computational genomics at UCLA. Part of this course (the second Short Course from July 30-August 3) will focus on population genetics and microbiome methods.

More details on the program can be found here: <http://computationalgenomics.bioinformatics.ucla.edu/-programs/2018-cgsi/> You can apply here: <http://computationalgenomics.bioinformatics.ucla.edu/-programs/2018-cgsi/2018-cgsi-application/> One somewhat unique and special feature of the Computational Genomics Summer Institute (CGSI) is the heavy focus on computational methods, rather than solely on new results.

We hope to see you in LA this summer!

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

“klohmueller@g.ucla.edu” <klohmueller@g.ucla.edu>

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## UCPHDenmark Archaeomics Aug13-17

Archaeomics Summer School (5 ECTS) 13-17 August 2018, Natural History Museum of Denmark, University of Copenhagen, Denmark

Instructors: Hannes Schroeder, Fernando Racimo, Gabriel Renaud, Marie Louise Jørkov, Matthew Collins and others

Since the publication of the first ancient human genome in 2010, archaeology has seen a significant rise in the use of various '-omics' methodologies. These changes have been facilitated by rapid developments in DNA and protein sequencing technologies and the rise of “big data”. This intensive 5-day summer course will provide

students with a broad but detailed introduction to these new methodologies and their application in archaeology, including ancient genomics and the analysis of ancient proteins. Lectures will be combined with hands-on computing sessions to give students first-hand experience working with high-throughput sequencing data. The course is free for all students at Danish universities. For all other students there is a course fee of 600 USD. Food and accommodation are not included in the course fee.

For more information visit on the course, accommodation, and on how to sign up please email us or visit our website at [www.archaeomics.ku.dk](http://www.archaeomics.ku.dk). Hannes Schroeder <[hschroeder@snm.ku.dk](mailto:hschroeder@snm.ku.dk)> Fernando Racimo <[fracimo@snm.ku.dk](mailto:fracimo@snm.ku.dk)>

Hannes Schroeder, DPhil Assistant Professor Natural History Museum of Denmark <<http://www.snm.ku.dk>> Section for Evolutionary Genomics University of Copenhagen Åster Voldgade 5-7 1350 Copenhagen, Denmark

[hschroeder@snm.ku.dk](mailto:hschroeder@snm.ku.dk)

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### UCPHDenmark NGSpopulationGenetics Aug6-10

Summer course in next-generation sequencing data analyses for medical and population genetics (5 ECTS) August 6th-August 10th 2018, University of Copenhagen, Denmark

Instructors: Emilia Huerta-Sánchez, Matteo Fumagalli, Benjamin Peter, Doug Speed, Fernando Racimo, Anders Albrechtsen and Ida Moltke

Topics:

The course is a comprehensive introduction to a number of topics and common research tools used in analyses of next-generation sequencing (NGS) data. Topics include: genetic drift, natural selection, population structure, Fst, linkage disequilibrium, association mapping, GWAS, f-statistics and admixture graph fitting. The main focus will be on humans, but the analysis methods are applicable to many other species as well. Lectures will be combined with hands-on computer exercises. The course is free for all PhD students at Danish universities. For all other students there is a course fee of 200 US dollars. Food and accommodation are not included in the course.

To sign up, please send an email to [\[summercourse@gmail.com\]\(mailto:summercourse@gmail.com\) For more information visit \[www.popgen.dk/popgen18\]\(http://www.popgen.dk/popgen18\) anders <\[albrecht@binf.ku.dk\]\(mailto:albrecht@binf.ku.dk\)>](mailto:cph-</a></p>
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### UHuddersfield UK EssentialComputingSkills Jun18-20

Next Generation Biologists: Essential Computing Skills for Molecular Biology (<http://nextgenbiologists.org>) is a BBSRC-STARs programme-funded project to introduce and train researchers in the essential skills and best practices in scientific computing and bioinformatics. The format of the materials and the nature of the delivery is based on the successful ‘Software Carpentry’ (<http://software-carpentry.org/>) blended-learning model where students learn by developing skills through hands-on live coding and peer programming sessions led by experienced Software Carpentry instructors and supported by a small team of helpers. This is the fourth workshop in the series.

**AUDIENCE** The workshop is aimed at researchers with little or no experience in programming and data analysis who nevertheless need these approaches in their research in the life sciences.

**ORGANISERS AND INSTRUCTORS** The main organisers of the workshops are Dr Mary J. O’Connell (@EvolMolly), Dr Martin Callaghan (both at the University of Leeds) and Dr Jarek Bryk (@jarekbryk at the University of Huddersfield). The project is a joint initiative of the University of Leeds and the University of Huddersfield. The instructors include Martin Callaghan, Jarek Bryk and Dr Alastair Droop (also from the University of Leeds).

**PRELIMINARY PROGRAMME** Monday Introduction to the fundamentals of UNIX, command-line interface and shell.

Tuesday Introduction to fundamentals of R with R Studio, including data and analysis reproducibility, concluded with example analysis of high-throughput data.

Wednesday A ‘hackathon’ day, during which participants will use skills learned in earlier days to solve a real-life data analysis problem of their choosing or a walk-through of an analysis of a real-life dataset using learned skills in shell and R.

**DATE** The workshop will be run on 18-20 June 2018 (Monday to Wednesday inclusive).



**VENUE** The workshop will take place at the University of Huddersfield, UK.

**COSTS** The workshop is free of charge for all BBSRC-funded researchers, as well as staff and students from the Universities of Leeds and Huddersfield. For all other participants a course fee of 170 will apply that will need to be paid before the workshop begins. Travel and accommodation costs are \*not\* covered by the organisers.

**HOW TO APPLY** To apply for a place on the workshop, prepare a 150 word summary of your curriculum vitae and a 150 word statement detailing why this course is of particular importance to your current research and submit them with the registration form: <https://goo.gl/1MzRpQ> by 25 May < <http://airmail.calendar/2018-05-25%2012:00:00%20BST> >. The selection committee will notify successful applicants by the end of 28th May. The workshop will be limited to 25 participants, who are expected to bring their own computers on the workshop.

More details about the project and the workshop are available on our website at <http://nextgenbiologists.org>. We are also on Twitter at @nextgenbiol (the 'l' is important :-).

See you on the workshop! The organisers

University of Huddersfield inspiring tomorrow's professionals.

Jarek Bryk <J.Bryk@hud.ac.uk>

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## UK Bioinformatics Using Linux Oct1-5

Introduction to Linux workflows for biologists (IBUL03)

This course will take place from the 1st - 5th October 2018 in Glasgow city and centre and will be delivered by Dr Martin Jones. You can subscribe to just the course and/or add an additional accommodation package in out near by accommodation for ease which included breakfast lunch and dinner on Monday and Thursday.

Course Overview:

Most high-throughput bioinformatics work these days takes place on the Linux command line. The programs which do the majority of the computational heavy lifting – genome assemblers, read mappers, and annotation tools – are designed to work best when used with a command-line interface. Because the command line can be an intimidating environment, many biologists learn

the bare minimum needed to get their analysis tools working. This means that they miss out on the power of Linux to customize their environment and automate many parts of the bioinformatics workflow. This course will introduce the Linux command line environment from scratch and teach students how to make the most of its tools to achieve a high level of productivity when working with biological data.

Monday 1st

Module 1: The design of Linux.

In the first session we briefly cover the design of Linux: how is it different from Windows/OSX and how is it best used? We'll then jump straight onto the command line and learn about the layout of the Linux file system and how to navigate it. We'll describe Linux's file permission system (which often trips up beginners), how paths work, and how we actually run programs on the command line. We'll learn a few tricks for using the command line more efficiently, and how to deal with programs that are misbehaving. We'll finish this session by looking at the built in help system and how to read and interpret manual pages.

Module 2: System management. We'll first look at a few command line tools for monitoring the status of the system and keeping track of what's happening to processor power, memory, and disk space. We'll go over the process of installing new software from the built in repositories (which is easy) and from source code downloads (which is trickier). We'll also introduce some tools for benchmarking software (measuring the time/memory requirements of processing large datasets).

Tuesday 2nd

Module 3: Manipulating tabular data. Many data types we want to work with in bioinformatics are stored as tabular plain text files, and here we learn all about manipulating tabular data on the command line. We'll start with simple things like extracting columns, filtering and sorting, searching for text before moving on to more complex tasks like searching for duplicated values, summarizing large files, and combining simple tools into long commands.

Module 4: Constructing pipelines. In this session we will look at the various tools Linux has for constructing pipelines out of individual commands. Aliases, shell redirection, pipes, and shell scripting will all be introduced here. We'll also look at a couple of specific tools to help with running tools on multiple processors, and for monitoring the progress of long running tasks.

Wednesday 3rd

Module 5: EMBOSS. EMBOSS is a suite of bioinformat-

ics command-line tools explicitly designed to work in the Linux paradigm. We'll get an overview of the different sequence data formats that we might expect to work with, and put what we learned about shell scripting to biological use by building a pipeline to compare codon usage across two collections of DNA sequences.

Module 6: - Using a Linux server. Often in bioinformatics we'll be working on a Linux server rather than our own computer— typically because we need access to more computing power, or to specialized tools and datasets. In this session we'll learn how to connect to a Linux server and how to manage sessions. We'll also consider the various ways of moving data to and from a server from your own computer, and finish with a discussion of the considerations we have to make when working on a shared computer.

Thursday 4th

Module 7: Combining methods. In the next two sessions – i.e. one full day – we'll put everything we have learned together and implement a workflow for next-gen sequence analysis. In this first session we'll carry out quality control on some paired-end Illumina data and map these reads to a reference genome. We'll then look at various approaches to automating this pipeline, allowing us to quickly do the same for a second dataset.

Module 18: Combining methods. The second part of the next-gen workflow is to call variants to identify SNPs between our two samples and the reference genome. We'll look at the VCF file format and figure out how to filter SNPs for read coverage and quality. By counting the number of SNPs between each sample and the reference we will try to figure out something about the biology of the two samples. We'll attempt to automate this analysis

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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>

## UK IntroToPython May21-25

PARTFUNDED SCHOLARSHIPS for the course “ Introduction to Python for biologists (IPYB05)”

This course will run from 21<sup>st</sup> - 25<sup>th</sup> May 2018 in Glasgow City Centre, Scotland, UK

<https://www.prinformatix.com/course/introduction-to-python-for-biologists-ipyb05/>

PR INFORMATIX ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE “ Introduction to Python for biologists (IPYB05)”

SCHOLARSHIPS CONTRIBUTE TOWARDS COURSE AND ACCOMMODATION FEES WITH 5 ALL INCLUSIVE PLACES (accommodation and meals included) AVAILABLE AT £475.00 (Fees have been subsidised by 40% from £800.00).

Applications should be sent to [oliver-hooker@prinformatix.com](mailto:oliver-hooker@prinformatix.com) and contain

the following.

1. Full name
2. Institute name
3. PhD subject title or Post doc research questions
4. Do you hold a funded position
5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Tuesday 1<sup>st</sup> May and decisions will be made by Wednesday 2<sup>nd</sup> May 2018

We still have a few 'normal' places available for anyone else interested.

Full course details are given below

Introduction to Python for biologists (IPYB05)

Delivered by Dr. Martin Jones

<https://www.prinformatix.com/course/introduction-to-python-for-biologists-ipyb05/>

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. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackle problems in their own research and (2) continue their Python education in a self-directed way. In biology Python is often applied to sequence analysis and data manipulation e.g. calculating base composition statistics, removing adapter sequences, translating DNA to protein, counting kmers, filtering tables etc. In this course we use these applications as examples during the exercises as a way of illustrating how to use the

tools that Python has because it makes sense given the background of most of the people who attend. However, it should be possible to apply what you learn to any type of programming problem.

Please email any questions to [oliverhooker@prinformatics.com](mailto:oliverhooker@prinformatics.com)

– Oliver Hooker PhD. PR informatics 2017 publications  
 - Ecosystem size predicts eco-morphological variability in post-glacial diversification. Ecology and Evolution. - The physiological costs of prey switching reinforce foraging specialization. Journal of animal ecology. [prinformatics.com](http://prinformatics.com) [twitter.com/PRinformatics](https://twitter.com/PRinformatics) [facebook.com/prstatistics/](https://www.facebook.com/prstatistics/) 6 Hope Park Crescent Edinburgh EH8 9NA +44 (0) 7966500340

Oliver Hooker <[oliverhooker@prinformatics.com](mailto:oliverhooker@prinformatics.com)>

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## UK Scholarships Python May28-Jun1

PARTFUNDED SCHOLARSHIPS for the course “Advanced Python for biologists (APYB02)”

This course will run from 28th May 1st June 2018 in Glasgow City Centre, Scotland, UK

<https://www.prinformatics.com/course/advanced-python-biologists-apyb02/> PR INFORMATICS ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE “Advanced Python for biologists (APYB02)”

SCHOLARSHIPS CONTRIBUTE TOWARDS COURSE AND ACCOMMODATION FEES WITH 5 ALL INCLUSIVE PLACES (accommodation and meals included) AVAILABLE AT pounds 475.00 (Fees have been subsidised by 40% from pounds 800.00).

Applications should be sent to [oliverhooker@prinformatics.com](mailto:oliverhooker@prinformatics.com) and contain

the following.

1. Full name
2. Institute name
3. PhD subject title or Post doc research questions
4. Do you hold a funded position
5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Tuesday 8th May and decisions will be made by Wednesday 9th May 2018

We still have 'normal' places available for anyone else interested.

Full course details are given below

Advanced Python for biologists (APYB02)

Delivered by Dr. Martin Jones

<https://www.prinformatics.com/course/advanced-python-biologists-apyb02/> 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.

Please email any questions to [oliverhooker@prinformatics.com](mailto:oliverhooker@prinformatics.com)

Oliver Hooker PhD. PR informatics 2017 publications  
 - Ecosystem size predicts eco-morphological variability in post-glacial diversification. Ecology and Evolution. - The physiological costs of prey switching reinforce foraging specialization. Journal of animal ecology. [prinformatics.com](http://prinformatics.com) [twitter.com/PRinformatics](https://twitter.com/PRinformatics) [facebook.com/prstatistics/](https://www.facebook.com/prstatistics/) 6 Hope Park Crescent Edinburgh EH8 9NA +44 (0) 7966500340

Oliver Hooker <[oliverhooker@prinformatics.com](mailto:oliverhooker@prinformatics.com)>

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## WellcomeUK HumanGeneticAnalysis Jul18-24

GENETIC ANALYSIS OF MENDELIAN AND COMPLEX DISORDERS

18-24 July 2018 Wellcome Genome Campus, Hinxton, Cambridge, UK APPLICATION AND BURSARY DEADLINE CLOSING SOON: 6 APRIL 2018! Summary: This intensive, residential, computational course

is aimed at scientists actively involved in genetic analysis of rare (Mendelian) or complex human traits who anticipate using state-of-the-art statistical analysis techniques on genetic data collected on related and unrelated individuals.

Course Organiser: Daniel E. Weeks (University of Pittsburgh, USA) Course Instructors: Heather Cordell (Institute of Genetic Medicine, Newcastle University, UK) Janet Sinsheimer (University of California, Los Angeles, USA) Eric Sobel (University of California, Los Angeles, USA) Joe Terwilliger (Columbia University, New York, USA) Simon Heath (Centre Nacional d'Anàlisi Gen<sup>2</sup>mica (CNAG), Barcelona, Spain) Guest Instruc-

tors: Najaf Amin (Erasmus Medical Centre, The Netherlands) Jin Zhou (University of Arizona, USA) Guest Speakers: Carl Anderson (Wellcome Trust Sanger Institute, UK) Inês Barroso (Wellcome Trust Sanger Institute, UK) Bursaries: Limited bursaries are available (up to 50% of the course fee). Please see our website for full details

URL: <https://coursesandconferences.wellcomegenomecampus.org/-events/item.aspx?e=706> Janet Sinsheimer PhD Professor Human Genetics, Biomathematics David Geffen School of Medicine at UCLA Professor Biostatistics Fielding School of Public Health, UCLA  
 “Sinsheimer, Janet” <JanetS@mednet.ucla.edu>

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## Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email [evoldir@evol.biology.McMaster.CA](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent 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  $\text{\LaTeX}$  do not try to embed  $\text{\LaTeX}$  or  $\text{\TeX}$  in your message (or other formats) since my program will strip these from the message.