
E v o l D i r

April 1, 2018

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

Foreword

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

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

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



Foreword	1
Conferences	2
GradStudentPositions	18
Jobs	47
Other	64
PostDocs	72
WorkshopsCourses	117
Instructions	139
Afterword	140

Conferences

Asilomar MolluscEvolution 2	Munich ReefEvolution Sep5-7 9
Bangalore EvolutionButterflyImmunology Jun11-14 .3	ParkCity Utah EvolutionaryMedicine Aug1-4 10
EntebbeUganda SpeciationInAncientLakes8 Jul29-Aug3 3	ParkCity Utah EvolutionaryMedicine Aug1-4 Absts 10
FortCollins DroughtStressAdaptation Jun21-22 4	ParkCity Utah EvolutionMedicine Aug1-4 10
Hawaii OriginsAdaptiveRadiation Jul22-25 Deadline 4	Portland GalaxyBioinformatics Jun25-30 11
Hungary SocialEvolution Apr19-22 5	PuertoRico EvolutionaryAntrhopology Nov1-4 12
ImperialC London EvolGenetics Apr10-12 6	Rennes Evolution Oct 13
London EvolGenetics Apr10-12 6	Sherbrooke Canada RECOMB-CG Oct9-12 13
Marseilles EvolutionaryBiology Sep25-28 DeadlineJun30 7	Toulouse EconomicsAndEvolution May24-25 14
MBL WoodsHole MolecularEvolution Jul19-29 7	UGottingen SensationEvolution Sep27-28 15
McMasterU EarlyLife Jun24-27 8	UK SexualSelection May 16
MilnerCentreBath Evolution Sep18-21 8	UMiami SEEC EcolEvolution Oct5-7 16
Monterey DeepSeaEvolution Sep9-14 8	UMontpellier PhylogenomicsSoftware Aug17 16
Montpellier OriginAgriculture Sep11-14 9	Warsaw HumanAndEvolution Sep24-26 Registra- tionOpen 17

Asilomar MolluscEvolution

Dear all

The next World Congress of Malacology will be in Asilomar conference grounds, Pacific Grove, California. The congress is organised by Unitas Malacologica in conjunction with the American Malacological Society, the Western Society of Malacologists, and our other partner societies. Asilomar is a stunning location and we are excited to welcome you there.

We are now seeking proposals for thematic symposia within the conference. The meeting includes all science done using any molluscs as subjects, as well as organismal biology of the molluscs themselves. Deadline for proposals is 1 May. <http://forms.calacademy.org/-wcm2019> We are particularly interested in symposium

topics that embrace (actually or theoretically) multiple molluscan classes. We ask you to suggest a few speakers, as indicative of the breadth of the topic. We will not contact any suggested speakers without your permission.

We expect symposia to last a half day or full day, but if you think your topic would extend beyond a day that's also welcome. The selected symposia are not being offered any funding support (we're sorry) but will be advertised prominently in the run up to abstract submission and registration, and we are happy help you recruit outside sponsorship for your symposium.

We also particularly encourage participation by early career scientists and international members as symposium organisers.

On behalf of the scientific programme committee, I am looking forward to your symposium ideas!

Here's the link to the online form again - deadline 1 May 2018. <http://forms.calacademy.org/wcm2019> 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

j.sigwart@qub.ac.uk

Bangalore
EvolutionButterflyImmunology
Jun11-14

Conference: ‘ Ecological Immunology in Butterflies, and underlying mechanisms’

Dear Colleagues,

Please see below information detailing the upcoming symposium “Ecological Immunology in Butterflies, and underlying mechanisms” to be held during the 8th Biology of Butterflies Conference, Bangalore, India, on June 11th to 14th. Both the symposium and the conference aim to attract researchers from the fields of Ecology and Evolutionary Biology.

Butterflies face challenges from wide range of organisms, from pathogenic fungi, viruses, and bacteria, to endo- and ecto-parasitoid wasps. An effective immune system is, hence, crucial. Activation of an immune response is, however, costly, and interactions with pathogens and parasites most likely have great fitness consequences on the butterfly hosts. Such adaptations may include modifications in the hosts’ immune strategies, fecundity, behaviours or other life-history traits.

This symposium aims to bring together people working on different facets of butterfly immunity. We will present the latest research on immune reactions, and the fundamental trade-offs between the investment into immune functions and other costly life-history traits in butterflies, using tool-boxes from molecular biology to ecology.

The invited speakers include: Prof. Jacobus de Roode, Emory University, USA. Prof. de Roode’s interests include how the host plant diet affects disease outcome in butterflies. (<http://deroodelab.org/>)

Dr. Christopher Wheat, Stockholm University, Sweden. Dr. Wheat will present his research on the microevolutionary selection dynamics acting on immune genes of the green veined white butterfly, *Pieris napi*. (<http://www.zoologi.su.se/en/about/staff/-person.php?suid=cwhea>)

The Conference organiser, and symposium organisers, Dr. Marjo Saastamoinen and Dr. Anne Duploux now welcome abstracts through the online registration form for both talk and poster contributions from anyone and any career level.

Please find all details about the conference, including registration form and fees here: <http://www.biologyofbutterflies.org/conference-registration>

Please send titles and abstracts for the symposium on Ecological Immunology in Butterflies through the Conference website <http://www.biologyofbutterflies.org/abstract-submission>, no later than 30th of April 2018. Please specify if you would like to present a talk or poster. Please specify the speaker’s affiliation and the names of all other authors of the study. Abstract should not be longer than 200 words.

For accommodation: <http://www.biologyofbutterflies.org/accommodation> We look forward to meeting you in Bangalore in June. Sincerely,

The organising committee: Marjo Saastamoinen Anne Duploux

Anne Duploux, PhD Organismal and Evolutionary Biology Research Program University of Helsinki Fi-00014 Helsinki, Finland

Web: www.anneduploux.net “Duploux, Anne M R” <anne.duploux@helsinki.fi>

EntebbeUganda
SpeciationInAncientLakes8
Jul29- Aug3

Dear colleagues, this is a reminder for the International Symposium “Speciation in Ancient Lakes 8” (SIAL 8) that will take place from 29 July 3 August, 2018 in Entebbe, Uganda. This will be the first time for SIAL to be held in Africa and we are looking forward to celebrate the 25th anniversary of SIAL at the shores of famous Lake Victoria.

Early bird registration ends on 31 March. Please, check the website for a preliminary program and details on registration and conference fees: sial-online.org/conferences/sial8.

Contact Christian.Albrecht@allzool.bio.uni-giessen.de for general information

Contact Bjoern.Stelbrink@allzool.bio.uni-giessen.de for registration and abstracts

Björn Stelbrink <Bjoern.Stelbrink@allzool.bio.uni-giessen.de>

FortCollins DroughtStressAdaptation Jun21-22

Registration is now open for a 2-day symposium Frontiers in Breeding for Drought 21-22 June 2018 in Fort Collins, Colorado

<http://plantbreedingfordroughttolerance.colostate.edu/symposium.html> Talks will span a variety of novel approaches in phenotyping, genetic discovery and analysis

Detlef Weigel, MPI Tuebingen Genetics and epigenetics of adaptation to the abiotic environment in *A. thaliana*

Malia Gehan, Danforth Center Utilizing Natural Variation for Crop Resilience Under Temperature Stress

Duke Pauli, University of Arizona Unraveling stress adaptive traits through the use of Phenomics

Alina Zare, University of Florida Machine Learning Methods for Remote Sensing and Phenotyping

Brook Moyers, Colorado State University Genetics of drought adaptation in rice

William Beavis, Iowa State University Redesigning Plant Breeding to Efficiently Transfer Discoveries of Genetic Adaptation to Drought

Chris Topp, Danforth Center Phenotyping technologies and computational tools for root structure-function and genetic analyses

Mike Olsen, CIMMYT Kenya Drought Tolerant Maize for Africa

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

Hawaii OriginsAdaptiveRadiation Jul22-25 Deadline

Invitation for consideration for oral presentation at the Hawaii AGA on Origins of Adaptive Radiation, July 22-25, 2018

The 2018 American Genetic Association Symposium, “*Origins of Adaptive Radiation*” is fast approaching, *July 22-25 in Waimea, Hawaii*. The meeting, which will explore processes at the early stages of adaptive diversification, includes speakers working on diverse systems, from African cichlids, sticklebacks, Anolis lizards, Galapagos finches and snails, Heliconius butterflies, Aquilegia plants, and Hawaiian honeycreepers, spiders, different insects, and trees. And covering concepts ranging from 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* (registration, accommodation & \$300 travel bursary). For this, we are particularly encouraging junior scientists to apply. *To be considered for an oral presentation, abstracts must be submitted by April 1st 2018*

- In addition, the AGA is offering *multiple free registration slots to graduate students* who submit an abstract. There are also a small number of travel bursaries (\$300 each) available, and will be awarded to select students based on their abstracts.

More details are provided below. If you have any logistical questions, please contact Anjanette Baker <theaga@theaga.org>. For any questions regarding the content of the symposium, please contact Rosemary Gillespie <gillespie@berkeley.edu>

Best wishes,

Rosemary Gillespie, AGA President

For full details, visit <http://www.theaga.org>. AGA symposia are small, friendly gatherings, and provide wonderful opportunities for students and researchers to engage with one another and share their science.

We will open with a pupu reception on Sunday night, and our Key Distinguished Lecturer, Ole Seehausen, will lead off two full days of talks on Monday and Tuesday. A luau reception with entertainment is planned for Tuesday night. Finally, an optional expert-led field trip to explore radiation processes at Volcanoes National Park will take place on Wednesday.

Registration is open! Registration cost includes receptions, lunches, and coffee breaks, as well as complimentary AGA membership and subscription to Journal of Heredity.

Invited Speakers:

Key Distinguished Lecturer: Ole Seehausen, Eawag Center, Switzerland Gordon Bennett, University of California, Merced Brian Bowen, Hawai'i Institute of Marine Biology

Rob Fleischer, Smithsonian Conservation Biology Institute Andrew Hendry, McGill University, Canada Scott Hodges, University of California, Santa Barbara

Henrik Krehenwinkel, University of California, Berkeley Jonathan Losos, Washington University Jim Mallet, Harvard University

Axel Meyer, University of Konstanz, Germany Anna Papadopoulou, University of Cyprus, Republic of Cyprus Christine Parent, University of Idaho

Karin Pfennig, University of North Carolina at Chapel Hill Dan Rubinoff, University of Hawai'i, Mānoa Dolph Schluter, University of British Columbia, Canada

Kerry Shaw, Cornell University Elizabeth Stacy, University of Hawai'i, Hilo Katie Wagner, University of Wyoming

theaga@theaga.org

Hungary Social Evolution Apr19-22

Hello

This is the last call for the conference on SOCIAL EVOLUTION in Hortobágy, Hungary 19-22 April 2018.

We are fortunate to have excellent young scientists and eminent evolutionary biologists, ecologists and behavioural biologists at the conference that will be opened by Prof József Pálincás, President of ELVONAL cutting edge program on Thursday 19th April. Friday and Saturday (20 & 21 April) will be dedicated to presentations and discussions. In addition, we'll have social events that include slide shows of Hungarian wildlife and Hungarian folk dancing, and of course, great food and wonderful scenery. We kept the cost low to allow students come along: the registration is 150 EUR that includes accommodation and all meals.

We only had a few places left: please contact workshop2018.hortobagy@gmail.com before 31 MARCH 2018.

See further details below. The conference is supported by ELVONAL programme, University of Debrecen and Hortobagy National Park.

===SOCIAL EVOLUTION Conference, 19-22 April

2018, Hortobágy, Hungary

Welcome to Hortobágy, a UNESCO-protected area and the first national park in Hungary. It has a unique wildlife, landscape and people, see further details at https://en.wikipedia.org/wiki/Hortob%C3%A1gy_National_Park We invited elite scientists from Hungary and abroad to discuss recent advances in the study of social evolution. The Workshop will also offer opportunities to young scientists and students to present their work, and discuss potential projects with senior scientists.

The provisional programme is as follows: Thursday 19 April - Arrival, Welcome reception

Friday 20 April - Full day scientific programme: presentations by senior speakers, and contributions by participants

Saturday 21 April - Full day programme: presentations by senior speakers, and contributions by participants

Sunday 22 April - Bird watching in Hortobagy and/or departure

In the evenings, we'll have social events (slide shows, evening discussions and folk dancing), so feel free to bring your partner.

The conference will take place in the Visitor Centre of Hortobagy National Park: <http://www.hnp.hu/hu-szervezeti-egyseg/turizmus/oldal/hnp-latogatokozpont> Accommodation will be in the National Parks' guesthouse approx 20 min walk, and meals will be in local restaurants. Registration will be around 150 EUR in total that includes 3 nights in shared rooms (2 or 4 person per room), and 3 breakfast, lunch and dinner each. We also offer reduced rate of registration of 20 EUR that does not cover accommodation or meals.

Hortobágy offers wonderful activities for everybody all year round. Shortly after our Workshop there will be the availability to visit the Puszta and learn about it's flora and fauna and the people who lives there, see: www.hnp.hu/en >From Budapest it takes about 2 hours to drive to Hortobágy, and from Debrecen about 30 min. Both Budapest and Debrecen have airports - WizzAir now offers direct flies to Debrecen from various European locations for a modest price. There are airport transfers available to and from both airports.

There is a train line connecting Hortobágy to Füzesabony and to Debrecen, approx. every other hour.

Professor Tamas Szekely Karola Szemán University of Bath & Debrecen University of Debrecen

Tamas Szekely <T.Szekely@bath.ac.uk>

ImperialC London EvolGenetics Apr10-12

Registration is now open for the Ecological Genetics Group 2018!

The meeting concentrates on evolutionary, ecological and population genetic issues in all types of organisms.

The 62nd Meeting of the Ecological Genetics Group will be held at the Skempton Building, Imperial College London between the 10th and 12th of April, 2018. The conference is sponsored by the British Ecological Society and the Genetics Society. There will be a full scientific and social programme throughout the three-day period of the conference. It brings together those working in the fields of population genetics, ecology and evolution from across Europe and beyond.

Talks and posters are welcome from all! For those of you still completing your MScs and PhDs, remember that you will have the chance to win the coveted best talk/poster prizes! The Ecological Genetics Group meetings have a long tradition of being friendly and relaxed, where young researchers studying for their PhDs can mix with established academics, and the organizing team will ensure that this tradition is upheld. It includes a free Natural History Museum Behind the Scenes Tour On Wednesday afternoon.

No matter what stage of your career, please consider presenting at EGG, we need you! Remember students- there is the chance to win the best student talk/ poster prizes!

If you would like to present either a talk or poster can you let Gemma Beatty (geb3@aber.ac.uk) know by the 17th March 2018.

<https://www.eventbrite.co.uk/e/ecological-genetics-group-62nd-annual-meeting-tickets-42942802077?aff=es2> Contact Email: geb3@aber.ac.uk

Best wishes, Kirsten Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University School of Biology Devonshire Building, 5th floor Newcastle NE3 7RU 0191 208 4852 kirsten.wolff@ncl.ac.uk <http://www.staff.ncl.ac.uk/kirsten.wolff/>

kirsten.wolff@newcastle.ac.uk

London EvolGenetics Apr10-12

Registration is now open for the Ecological Genetics Group 2018!

The meeting concentrates on evolutionary, ecological and population genetic issues in all types of organisms.

The 62nd Meeting of the Ecological Genetics Group will be held at the Skempton Building, Imperial College London between the 10th and 12th of April, 2018. The conference is sponsored by the British Ecological Society and the Genetics Society. There will be a full scientific and social programme throughout the three-day period of the conference. It brings together those working in the fields of population genetics, ecology and evolution from across Europe and beyond.

Talks and posters are welcome from all! For those of you still completing your MScs and PhDs, remember that you will have the chance to win the coveted best talk/poster prizes! The Ecological Genetics Group meetings have a long tradition of being friendly and relaxed, where young researchers studying for their PhDs can mix with established academics, and the organizing team will ensure that this tradition is upheld. It includes a free Natural History Museum Behind the Scenes Tour On Wednesday afternoon.

No matter what stage of your career, please consider presenting at EGG, we need you! Remember students- there is the chance to win the best student talk/ poster prizes!

If you would like to present either a talk or poster can you let Gemma Beatty (geb3@aber.ac.uk) know by the 17th March 2018.

<https://www.eventbrite.co.uk/e/ecological-genetics-group-62nd-annual-meeting-tickets-42942802077?aff=es2> Contact Email: geb3@aber.ac.uk

Best wishes, Kirsten Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University School of Biology Devonshire Building, 5th floor Newcastle NE3 7RU 0191 208 4852 kirsten.wolff@ncl.ac.uk <http://www.staff.ncl.ac.uk/kirsten.wolff/>

kirsten.wolff@newcastle.ac.uk

Marseilles Evolutionary Biology Sep25-28 Deadline Jun30

Dear all , the dead line for the next evolutionary biology meeting at Marseilles is June 30

For those that don't know the meeting, the Evolutionary Biology Meeting at Marseilles goal is to gather together International scientists interested in the mechanisms of evolution that generate the incredible diversity of living things found on Earth (and possibly beyond)

The meeting Will take place on September 25-28 2018 in Marseilles (Souh of France) more info : aeeb.fr (follow the evolutionary biology meeting link)

More precisely the following subjects will be discussed:

Evolutionary biology concepts and modeling; Biodiversity and Systematics; Comparative genomics ans post-genomics (at all taxomic levels); Functional phylogeny; Environment and biological evolution; Origin of life and exobiology; Non-adaptative versus adaptative evolution; The « minor » phyla: their usefulness in evolutionary biology knowledge; Convergent evolution Evolution of complex traits (Evo-Devo) education

contact : Marie-Hélène Rome marie-helene-rome@univ-amu.fr

Pierre Pontarotti DR CNRS

1 Aix Marseille Univ, IRD, APHM, MEPHI, IHU Méditerranée Infection, Marseille France Evolutionary Biology team. 2 CNRS tel 33 (0) 4 13 7 32425 http://aeeb.fr/?page_id=1013 we are organizing the 22nd evolutionary biology meeting at Marseilles September 25-28 2018 aeeb.fr

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

MBL WoodsHole Molecular Evolution Jul19-29

Founded in 1988, the Workshop on Molecular Evolution is the longest-running workshop if its kind. The 2018 workshop will be held July 19-29, and this will be its

30th anniversary at the Marine Biological Lab in Woods Hole, MA. The Workshop is the premier program for integrating the methods, theory, and applications of molecular phylogenetics, statistical genetics, molecular evolution, and related disciplines. Students work closely with internationally-recognized scientists, receiving (i) high-level instruction in the principles of molecular evolution and evolutionary genomics, (ii) advanced training in statistical methods best suited to modern datasets, and (iii) hands-on experience with the latest software tools (often from the authors of the programs they are using). The material is delivered via lectures, discussions, and bioinformatic exercises motivated by contemporary topics in molecular evolution. A hallmark of this workshop is the direct interaction between students and field-leading scientists. The workshop serves graduate students, postdocs, and established faculty from around the world seeking to apply the principles of molecular evolution to questions of both basic and applied biological sciences. A priority of this workshop is to foster an environment where students can learn from each other as well from the course faculty.

As the course progresses, participants learn how to use the following software to address questions concerning the origins, maintenance, and function of molecular variation: ASTRAL, BEAST2, BEST, FASTA, FigTree, GARLI, IQTree, MIGRATE, MAFFT, MP-EST, RaxML, RevBayes, PAML, PAUP*, SNaQ, and SVD Quartets. Students will have the opportunity to work with software on their own laptops as well as receive training on how to use the same programs on a high performance computer cluster.

In 2018 the course instructors include Cécile Ané, Peter Beerli, Joseph Bielawski, Belinda Chang, Casey Dunn, Scott Edwards, Laure Eme, Deise Josely Pereira Gonçalves, Tracy Heath, Mark Holder, John Huelsenbeck, Lacey Knowles, Laura Kubatko, Michael Landis, Paul Lewis, Emily Jane McTavish, Bui Quang Minh, Suman Neupane, David Swofford, Noor White, Rachel Williams and Anne Yoder.

Deadline for applications is April 6, 2018: <https://ws2.mbl.edu/studentapp/studentapp.asp?courseID=-MOLE> More information on the Workshop is available on the dedicated course website: https://molevol.mbl.edu/index.php/Main_Page The dates for the Workshop are designed to allow students to segue directly into the Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) course, though please note that applications must be submitted to, and are evaluated separately from, those submitted to the Workshop on Molecular Evolution.

For further information, please contact Workshop co-

Directors:

Joseph Bielawski (j.bielawski@dal.ca) and/or Mark Holder (mtholder@ku.edu)

“J.Bielawski@dal.ca” <J.Bielawski@dal.ca>

McMasterU EarlyLife Jun24-27

The Origins Institute at McMaster University is running a research conference on Science of Early Life from June 24th-27th 2018. We now invite Registration and Abstract submission (deadline 1st May) via the conference web site:

<http://origins.mcmaster.ca/early-life> The conference will present leading research in the Origins of Life, covering experimental, observational, and theoretical aspects.

Topics

- Astrochemistry
- Prebiotic Chemistry
- RNA World
- Life in the Laboratory
- Computational and Mathematical Modelling
- Linking Geology and Chemistry

The conference will highlight the new Origins of Life Laboratory at McMaster, which has facilities for investigation of nucleic acid and membrane biochemistry and biophysics in controlled environments that simulate conditions on the early Earth and other planets. There will be a School for Graduate Students on Sun 24th June - The RNA World in Theory and Practice.

A full list of confirmed invited speakers is on the web site <http://origins.mcmaster.ca/early-life> Please encourage your students and colleagues to attend. I hope to see you at the conference.

Paul Higgs.

Director, Origins Institute, McMaster University,
Hamilton, Ontario, Canada.

“Higgs, Paul” <higgsp@mcmaster.ca>

MilnerCentreBath Evolution Sep18-21

The Milner Centre for Evolution at the University of Bath, UK is delighted to announce the details of its inaugural conference, \$B!H(BEvolution in the 21st Century“. Details and registration here:

<http://www.milnercentre.org/> The conference runs from Tuesday 18th-Thursday 20th September 2018, although people might like to stay on for the official opening on 21st and public lecture that evening. Keynote speakers are Neil Shubin, Peter and Roemary Grant, Hanna Kokko and Gil McVean. The public lecture will be delivered by Alice Roberts.

Aside from keynotes there are 20 lecture slots. Speakers will be selected from submitted abstracts. There will be one lecture slot for the Milner Prize lecturer (for application details see <http://www.milnercentre.org/-milner-prize/>).

For further enquiries please contact Laurence Hurst (l.d.hurst@bath.c.uk)

Laurence D. Hurst

Professor of Evolutionary Genetics Director of The Milner Centre for Evolution Department of Biology and Biochemistry University of Bath Bath Somerset, UK BA2 7AY

tel: +44 (0)1225 386424 fax: +44 (0)1225 386779 email: l.d.hurst@bath.ac.uk website: <http://-people.bath.ac.uk/bssldh/LaurenceDHurst/Home.html> ”Laurence D. Hurst“ <laurence@ldhurst.plus.com>

Monterey DeepSeaEvolution Sep9-14

Hi All,

This is one of my favorite meetings and it only happens once every 3 years. It is a great place to exchange ideas about any biology of the deep sea or open ocean.

>From Steve Haddock - The next Deep-Sea Biology Symposium will be held in Monterey, California on 9-14

September 2018, and some important deadlines are fast approaching. Early registration rates, abstract submissions, and travel award requests are due on March 30th! Please visit <http://dsbs2018.org> for more information. If you need a pre-acceptance letter for an abstract, or wish to register with the undergraduate student discount, please email the organizers at dsbs@dsbs2018.org

Hope to see you there, Karen 'X Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 osbornk@si.edu <http://invertebrates.si.edu/osborn/> <http://orcid.org/0000-0002-4226-9257> SMITHSONIAN INSTITUTION NATIONAL MUSEUM OF NATURAL HISTORY Facebook < <https://www.facebook.com/nmnh.fanpage/> > | Twitter < <https://twitter.com/NMNH> > | Instagram < <https://www.instagram.com/smithsonianmnh/> >

Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012, Washington, D.C. 20013-7012 USA

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

“Osborn, Karen” <OsbornK@si.edu>

His most famous book “Crops and Man”, 1975, remains a reference and has been the bedside book of generations students in plant breeding, especially in France, where J.R. Harlan’s influence was very strong in the scientific community dealing with plant genetic resources.

On invitation of the UC Davis, the Montpellier scientific community has applied in 2016 for the third edition of the Harlan Symposium, a prestigious, recurrent but rare event, organized in 1997 and 2008. This application was selected after a competitive process. The originality of the Harlan symposium lies in the multidisciplinary aspects of the science (from archeology to genetics and agroecology), the variety of biological models (plants, animals, microorganisms) and the broad temporal scale (from the origin of agriculture to the current problems of use of agricultural biodiversity). The Third Harlan Symposium will be influenced by the research thematic of the South countries, given the Mediterranean and tropical orientation of the research teams involved.

Information about the symposium E-mail : contact@harlan3symposium.org

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

Montpellier Origin Agriculture Sep11-14

Subject: Montpellier.HARLANIII_OriginOfAgricultureandGr.Sep11-14. Third Jack R. Harlan International Symposium Dedicated

to the Origins of Agriculture and the Domestication, Evolution,

and Utilization of Genetic Resources

<https://sites.google.com/site/harlan3symposium2018>
Montpellier will have the honor of hosting the Third Jack R Harlan International Symposium on the Origins of Agriculture and Domestication, evolution and utilization of genetic resources.

The Harlan Symposium was created by the University of California (UC Davis, USA) as a tribute to Jack R. Harlan, who was an American botanist and agronomist (1917-1998). J.R. Harlan was a pioneer in the study of origin agriculture and crops, showing the importance of the relationship between the activity from human development and the evolution of agricultural biodiversity.

Munich Reef Evolution Sep5-7

Dear all,

registration and abstract submission are now open for the 5th Young Reef Scientists Meeting, September 5th-7th in Munich (Germany).

The aim of the meeting is to provide master students, PhD candidates and early-career researchers with an opportunity to present their work, share and discuss methodological approaches, and exchange ideas..

The meeting is open to all fields related to coral reef research (e.g. biology, ecology, evolution, chemistry, geology, paleontology, modelling, social sciences, conservation, etc.).

Further information can be found here: <http://www.en.palaeontologie.geowissenschaften.uni-muenchen.de/young-reef-scientists-meeting/index.html>

Best Regards

Nicola Conci

Department für Geo- und Umweltwissenschaften
Paläontologie & Geobiologie Richard-Wagner-Str. 10
80333 München

+49 (0) 89 2180 17935 n.conci@lrz.uni-muenchen.de

Nicola Conci <nicola.conci@my.jcu.edu.au>

ParkCity Utah EvolutionaryMedicine Aug1-4

The abstract deadline is looming...March 31...for the 4th annual meeting of the International Society for Evolution, Medicine, and Public Health. <http://isemph.org>

This year's meeting will be August 1-4, 2018 in a spectacular mountain town just above Salt Lake City, Park City, Utah, .

This interdisciplinary conference is an opportunity for research biologists, students, clinicians and public health professionals to share their research and advance the goals of the society: to use evolutionary insights to improve medical research and practice and to advance evolutionary biology.

The conference will be anchored around presentations by six internationally-celebrated keystone speakers. The conference features special symposia on Alternatives to Antibiotics, The Microbiome, Evolutionary Health Behavior, and Evolution in Emergency Medicine and Critical Illness, Cancer, and Human Genomics. A Pre-Conference on Wilderness Medicine - Human Adaptation to Extreme Environments will take place on August 1st, 2018 Please join us for this exciting meeting!

Download a poster for ISEMPH 2018 here and share widely. <https://isemph.org/resources/Documents/-2018%20Poster%20Final.pdf> ISEMPH 2018 is accepting abstracts to be considered for poster or platform presentation now. Submit today by clicking the below link <https://easychair.org/cfp/ISEMPH2018> *Key dates* - Abstract Submission Deadline March 31, 2018 - Early Bird Registration Deadline April 30, 2018 - Conference Begins August 1-4, 2018 *Venue* The conference venue is the Yarrow DoubleTree Hotel in Park City, Utah. Lodging information and additional conference details are here: [*https://isemph.org/Location-and-Lodging](https://isemph.org/Location-and-Lodging) <<https://isemph.org/Location-and-Lodging>>*

Travel Grants Travel grants are available for students submitting abstracts, based on scientific merit, need, and underrepresented categories in STEM. Contact conference director Janice.mancuso@gmail.com for details. Learn more: <https://isemph.org/annualmeeting> rمنesse@gmail.com

ParkCity Utah EvolutionaryMedicine Aug1-4 Absts

Dear all,

Abstract submissions are open for the International Society for Evolutionary Medicine & Public Health (ISEMPH) 2018 meeting, August 1-4th in Park City Utah. We have a fantastic line up of keynotes, including Val Curtis, Chris Kuzawa, Maria Gloria Dominguez-Bello, Andrew Read, Katie Hinde & Jacob Scott. See the website for more: <https://isemph.org/annualmeeting>
Best wishes, Gillian

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

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

ParkCity Utah EvolutionMedicine Aug1-4

Dear list members,

As a member of the 2018 Program Committee for the International Society for Evolution, Medicine, and Public Health <<http://isemph.org/>> I am delighted to announce our 4th annual meeting this year in Park City, Utah, August 1-4, 2018. This interdisciplinary conference is an opportunity for researchers, students, clinicians and public health professionals to share their research and advance the goals of the society: to use evolutionary insights to improve medical research and practice and to advance evolutionary biology.

The conference will be anchored around presentations by six internationally-celebrated keystone speakers. In addition, the conference features presentations by winners of the prestigious Omenn and Williams prizes. Special symposia organized by members of the program committee are: The future of evolutionary medicine, Evolution and health behavior, Evolution and medicine in light of the microbiome, Adaptation and maladaptation in

sepsis and critical illness, Evolution and cancer, and Novel solutions to chemotherapeutic resistance. A Pre-Conference on Wilderness medicine - Human adaptation to extreme environments will take place on August 1st, 2018.

Please join us for this exciting meeting! You can download a poster for ISEMPH 2018 here < <https://isemph.org/resources/Documents/-2018%20Poster%20Final.pdf> >. ISEMPH 2018 is accepting abstracts to be considered for poster or platform presentation now. Submit today by clicking here < <https://easychair.org/cfp/ISEMPH2018> >.

Key dates - Abstract Submission Deadline March 31, 2018 - Early Bird Registration Deadline April 30, 2018 - Conference Begins August 1-4, 2018

Venue The conference venue is the Yarrow Double-Tree Hotel in Park City, Utah. Lodging information and additional conference details are here: <https://isemph.org/Location-and-Lodging> Travel Grants Travel grants are available for students submitting abstracts, based on scientific merit, need, and underrepresented categories in STEM. Contact conference director Janice.mancuso@gmail.com for details. Learn more: <https://isemph.org/annualmeeting> Thanks and best wishes, Gillian

Dr Gillian Pepper Centre for Behaviour and Evolution Institute of Neuroscience Henry Wellcome Building Newcastle University Framlington Place Newcastle Upon Tyne, UK NE2 4HH

Email: gillian.pepper@ncl.ac.uk Mobile: 07951 295 751 Website: <http://gillianpepper.com/> Gillian Pepper <Gillian.Pepper@newcastle.ac.uk>

Portland GalaxyBioinformatics Jun25-30

GCCBOSC 2018 - <https://gccbosc2018.sched.com/> - June 25-30, in Portland, Oregon, United States

GCCBOSC brings together these events: - Bioinformatics Open Source Conference (BOSC 2018) - Galaxy Community Conference (GCC2018)

GCCBOSC 2018 (<https://gccbosc2018.sched.com/>) brings together the Bioinformatics Open Source Conference (BOSC) and the Galaxy Community Conference GCC into a unified event, June 25-30, in Portland, Oregon, United States.

GCCBOSC features two days of training, a two day meeting, and finishes with several days of intense collaboration at CollaborationFest Core and Encore events. The meeting features joint and parallel sessions, and shared keynotes, poster, demo, and birds-of-a-feather sessions.

Oral presentation abstracts are due Friday, March 16

Oral presentation abstracts are being accepted through Friday, March 16. If you are working in data-intensive life science research, then there is no better place to present your work to and learn from hundreds of other researchers addressing challenging research questions at the intersection of life science and computing.

Submit an abstract now - <https://easychair.org/-conferences/?conf=gccbosc2018> Early Registration ends May 11

Early registration is now open. Register by May 11 and get half off registration costs. Early registration is quite affordable, with early registration for students and post-docs averaging just \$66/day. Travel fellowships are available from both OBF and the Galaxy Community Fund. On-campus conference housing registration is also open. Nightly rates drop the longer you stay, and there are 20 and 40% discounts for shared rooms.

Register for GCCBOSC 2018 - <https://-gccbosc2018.eventbrite.com/> Book housing - <https://-gccbosc2018housing.eventbrite.com/> Registration and Housing info - <https://galaxyproject.org/events/-gccbosc2018/register/> We hope to see you in Portland!

GCCBOSC 2018 Organizing Committee

Links

Conference Info - Home page <https://-gccbosc2018.sched.com/> - Info Hub <https://-galaxyproject.org/events/gccbosc2018/> Registration & Abstract Submission - Submit an abstract <https://easychair.org/conferences/-?conf=gccbosc2018> - Register <https://-gccbosc2018.eventbrite.com/> - Book conference housing <https://gccbosc2018housing.eventbrite.com/> - Travel fellowships <https://galaxyproject.org/-events/gccbosc2018/register/#travel-fellowships> Schedule - Galaxy Training Day, Monday, June 25 <https://gccbosc2018.sched.com/2018-06-25/-overview/> - All topics Training Day, Tuesday, June 26 <https://gccbosc2018.sched.com/2018-06-26/-overview/> - BOSC and GCC Meetings with joint and parallel tracks, Wednesday-Thursday, June 27-28 <https://gccbosc2018.sched.com/overview/-type/D.x+Conference+-+All> - CollaborationFest:

Core, Friday-Saturday, June 29-30 & CollaborationFest: Encore, Sunday-Monday, July 1-2 <https://galaxyproject.org/events/gccbosc2018/collaboration/>
Dave Clements <clements@galaxyproject.org>

PuertoRico EvolutionaryAnthropology Nov1-4

DEADLINE APPROACHING:

CALL FOR SYMPOSIUM PROPOSALS ALAB-2018, Mayagüez, Puerto Rico (due March 30, 2018 at www.pr-science.org) 15th Congress of the Latin American Association for Biological Anthropology (ALAB) The ALAB is a corporation that brings together scholars interested in the fields of Physical Anthropology and Human Biology. Its members can be located in Latin American countries or elsewhere if their investigations relate to Latin America.

The ALAB congresses are held every two years since 1990, offering Latin American researchers and to those interested in anthropological studies on Latin America a periodic opportunity for the discussion of scientific experiences and issues linked to the development of the discipline in a local, regional and continental context.

The overall objective of the Congress is to bring together scholars in our field in a healthy environment for the contact, discussion of problems and new ideas, and the development of collaborative networks of researchers and students.

We will celebrate the fifteenth Congress of the ALAB in Mayagüez, Puerto Rico from November 1st to 4th, 2018. It will be the first time that the ALAB holds its Congress in the Caribbean. We expect a dynamic discussion of all the fields of action of biological anthropology, among them: Nutrition and growth and child development Nutrition, health and demographics of ancient peoples The Peopling of the Americas The settlement of Mesoamerica and the circum-Caribbean Forensic anthropology and human identification Mortuary rituals and treatment of corpses in ancient civilizations Genetics of modern populations Paleogenomics Biocultural Anthropology African ancestry in the Caribbean Primatology Resources and strategies for teaching biological anthropology Bioarchaeology and cultural ecology Reproductive health Submit your symposium title and description to ALAB-2018 at www.pr-science.org In the submission form, please indicate why this particular

symposium or panel discussion is timely and necessary and also how it is likely to be of interest to a broad range of researchers in the fields of biological anthropology.

Symposium Overview: “ Each symposium will consist of one or two one-and-a-half hour sessions. Each session will consist of one invited speaker and 3 contributed speakers, or no invited speaker and 5 contributed speakers, but all symposiums will have at least one invited speaker.

” The local organizing committee (LOC) may suggest one additional invited speaker per symposium (Based on symposium title), at no cost to the symposium.

“ The symposium organizers will be responsible for selecting at least one invited speaker for their symposium.

” The symposium organizers will select the contributed speakers from submitted abstracts.

“ The final decision on the selection of symposia, invited and contributed talks will be made by the LOC.

Invited Speakers: We ask you to bring 'invited speakers' of high quality capable of delivering an interesting talk of wide interest. Please indicate whether they have been approached and/or whether they have confirmed their participation and the likely topic for their talk.

(e.g. Prof A.N. Other - confirmed or approached and likely to speak but not yet confirmed) Important Dates: Call for Symposia and Discussion Panels will close on Thursday March 15th 2018.

Successful Symposium and Discussion Panel applications will be confirmed on April 1st 2018.

The Online Abstract Submission will open on April 5th 2018.

The LOC will make its decision on proposals received based on its standards of merit and wide interest. Symposium and discussion panel submissions from scientists in the Caribbean and Latin America are encouraged.

If you have any questions, email us at cohemis@uprm.edu Subject Line: ALAB's 15th Congress, 2018 Symposium or Discussion Panel Submission Please Note: - Each successful symposium will be funded with \$500 USD to help with the costs of inviting speakers to the meeting and waiver of the registration. If you have any queries about this please email the ALAB's 15th Congress secretary at cohemis@uprm.edu - Sponsored symposia and discussion panels are encouraged, however, please contact our Exhibition and Sponsorship Manager Yamarie Hernández (cohemis@uprm.edu) before enquiring about sponsor prospectus and beginning sponsorship discussions.

Taras K Oleksyk, Ph.D.

Associate Professor of Biology University of Puerto Rico
Mayaguez, PR 00680 taras.oleksyk@upr.edu

Taras K Oleksyk <taras.oleksyk@upr.edu>

Rennes Evolution Oct

Sfecologie 2018 - Rennes, Conference announcement

Dear Colleagues,

We are delighted to invite you to Sfecologie2018 International Conference on Ecological Sciences (<https://sfecologie2018.sciencesconf.org/>), the conference of the French Society of Ecology and Evolution (Sfe????) that will take place in Rennes in October 2018. The conference will be held at the historic Couvent des Jacobins (<http://centre-congres-rennes.fr/>), in the old part of the city of Rennes, ensuring convenient public transportation for the attendees.

This meeting will promote and support exchanges around the latest developments in research and the most exciting challenges raised from the different disciplines of ecology and evolution. Contributions will be welcome on any aspect of ecology and evolution, including focused empirical and theoretical studies, to engage and strengthen fruitful collaboration and intellectual exchanges.

The deadline for the submission of abstracts for oral and poster presentations is: 2018, May 1st (<https://sfecologie2018.sciencesconf.org/submission/submit>)

This 4-days conference will include a full range of academic sessions, plenary lectures, social events and field trips within and beyond Rennes.

The organizing committee

–

David RENAULT Universite de Rennes 1, Membre junior de l'Institut Universitaire de France UMR CNRS 6553 EcoBio 263 Avenue du Gal Leclerc, CS 74205, 35042 Rennes Cedex Tel: 02 23 23 66 27 Website: <https://sites.google.com/site/davidrenaultecobio/home> Join us at Sfecologie2018! More information at <https://sfecologie2018.sciencesconf.org/> David RENAULT <david.renault@univ-rennes1.fr>

Sherbrooke Canada RECOMB-CG Oct9-12

RECOMB-CG 2018, FIRST 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)

Gwenaél 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 Chindelevitch (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)

— / —

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>

Toulouse EconomicsAndEvolution May24-25

Dear colleagues,

Registrations for the 6th Toulouse Economics and Biology Workshop - Evolution, Cognition and Rationality, May 24-25 are now open. Please register [HERE](#)

We will circulate a preliminary program shortly.

The speakers are:

Immanuel Bomze, University of Vienna - Operations Research

Joanna J. Bryson, University of Bath & Princeton University - Computer Science

Noam Brown, Carnegie Mellon University - Computer Science

Iain Couzin, Max Planck Institute for Ornithology & University of Konstanz - Biology

Audrey Dussutour, CNRS University Toulouse III - Biology

Yuval Heller, Bar-Ilan University - Economics

Cecilia Heyes, University of Oxford - Biology & Psychology

Peter Gardenfors, Lund University - Cognitive Science

Alex Kacelnik, University of Oxford - Biology

Marc Mezard, ENS Paris Sud University - Physics

Erik Mohlin, Lund University - Economics

Arthur Robson, Simon Fraser University - Economics

Ariel Rubinstein, Tel Aviv University - Economics

Aldo Rustichini, University of Minnesota - Economics

Besides the plenary sessions, there will be a poster session to which post-docs and Ph.D. students are most welcome to submit applications (abstract + CV + cover letter) to econbio_poster@iast.fr no later than March 30, 2018. A limited number of travel grants will be available. To apply, please join a cover letter explaining why you are applying for a grant and why you are interested in attending the workshop.

For any further information please contact us directly at econbio@iast.fr or visit our website <https://www.iast.fr/conferences/2018-6th-toulouse-economics-and-biology-workshop> We look forward to seeing you in May!

Organizers: Ingela Alger and Jorgen Weibull,

Co-organizers: Lauriane Rat-Fischer and Slimane Dridi

Administrative assistants: Cynthia Diaz and Aline Couratier

The Toulouse Economics and Biology Workshop
<econbio@iast.fr>

UGöttingen SensationEvolution Sep27-28

Dear colleagues, PIs and students,

the GOEvol consortium proudly presents its 6th meeting #Sensation @GOEEvolution 2018 taking place in Göttingen from September 27th to 28th 2018 (<http://goevol.uni-goettingen.de/index.php?id=meeting20160>).

The perception of environmental stimuli, their processing and integration is essential for any organism. Apart from the more familiar senses like hearing, seeing or tasting, there are sensory tasks performed by highly specialized animals, such as echolocation in bats or the perception of polarized light in insects. Sensory processing consequently also differs strongly between species. However, at the same time there are astonishing similarities between sensory modalities of phylogenetically distant animal groups, such as the shared cellular structure of light-sensitive organs or the genetic control and

developmental origin of sensory cells. With methodological innovation, more and more species can be used for detailed analyses, which further expand the understanding of the evolution of sensation.

Because of the diversity of research and various methodologies in multiple (emerging) model organisms in the field of evolution of sensation we want to bring together scientists from a broad range of fields to reveal commonalities across disciplines.

Following the GOEvol tradition, we aim for an interdisciplinary symposium with an informal atmosphere with plenty of possibilities for social networking. If you enjoy small interactive meetings and the topic suits you, come along!

There are several slots for contributing talks and poster presentations. We strongly encourage interested students and researchers from all levels (Bachelor, Master, PhD and above) to register and apply for talks and poster presentations.

Moreover, we want to support parents to participate. Therefore, depending on the demand, we will be able to provide childcare as well as designated rooms for nursing.

Please book hotel rooms as early as possible since there is a conflicting fare in Hannover. Hotel rooms are extremely rare.

Registration is possible from March 15th to July 15th 2018 following this link:

<http://goevol.uni-goettingen.de/index.php?id=-addgroup0> Costs to register are 10 euro for students, 20 euro for Postdocs and PIs.

Please post any question either via email at goevolnetwork@gmail.com or via Twitter @GOEEvolution.

Invited speakers:

Sally Leys (University of Alberta, Canada)

Michael Bok (University of Bristol, UK)

Tobias Kaiser (MPI for Evolutionary Biology, Plön, Germany)

Robert Barton (University of Durham, UK)

Mirjam Knörschild (Free University of Berlin, Germany)

Brigitte Schönemann (University of Cologne, Germany)

Best regards,

The GOEvol Team <https://goevol.uni-goettingen.de/>
Twitter: @GOEEvolution

On behalf of the GOEvol organizing team,

Max S. Farnworth

Georg-August-University of Göttingen
 Johann-Friedrich-Blumenbach Institute of Zoology and
 Anthropology
 Department of Evolutionary Developmental Genetics
 Göttingen Center for Molecular Biosciences (GZMB)
 Justus-von-Liebig-Weg 11
 37077 Göttingen
 E-mail: max.farnworth@biologie.uni-goettingen.de
 Phone: +49 551 39 10124
http://www.researchgate.net/profile/Max_Farnworth
 Twitter: @StephesMax
 m789farnworth@t-online.de

UK SexualSelection May

Dear all

Can I draw your attention to this meeting, one of the Royal Society Theo Murphy meetings. Held at Chicheley Hall in Buckinghamshire, UK. We have a stellar line up of speakers, both specialists in sexual selection in extant organisms as well as palaeontologists.

Sexual selection is potentially an important driver of macroevolutionary processes like speciation and extinction, but this has rarely been tested using the fossil record. This meeting will bring biologists and palaeontologists together to discuss sexual selection's role in macroevolution, how to detect it in extinct animals and how to measure its influence on the history of life across geological time

<https://royalsociety.org/science-events-and-lectures/-2018/05/sexual-selection/> All welcome and plenty of places available. The conference itself is free, you can stay at the centre (for a fee) or organise your own accommodation nearby.

Best wishes

Rob Knell

Reader in Evolutionary Ecology School of Biological and Chemical Sciences Queen Mary University of London
 research website <http://webspaces.qmul.ac.uk/rknell/>
 r.knell@qmul.ac.uk

UMiami SEEC EcolEvolution Oct5-7

Call for Symposium Proposals

The University of Miami is excited to host the 2018 Southeastern Ecology and Evolution Conference (SEEC) from October 5 -7, 2018 in Miami, Florida. The SEEC is a regional, student-run meeting that provides undergraduates, graduate students, and post-docs an opportunity to present research in ecology and evolution. This conference is open to anyone with an interest in ecology and evolution research in the southeastern region of the United States.

The conference will feature outstanding plenary speaker: Dr. Daniel Simberloff, University of Tennessee. Some of his research interests include biogeography, invasive species, and statistical ecology.

As part of the conference, individuals are invited to attend workshops on Biological Invasions and Modern Applications.

Abstracts are due by June 1st 2018. Early registration will start on July 1st, for \$45, after you hear back from our conference committee about the acceptance of the submitted abstract. There will be cash prizes awarded to the best talks and posters. Further details about the conference, abstract submission instructions, and registration information can be found at <https://seeconference2018.wordpress.com/>

Questions or inquiries can be directed to SEEC 2018 (email: SEEC.Host@gmail.com)

“Kula, Alexander” <axk750@miami.edu>

UMontpellier PhylogenomicsSoftware Aug17

We are pleased to announce a half-day Phylogenomics Software Symposium, which will be held at the Institut des Sciences de l'Evolution - Montpellier, on the University of Montpellier campus.

This symposium will take place on August 17, the day before the Evolution 2018 meeting begins.

The conference will include two sessions of invited talks and one session of contributed talks. The invited talks will describe recent breakthroughs in methods and software that address challenges in phylogenetics using large and heterogeneous sequence datasets.

Contributed talks will be selected from submitted abstracts; these may also describe advances in software, novel challenges, or discoveries made using new methods.

Travel awards are available, and registration in advance is required.

Please see <http://tandy.cs.illinois.edu/2018-Symposium.htm> for more information.

Tandy Warnow Founder Professor of Computer Science Associate Head of Department Member of the Carl R. Woese Institute for Genomic Biology Affiliate of the National Center for Supercomputing Applications Affiliate of Coordinated Sciences Laboratory Affiliate of Electrical and Computer Engineering, Mathematics, Statistics, Entomology, Plant Biology, Animal Biology, and PEEC (Program in Ecology, Evolution, and Conservation Biology) 3235 Siebel Center (CS Office) 3402 Institute for Genomic Biology (IGB office) <http://tandy.cs.illinois.edu> “Warnow, Tandy” <warnow@illinois.edu>

Warsaw HumanAndEvolution Sep24-26 RegistrationOpen

Polish Society for Human and Evolution Studies (PTNCE) has a great pleasure to invite you to its annual international conference PTNCE2018, which will be held in Warsaw (Poland) between the 24th and 26th of September 2018.

Registration and abstract submission opened on the 5th of March 2018. Abstract submission for talks and posters closes on the 15th of June 2018. Early bird registration with reduced conference fees closes on the 4th of July 2018.

Please visit: <http://www.ptnce2018.pl/registration> to

register.

PTNCE conference, as well as the Society in general, aims at associating scientists and students of various scientific disciplines interested in the application of the evolutionary perspective in the following research areas: biology, ecology, human behaviour and culture studies. By creating an idiosyncratic evolutionary platform we intend to break the barriers between traditional divisions in human studies.

We are pleased to announce our distinguished plenary speakers for the PTNCE2018 conference: Russell Gray, Max Planck, Jena (evolutionary linguistics), Johannes Krause, Max Planck, Jena (archaeogenetics), Jan Havlicek, Charles University, Prague (social perception) and Grazyna Jasienska, Jagiellonian University, Cracow (reproductive ecology).

At the conference website www.ptnce2018.pl you will find further information about the speakers and the conference. Gradually we will be publishing more information about the conference program as well as travel and accommodation tips. Therefore, we encourage you to keep checking the website updates.

If you have any questions, please do not hesitate to contact the organizing team at ptnce2018@gmail.com.

We will be very grateful for forwarding this message and/or spreading information about the conference among all potentially interested people, research groups and institutions.

Kind regards,

Prof. Bogusław Pawłowski University of Wrocław
President of the Polish Society for Human and Evolution Studies

&

Martyna Molak, PhD Polish Academy of Sciences Head of the PTNCE2018 Conference Organising Committee

Conference organizers: Polish Society for Human and Evolution Studies Museum and Institute of Zoology Polish Academy of Sciences Centre of New Technologies University of Warsaw

PTNCE2018 <ptnce2018@gmail.com>

GradStudentPositions

BarcelonaCRAG PlantPaleogenomics 18	QMU London PhD BehaviouralDifferencesChicks . . 32
BarllanU Israel WildRockHyrax 19	StockholmNHM Palaeogenomics 32
Berlin 11 Biodiversity 19	StockholmU EvolutionCognition 33
BournemouthU SalmonidEvolution 21	StockholmU LifeHistoryEvolution 34
BrandonU EvolutionPesticideResistance 21	StockholmU WinterEvolutionaryEcology 34
CanMuseumNature Ottawa PlantSystematics 21	UAberdeen ExperimentalEvolutionMicrobes 35
EAWAG Switzerland Daphnia 22	UAucklandNZ EvolBirdSong 36
Europe 15 ITN IGNITE CompGenomicsInverts . . . 23	UBielefeld RaptorMalariaGenomics 37
Europe 15 ITN IGNITE CompGenomicsInverts dead- lineFeb28 23	UGroningen ExperimentalEvolutionMicrobes 38
GhentU AvianSpeciation 24	ULausanne 2 MicrobialEvolution 39
KielU ComputationalEvolutionaryGenomics 25	ULausanne EvolutionaryGenomicsNeurogenetics . 105
Leibniz Berlin 2 WildlifeFitness 26	UMassachusetts Lowell EvolutionVertJaw 41
LouisianaStateU ConservationGenetics 26	UMuenster MolecEvolutionNasonia 41
MasseyU 2 PlantEvolution 27	UOslo 2 ancientDNA Conservation 42
MaxPlanck Jena 5 EvolutionaryBiology 28	UOtago NewZealand EvolutionaryGenomics 43
MPIO Seewiesen EvolutionCognition 28	UPrague ArabidopsisAdaptation 44
NewZealand 2 EvolutionaryEcol 29	USunshineCoast Aust EvolutionaryRobotics 44
Norway ComparativeGenomicRegulation 30	UWageningen HyperparasitoidEvolution 45
Portugal Archaeogenetics 30	UWesternAustralia SeagrassAdaptation 46
Portugal EvolutionaryGenomics 31	UZurich PlantAdaptation 47
QMUL London EvolutionChickBehaviour 31	

BarcelonaCRAG PlantPaleogenomics

Graduate position on plant palaeogenomics available in Barcelona.

The Botigue lab for “Genomics of ancient crops and domestication” in the Centre for Research in Agricultural Genomics (CRAG) in Barcelona is offering a PhD position under the International CRAG Severo Ochoa Program to work on the genomic analysis of ancient emmer wheat from Egypt with the goal to better understand plant domestication.

PROJECT DESCRIPTION: Plant domestication is a topic of interest in a broad range of research fields such as agronomics, genome evolution, archaeology or anthropology. Past limitations in the study of the early domestication process can now be overcome by including ancient samples in crop genomic analysis. Our lab

has access to emmer wheat samples excavated in Egypt dated from the Neolithic up to the Roman period. This project aims to extract the DNA from these ancient samples and sequence it to perform downstream genomic analyses that will allow us to answer several questions regarding wheat domestication. Specifically, the PhD candidate will use cutting-edge bioinformatic and statistical tools under a population genetics framework to work on i) investigating the genomic architecture of Egyptian wheat population through time, including modern wheat; ii) characterizing known phenotypic traits in the ancient samples such as the non-shattering phenotype, and iii) identifying regions of the genome selected during domestication through the comparison of the observed evolution of allele frequencies and computational simulations.

This project is a collaborative effort with University College London and Warwick University and presents an opportunity to learn and develop a wide range of techniques to perform genomic analysis and computational modeling. As a result, new aspects of cereal domestication will be discovered, and a step forward in the identification of genomic regions of interest for

domestication will have been made. Furthermore, the PhD student will analyse for the first time genetic data from ancient specimens from different time periods.

REQUIREMENTS: The CRAG Severo Ochoa program is aimed at international students who have completed one of the following options by September 2018:

- studies that lead to an official Spanish (or from another country of the European Higher Education Area) university degree in Biology, Biochemistry, Biotechnology, or related areas and that have 300 credits (ECTS), of which at least 60 must correspond to master level.
- a degree in a non-Spanish university not adapted to the European Higher Education Area that gives access to doctoral studies in Biology, Biochemistry, Biotechnology or related areas.

Candidates are selected exclusively on merit, on the basis of their curriculum. Academic grades and the curriculum of applicants are evaluated, as well as reference letters and a motivation letter. No selection criteria for positive or negative discrimination are applied. Applicants should have obtained a degree after January 2015. Candidates cannot be in possession of a PhD Degree. Candidates cannot have been hired as predoctoral students for more than 12 months before the start of the CRAG "Severo Ochoa PhD Program. Candidates cannot have started a pre-doctoral fellowship funded by the Spanish "Plan Estatal de Investigacion, Desarrollo e Innovacion Tecnologica" or any previous "Plan Nacional".

CONTACT For questions about the position and further information about the project, contact Laura Botigue, Email: laura.botigue@cragenomica.es

HOW TO APPLY Applications should be done using CRAG's online application system. Please follow the link below to obtain further information about the PhD program and how to access the online application system: <https://www.cragenomica.es/2018-international-crag-severo-ochoa-phd-program> Closing date: 30 April 2018

Laura Botigue <rb.laura@gmail.com>

BarIlanU Israel WildRockHyrax

We are looking for an enthusiastic and fit graduate student (MSc or PhD) for a funded multidisciplinary project on sperm competition, vocalisations, and sexual selection in wild rock hyrax. The project involves cap-

turing, marking, sampling, observing, and carrying out manipulation experiments while in the field, in the Ein Gedi Nature Reserve, near the Dead Sea, Israel. The ideal applicant has a strong background in behavioural ecology, field experience handling wildlife, and an ability to work both independently, and as part of a team. Experience with sperm or sound analysis is an asset. Financial support includes a scholarship from Bar Ilan University, tuition, and TAship. For more information, please contact Dr. Lee Koren (Lee.Koren@biu.ac.il). Please include a CV and a cover letter with field experience and interests.

Thanks and best wishes,

Lee

Lee Koren, PhD The Mina and Everard Goodman Faculty of Life Sciences Bar-Ilan University Ramat Gan, 5290002 Israel Institute of Nanotechnology and Advanced Materials (Building 206) Office B-940; Lab B-935 (9th floor) Telephones: office +972-3-7384371 lab +972-3-7384372 Skype: leezik Lee.Koren@biu.ac.il <https://leekoren.wixsite.com/korenlab> Lee Koren Lab (Facebook page) @LeeKoren2 (Twitter)

Lee Koren <Lee.Koren@biu.ac.il>

Berlin 11 Biodiversity

The DFG-funded Research Training Group RTG 2118 "Integrating Biodiversity Research with Movement Ecology in Dynamic Agricultural Landscapes [BioMove]" (Speaker: Prof. Dr. Florian Jeltsch) at the *University of Potsdam (UP)*, the *Freie Universität Berlin (FU)*, the *Leibniz Institute for Zoo and Wildlife Research (IZW, Berlin)*, and the *Leibniz Centre for Agricultural Landscape Research (ZALF, Müncheberg)* offers several positions:

- *At the University of Potsdam* -

7 doctoral candidates (PhD)

/- Intra-specific trait variation in movement behaviour as mechanisms for species coexistence - Mobile link functions in unpredictable agricultural landscapes - Indirect, tri-trophic Effects of Fear on Biodiversity - Obstacles to plant gene-flow across an agricultural landscape: habitat filtering and recruitment limitation vs. dispersal limitation - Stabilizing biodiversity by zooplankton dispersal through space and time - Zooplankton dispersal and colonization in a meta-community pond system -

From individual home-range formation to community dynamics: a novel, allometric modelling approach to explore biodiversity loss caused by landscape changes/

Registration Number: 225/2018

26 hours per week (65%) for three years

The salary scale is in accordance with the German public service 13 TV-L (area east). Contracts are time-limited according to Section 2 subsection 1 of the Academic Fixed-Term Contract Law (WissZeitVG).

Under the laws of the federal state of Brandenburg, employees under this contract are permitted to dedicate at least 33% of their contract time for their scientific qualification.

*At the Leibniz Institute for Zoo and Wildlife Research (IZW), Berlin*

2 doctoral candidates (PhD)

/-Pathogen evolution in changing landscapes// // - Equalizing and stabilizing mechanisms in regulating the co-existence of aerial-hawking bat species in agricultural landscape/

Salary is according to TVöD Bund (25,35 hours per week 65%), 3-year contract.

*At the Freie Universität Berlin*

1 doctoral candidate (PhD)

/-Tradeoffs between growth rate, attachment and competitiveness as a source of equalizing effects in nectar yeast communities/

Salary is according to TV-L FU E13 (65%), 3-year contract.

- - -

--

*At the Leibniz Centre for Agricultural Landscape Research (ZALF) Müncheberg*

1 doctoral candidate (PhD)

/- Trade-offs between dispersal ability and niche competition of co-occurring microorganisms in the phyllosphere of host plants/

26 hours per week (65%) for three years

The salary is in accordance with the German public service 13 TV-L (area east). Contracts are time-limited according to the Academic Fixed-Term Contract Law (WissZeitVG).

All positions begin on October 1st, 2018.

*BioMove*links innovative individual research projects that overcome the apparent gap between movement

ecology and biodiversity research, employing a joint conceptual framework. It strategically combines empirical, experimental and modelling approaches to advance our mechanistic understanding of how biodiversity patterns emerge and how they feed back on the active and passive movement of organisms. This will improve our ability to predict biodiversity responses to ongoing changes in land use or climate. Projects cover different spatial and temporal scales and groups of organisms ranging from bacteria, fungi, plankton, plants, and insects to birds and mammals (for more details see <http://www.biomove.org>).

Doctoral candidates will also strongly profit from a unique qualification program specifically tailored to bridge between state-of-the-art concepts and methods in movement ecology and biodiversity research, supplemented by a broad range of soft skill workshops.

Candidates should fulfill the following requirements:

*

A very good M.Sc. degree (or equivalent) in Ecology, Zoology, Botany, Conservation, Behavioural or Evolutionary Biology, Microbiology, Epidemiology (or other natural sciences if mechanistic modelling was involved). Candidates that have not yet finished their Master thesis can submit a current and informative study record.

*

Very good English skills (written and spoken)

*

Very good statistical and analytical skills (preferentially sound knowledge in R)

*

Experience in one or more of the following areas is expected: experimental field and laboratory studies, mathematical or computer simulation modelling, telemetry, molecular ecology.

*

A strong interest in interdisciplinary research and the willingness to engage in scientific exchange with other disciplines is essential for applicants.

The University of Potsdam, the Freie Universität Berlin, the Leibniz Institute for Zoo and Wildlife Research and the Leibniz Centre for Agricultural Landscape Research strives to maintain gender balance among

— / —

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>

BournemouthU SalmonidEvolution

BournemouthU.SalmonidEvolutionaryEcology

PROJECT TITLE:

Interactions of wild, translocated and hatchery-reared juvenile salmonids: implications for management

PROJECT SUMMARY:

We welcome applications for a funded PhD studentship in Professor Rob Britton's group at Bournemouth University, UK. The project will involve stream-scale manipulation experiments to test whether wild fry translocations can be used instead of hatchery fish stocking to increase juvenile recruitment in wild Atlantic salmon populations. The goal of the project is to understand how the demographic benefits of stocking can be achieved without the evolutionary risks associated with hatchery rearing, artificial selection and maladaptation to the wild. The research will be conducted in collaboration with Inland Fisheries Ireland, with extensive fieldwork throughout the River Erriff National Salmonid Index Catchment near Galway, Ireland.

INFORMATION AND CONTACTS:

Application deadline: 2 April 2018

Project description and application guidelines:

<https://www1.bournemouth.ac.uk/study/courses/-phd-studentship-interactions-wild-translocated-hatchery-reared-juvenile-salmonids-implications-management>

Direct all inquiries to Rob Britton: rbritton@bournemouth.ac.uk

Kyle A Young <kayoung1969@gmail.com>

BrandonU EvolutionPesticideResistance

M.Sc. Position at Brandon University

The Cassone lab at Brandon University is seeking a highly motivated M.Sc. student to work on projects related to the evolution of pesticide resistance in wireworm.

The successful applicant will gain valuable experience conducting field work and using cutting-edge molecular biology tools. This collaborative position is funded for two years and includes stipend support.

Interested students are encouraged to contact Dr. Cassone directly for further information (cassoneb@brandonu.ca). Please include a brief statement of interest and a CV in your email.

Closing Date: Open until filled Start Date: Summer 2018 preferred

Founded in 1899, Brandon University is a small but thriving institution located in southwestern Manitoba. Students have access to fully renovated labs, greenhouse and growth chamber facilities, as well as state-of-the-art molecular and computational equipment.

Bryan Cassone <CassoneB@BrandonU.CA>

CanMuseumNature Ottawa PlantSystematics

Call for Applications - PhD Fellowship in Arctic Plant Systematics (University of Ottawa and Canadian Museum of Nature)

We are seeking a highly motivated PhD student to conduct research in the field of plant systematics, with an Arctic geographical focus.

The candidate will be enrolled at the University of Ottawa in the joint graduate program in biology (Ottawa Carleton Institute for Biology).

Research will be conducted at the Canadian Museum of Nature's Natural Heritage Campus (1740 Pink Road, Gatineau, Quebec) in the National Capital Region. The successful candidate will have access to the Museum's excellent facilities designed to support projects in taxonomy, systematics, evolution and ecology, including the world's most comprehensive collection of Canadian Arctic plants in the National Herbarium of Canada.

Research Project Description

The successful candidate will develop a project focused on a circumpolar and/or Arctic-alpine vascular plant species complex (or multiple congeneric species complexes) in which species boundaries are poorly understood, with an aim to make progress in resolving the evolutionary history of the complex from multiple perspectives (e.g., phylogenetic, phylogeographic, taxonomic).

Examples of complicated Arctic genera in particular need of further study include but are not limited to *Draba* (Brassicaceae), *Taraxacum* (Asteraceae), *Potentilla* (Rosaceae), *Papaver* (Papaveraceae), and *Calamagrostis* (Poaceae).

The project will be multi-faceted and will combine herbarium-based study of morphological variation in the National Herbarium of Canada, molecular study in the museum's Laboratory of Molecular Biodiversity, and field work in the Arctic and possibly other ecozones. It may also be necessary to visit other museums and herbaria in Canada and abroad to study type and other material.

Qualifications

An ideal candidate will have previous training and experience in botany or plant biology and a strong interest in plant biodiversity, evolution, phylogeny and taxonomy.

The candidate must meet the University of Ottawa's eligibility criteria, described here: http://catalogue.uottawa.ca/en/graduate/doctorate-philosophy-biology/#t_ext

The fellowship is available to Canadian citizens and permanent residents.

Funding

The position is fully funded by the Canadian Museum of Nature's Scientific Training Program for three years (\$25,000/year), plus \$5,000/year in funds to support research costs.

Deadline

The University of Ottawa application deadline for Canadian students to begin the doctorate program in Fall 2018, is 1 June 2018. See here: <http://www.uottawa.ca/graduate-studies/programs-admission/apply/specific-requirements>

Interested students should contact Drs. Lynn Gillespie (lgillespie@nature.ca) and Jeff Saarela (jsaarela@nature.ca) by email ASAP (before 15 May 2018) to discuss this opportunity, prior to submitting an application to the University. In your initial message, please include a description of your research interests and motivation, your CV and contact information for two references.

Dr. Lynn Gillespie, Research Scientist, Canadian Museum of Nature, and Adjunct Professor, University of Ottawa

Dr. Jeff Saarela, Research Scientist and Director, Centre for Arctic Knowledge and Exploration, Canadian Museum of Nature

21 March 2018

Jeff Saarela <jsaarela@nature.ca>

EAWAG Switzerland Daphnia

PhD position : Host-parasite interactions in hybridizing *Daphnia*, from correlations to experiments

Deadline extension!

The PhD student will participate in a collaborative research project with PD Dr Piet Spaak (Eawag) and Prof. Justyna Wolinska (Leibniz-Institute of Freshwater Ecology and Inland Fisheries, IGB in Berlin, Germany), financed by the Swiss and German Science Foundations (SNF & DFG).

Eutrophication is a worldwide environmental problem accelerated by global warming, affecting the stability of aquatic ecosystems and having long consequences. We will investigate if and how eutrophication affects two interacting evolutionary processes: disease spread and interspecific hybridization. We will use water fleas (*Daphnia*), a well-established model in both host-parasite and hybridization research. This project is a combination of a field survey, a mesocosm experiment (where trophic conditions will be manipulated), the transcriptional profiling of *Daphnia* exposed to stressful eutrophic conditions, and the development and application of molecular markers to study parasite evolution in eutrophic environments. Overall, through the unique combination of expertise and methods, this project will improve our understanding of disease spread and biodiversity loss under different trophic conditions and, consequently, might provide tools for management of aquatic ecosystems.

Within the project this position focuses on interspecific hybridization. The main task will be participation in a large-scale field study and mesocosm experiment; data collection and processing. The student will screen the dynamics of natural and experimental *Daphnia* communities, using microsatellite and SNP markers. Also, the student will conduct a large laboratory experiment to assess *Daphnia* stress responses; here, RNA-Seq methods will be applied. The PhD student will take advantage of the draft *D. galeata* genome.

Although the student will be hosted primarily at Eawag, exchange stays are planned at IGB. Moreover, generous funds are available to cover attendance at national and international conferences. He/she will be enrolled at the Swiss Federal Institute of Technology (ETH) in Zürich.

The position will be for a period of four years, and should start as soon as possible (spring / early summer 2018).

The ideal candidate should have good molecular skills and a strong background in evolutionary biology, ecology or related fields. In addition, knowledge of statistics, bioinformatics and/or population genetics will be highly advantageous. Excellent communication and writing skills in English, good work ethic, and creative thinking are desired. A Master's Degree (or equivalent) in biology or a related subject is necessary for admission. The working language in the group is English.

Eawag offers a unique research and working environment (<http://www.eawag.ch/en/aboutus/working/-researchenvironment/>) and is committed to promoting equal opportunities for women and men and to support the compatibility of family and work. Applications from women are especially welcome. For more information about Eawag and our work conditions please consult www.eawag.ch and www.eawag.ch/en/aboutus/-working/employment. For further information please consult Piet Spaak (spaak@eawag.ch). The application should be submitted by 16 April 2018.

Please submit your application including a motivation letter with a description of pertinent experience, a complete CV (incl. publication list), the names (with e-mail addresses) of three potential referees, and copies of certificates of academic qualifications via the Eawag Jobs & Career webpage, any other way of applying will not be considered. The link below will take you directly to the application form.

<https://apply.refline.ch/673277/0589/pub/1/-index.html>
 Piet Spaak Eawag Aquatic Ecology
 Äberlandstrasse 133 8600 Dübendorf Switzerland
 Phone: +41 58 765 —56 17

spaak@eawag.ch <http://www.eawag.ch/abteilung/eco/-schwerpunkte/zooplankton-oekologie-und-evolution/>
 “Spaak, Piet” <Piet.Spaak@eawag.ch> “Spaak, Piet”
 <Piet.Spaak@eawag.ch>

Europe 15 ITN IGNITE CompGenomicsInverts

Applications for 15 ESR/PhD positions in @MSCACTIONS project ITN IGNITE “Comparative Genomics of Non-Model Invertebrates” have been re-opened for a brief period - final application deadline now 3rd April

2018 (12pm/noon CET)!

Positions are available in institutions and companies in the network for a maximum duration of 36 months. All positions will open on 1st July 2018 or as soon as possible thereafter.

Europe is home to world-leading expertise in invertebrate genomics and the aim of IGNITE is to gather together this European excellence to train a new generation of scientists skilled in all aspects of invertebrate genomics.

The well-trained genome scientists emerging from IGNITE will be in great demand in universities, research institutions, as well as in software, biomedical, agrofood and pharmaceutical companies. Through their excellent interdisciplinary and intersectoral training spanning from biology and geobiology to bioinformatics and computer science, our graduates will be in a prime position to take up leadership roles in both academia and industry in order to drive the complex changes needed to advance sustainability of our knowledge-based society and economy.

To apply and for general information about the positions, please visit our central application tool available here:
 < <https://portal.graduatecenter-lmu.de/ocgc/ignite> >

For a detailed description of the individual projects please see: < <http://www.itn-ignite.eu/projects/> >

In behalf of the IGNITE coordinator and the entire consortium.

Best wishes Michael

Dr. Michael Eitel Project Manager IGNITE Innovative Training Network

Dr. Michael Eitel Molecular Geo- & Paleobiology Lab
 Department of Earth & Environmental Sciences, Division of Paleontology & Geobiology
 Ludwig-Maximilians-Universität München
 Richard-Wagner-Straße 10 D-80333 München Germany

<http://www.itn-ignite.eu> pm@itn-ignite.eu Phone: +49 (89) 2180-6733 Fax: +49 (89) 2180-6601

Michael Eitel <m.eitel@lmu.de>

Europe 15 ITN IGNITE CompGenomicsInverts deadlineFeb28

Dear all,

This is a reminder that the (strict) deadline for applying to the 15 PhD positions in the Innovative Training Network IGNITE (Comparative Genomics of Non-Model Invertebrates) is tomorrow February 28, 23:59 CET. This includes one PhD position in my group entitled “Using chromosome conformation capture to assemble genomes to perfection”, i.e. applying contact genomics to generate completely assembled genomes (from telomeres to telomeres). Experience in computer science, bioinformatics, genomics and/or statistics would be highly desirable for this position.

Here is the link to the description of the project (which includes the sequencing and assembly of a chaetognath genome in order to better understand the evolution of these enigmatic metazoans): http://www.itn-ignite.eu/projects/11559_esr-project-5-using-chromosome-conformation-capture-to-assemble-genomes-to-perfection/ For details of the 15 PhD projects available, see: <http://www.itn-ignite.eu/projects/> Applicants should have a master degree or equivalent in a relevant field, but cannot already possess a doctoral degree. For the position in my group, the successful applicant will be registered in the PhD programme of the Université libre de Bruxelles. Candidates of all nationalities may apply, but must not have lived in Belgium for more than 12 months in the 3 years immediately prior to their appointment. The fellow will receive a competitive salary, including a mobility allowance, a family allowance (if applicable) and comprehensive social benefits.

Application website: <http://portal.graduatecenter-lmu.de/ocgc/user/register> Best regards, Jean-François

– Jean-François Flot Associate Professor Evolutionary Biology & Ecology - C.P. 160/12 Université Libre de Bruxelles Avenue F.D. Roosevelt 50 B-1050 Brussels - Belgium <http://ebe.ulb.ac.be/ebe/Flot.html> “jflot@ulb.ac.be” <jflot@ulb.ac.be>

GhentU AvianSpeciation

PHD POSITION TO STUDY LATERAL PROCESSES IN AVIAN SPECIATION

The Terrestrial Ecology Unit (TEREC) at Ghent University is a vivid lab, where students and researchers apply first principles of individual-based ecology to predict how natural populations are affected by long- and short-term environmental change. We believe that innovation in research can only be propelled by amalgamating skills

and perspectives from different disciplines into an overarching framework. For our new project Zosteromics, launched by Prof. Luc Lens and Dr. Jan O. Engler, we want to capitalize on the newest developments in genomics and computational biology paired with classical ecological work to understand how avian speciation works in complex and changing environments.

The “great speciator” bird genus *Zosterops*, also known as white-eyes, shows a remarkable speciation rate which is unprecedented in birds and one of the highest among vertebrates. This diversification is partly driven by adaptation to rapidly changing environments - yet, the exact processes remain unknown. Therefore, these iconic birds pose an ideal study system to learn more about speciation in a changing world.

Within the Zosteromics project, we have one fully funded PhD position available to work at TEREC alongside a multilateral consortium of experts (see below). The position is available for 2+2 years and a salary range of 1900 - 1950euro / Month (+ benefits). The preferred, yet negotiable, starting date is 1st of October 2018. The PhD can be conducted in one of two topics.

Topic 1: Genomics of white-eye diversification

Recent insights into rapid species diversification using genomic tools question the notion of vertical processes as leading evolutionary force in favor of network-like structures in which vertical and lateral evolutionary drivers act in concert, e.g. when hybridization leads to adaptive introgression. Using de novo assemblies and whole-genome resequencing of different highland-lowland white-eye lineages across East African sky-islands you will study the role of lateral processes and understand the evolutionary role of genes introgressed that way. This topic will be jointly performed with Asst. Prof. Alexander Suh, Dept. of Ecology and Genetics, Uppsala University, Germany.

Topic 2: Simulating speciation in dynamic environments

Different speciation models aim to formally describe evolution along elevational gradients. To assess how these speciation models describe white-eye diversification, you will implement a Mechanistic Simulation Model that is spatially-explicit, individual-based, and stochastic, incorporating all processes relevant for biodiversity dynamics. You will run the model under neutral and adaptive (informed by genomic outcomes) conditions to understand the role of lateral processes of speciation in changing environments. This topic will be jointly performed with Prof. Juliano Cabral, CCTB, University of Wurzburg, Germany.

Candidates should have an excellent MSc degree in a relevant field, are self-driven, and eager to work in an

interdisciplinary and multilateral team. Next to quantitative skills relevant for the respective topic, we expect generally high writing and verbal communication skills to present results of your work in academic journals and at international conferences.

To apply send your complete application, including motivation letter, full CV, publication list, and contact details of two references alongside your preferred topic to Zosteromics@ugent.be.

Deadline is 3rd of April 2018.

Links:

Project Page: [http://www.ecology.ugent.be/terec/-research.php?page=project&project=FWO 2017b](http://www.ecology.ugent.be/terec/-research.php?page=project&project=FWO%202017b)

The Avian Ecology and Evolution group @ TEREC: <http://www.ecology.ugent.be/terec/-research.php?page=aee> Suh Lab (Uppsala): <http://www.ieg.uu.se/evolutionary-biology/suh/> Cabral Lab (Wurzburg): <http://www.ctb.uni-wuerzburg.de/research/ecosystem-modeling/people/juliano-sarmiento-cabral/>

Jan O. Engler FWO PostDoc Fellow Terrestrial Ecology Unit Ghent University

Twitter: @engler_j

Jan Engler UGhent <JanOliver.Engler@ugent.be>

KielU Computational Evolution- ary Genomics

The Genomic Microbiology Group of Prof. Tal Dagan in the Institute of Microbiology at Kiel University, Germany, invites applications for a:

PhD position in computational evolutionary genomics

The position is offered within the International Max Planck Research School (IMPRS) for Evolutionary Biology

Application deadline is March 25, 2018.

Research topic: Phylogenetic tree rooting and inference of lateral gene transfer Phylogenetic trees are used to describe and investigate the evolutionary relations between entities. In most tree reconstruction methods the inferred phylogeny is unrooted, and the ancestral relations between the taxonomic units are not resolved. The determination of ancestor-descendant relations in an unrooted tree is achieved by the infer-

ence of a root node, which a priori can be located on any of the branches of the unrooted tree. Recently we introduced the Minimal Ancestor Deviation (MAD) rooting method, which operates on any phylogenetic tree with branch lengths (Tria et al. (2017) *Nat Ecol Evol* 1:0193). The new method explicitly quantifies the major confounding factor - rate variation among lineages - to achieve unprecedented accuracy and consistency. The PhD candidate will take part in further developing this rooting method and researching the applicability of the method for reconstructing donor-recipient relations in gene transfer events during prokaryote evolution. The project requires background in molecular evolution and programming skills.

Research Group: The PhD candidate will work in the Genomic Microbiology group led by Prof. Tal Dagan (<http://www.uni-kiel.de/genomik>) that is focused on microbial genome evolution. The group is international and multidisciplinary with both computational and experimental working scientists. For enquiries regarding the position and research topic please contact Prof. Tal Dagan: tdagan@ifam.uni-kiel.de

The IMPRS graduate school is dedicated to highest level of research and training in all areas of contemporary Evolutionary Biology. It is a joint initiative of the Max Planck Institute for Evolutionary Biology, the University of Kiel and the Helmholtz Center for Ocean Research Kiel (GEOMAR). The school offers an internationally competitive research environment with state of art facilities. The participating groups are working on a broad variety of scientific topics including molecular, behavioral, theoretical and organismal approaches.

The graduate program starts with a rotation period of three months followed by a PhD project of three years including seminars, courses and workshops. The language of the graduate school is English. Financial support is provided throughout the program.

To obtain further information about the PhD program and application details (only online application possible), please visit our website at <http://www.evolbio.mpg.de/-imprs>. Well-motivated and highly-qualified students from all countries are welcome to apply. A Master of Science degree or a Diploma as well as a strong interest in Evolutionary Biology and flexibility in the research project are prerequisites for entering the program. We are looking forward to your online application for a PhD fellowship in the beautiful landscape of Northern Germany.

The deadline for applications is March 25, 2018. The selection week will be held from June 25 29 and the program itself starts on September 17, 2018.

For information regarding the program contact: Dr. Kerstin Mehnert, August-Thienemann-Str. 2, 24306 Plön, Germany email: imprs@evolbio.mpg.de phone: +49(0)4522 763 233

The coordinator Kerstin Mehnert

The steering committee Tal Dagan, Thorsten Reusch, Hinrich Schulenburg, Eva Stukenbrock, Diethard Tautz and Arne Traulsen

“tdagan@ifam.uni-kiel.de” <tdagan@ifam.uni-kiel.de>

Leibniz Berlin 2 WildlifeFitness

The Leibniz Institute for Zoo and Wildlife Research (Leibniz IZW) in Berlin is Germany’s premier wildlife research institute. The Leibniz IZW focuses on the life histories and mechanisms of evolutionary adaptations of mammals and birds, their limits and their conservation in natural and anthropogenically influenced environments. The institute operates within the fields of evolutionary ecology, evolutionary genetics, ecological dynamics, wildlife diseases, reproduction biology and reproduction management. The Department of Ecological Dynamics offers the following 2 PhD-positions (50%) in Modelling with projects entitled:

Project 1: The long-term consequences of early life environments on behaviour and fitness

Project 2: Effects of variation in vital rates on population and community dynamics The aim of both projects is to better understand how and when environmental conditions shape fitness-related traits (e.g. survival probability), and how environmentally driven variation in fitness-related traits in turn affects population and community dynamics. By investigating these questions at the level of individuals and populations/communities, using data-driven analyses, simulations and meta-analyses, we aim to advance the general understanding of how different levels of organization respond to changes in environments.

Requirements for both positions: * Completed MSc in ecological modelling, behavioural ecology, evolutionary ecology, computational biology or bioinformatics * Excellent programming skills in R * A solid background in statistical analyses and modelling * Reliability, high motivation and efficiency; ability to work independently and as part of a team; * Strong organizational and communication skills; willingness to engage in collaboration for successful and timely implementation of the project

and publication of results; * Proficiency in English.

Beneficial for both positions: * Experience in analyzing individual based, longitudinal data sets, simulations, population modelling, individual-based modelling, meta-analyses, social network analyses * Programming skills in Netlogo / Python * A strong interest in behavioural ecology, population ecology, and evolution

We offer state-of-the-art methodology and a stimulating research environment in an interdisciplinary, collaborative project. The two positions will start 1st June 2018 and are limited to three years. Working hours comprise 19.5 hours per week, with salary according to TVöD (Bund). The place of work is the Leibniz IZW Alfred-Kowalke-Str. 17, 10315 Berlin. As a member of the Leibniz Association the IZW is an equal opportunity employer, determined to increase the proportion of women in science, and particularly encourages women to apply. Preference will be given to disabled applicants with the same qualifications.

Enquiries or further questions should be directed to Dr. Sarah Benhaiem for Project 1 (benhaiem@izw-berlin.de) and Dr. Viktoriia Radchuk for Project 2 (radchuk@izw-berlin.de). Applicants should submit 1) a letter of motivation in which they indicate to which project they apply, and highlight particular skills for this position, 2) a CV, 3) copies of relevant degrees, 4) a potential list of publications and 5) the names and contact details of two referees no later than 15th April 2018 via the IZW’s (www.izw-berlin.de) online-job-market (button “Apply online”). Interviews will take place on the 24th of April.

We are looking forward to your application!

“Vollberg, Stephanie” <vollberg@izw-berlin.de>

LouisianaStateU ConservationGenetics

Professors in the School of Renewable Natural Resources, Louisiana State University may each nominate a prospective student for a Board of Regents PhD fellowship beginning in Fall 2018. I would like to nominate an outstanding student to compete for this fellowship and work in my lab. The fellowship pays 30K/year for four years, and includes a tuition waiver. Active research programs in my lab (<http://www.rnr.lsu.edu/people/-taylor/default.htm>) focus on conservation genetics, particularly the relationship between immunogenetic vari-

ation and fitness, population-level genetic variation in threatened species and species of management concern, historical genetic variation (using museum DNA), and genetic aspects of behavioral ecology (inbreeding avoidance, extra-pair paternity). Interested students should contact Sabrina Taylor at staylor@lsu.edu to discuss potential projects: as long as the project is in the field of conservation genetics, it can be tailored to suit a prospective student's interests. Applicants must be US citizens/residents. All qualified U.S. citizens and residents must apply before Mar 30, 2018. Fellowship offers will be made by April 15, 2018 and students who accept will then be asked to apply to the LSU Graduate School. LSU is an Equal Employment Opportunity employer.

Sabrina Taylor Associate Professor School of Renewable Natural Resources RNR Bldg. Room 227 (Office 331) Louisiana State University and AgCenter Baton Rouge, LA, 70803, USA 225-578-4137, fax 4227 <http://www.rnr.lsu.edu/people/taylor/default.htm> "Taylor, Sabrina S" <staylor@agcenter.lsu.edu>

MasseyU 2 PlantEvolution

Two fully-funded PhD Scholarships

Investigating native plants derived from whole-genome duplication events and understanding why they are successful

Project description: We are seeking two highly-motivated PhD students for a project that seeks to understand why plants with multiple sets of chromosomes (polyploidy) are so common in New Zealand and elsewhere. The three-year project is part of a new Royal Society of New Zealand Marsden Fund grant. Specifically, we want to determine the relative roles of genetic differentiation, genomic downsizing, trait innovation and novel ecological opportunities in the evolutionary success of many polyploid species. Our prediction is that polyploidy creates both costs and opportunities for plants which limit the type of environments they can occupy. The idea is to investigate plant lineages in New Zealand with well-documented and different levels of chromosome duplication. With the research team, the aim is obtain information on genome size, gene expression, phylogenetic relationships, ecophysiological and trait features, and undertake process-based niche modelling across ploidy levels in six representative lineages (e.g. *Asplenium*, *Poa*, *Plantago*, *Schizoclema*, *Leptinella*, *Veronica*).

This is an ideal PhD opportunity in evolutionary ecology and the students will gain experience in genomic analysis, comparative phylogenetics, trait analysis, and species distribution modelling, depending on their interests.

Project Supervisors: Professor Bill Lee, School of Biological Sciences, University of Auckland and Landcare Research, Dunedin, New Zealand; Dr Jen Tate, Massey University, Palmerston North; Dr Heidi Meudt and Dr Patrick Brownsey, Museum of New Zealand Te Papa Tongarewa, Wellington. The PhD students will also gain experience working with Professor Dirk Albach (Carl von Ossietzky-University Oldenburg, Germany) and Dr Andrew Tanentzap (University of Cambridge, UK).

Funding: Funding includes a tax-free stipend, full tuition fees, and operational expenses for travel, conference attendance and research expenses over the 3-year programme. Both international and domestic students are eligible. One PhD (ecophysiology, species distribution modelling) will be run from the University of Auckland but will include time at Landcare Research in Dunedin, while the other (phylogenetics, genomics) will be based at Massey University, Palmerston North.

Requirements: Applicants should have completed a degree with a significant research component (e.g. MSc or BSc Honours), and have an excellent academic record. Applicants need to have a background either in plant ecology, ecophysiology, phylogenetics or computational biology.

Applicants should email their CV, academic transcripts, a cover letter stating why you are interested in the position and how your qualifications and experience make you a good fit for the proposed research, and the contact details for at least two referees to Prof. Bill Lee (wg.lee@auckland.ac.nz or leew@landcareresearch.co.nz). Applications close on 1st April 2018.

Jennifer A. Tate, Ph.D.

Senior Lecturer in Plant Systematics and Evolution

Curator, Dame Ella Campbell Herbarium (MPN)

Massey University

Institute of Fundamental Sciences

Private Bag 11222

Palmerston North

New Zealand

Phone: 64-6-350-5515 ext. 84718

FAX: 64-6-350-5682

Homepage

j.tate@massey.ac.nz

“Tate, Jennifer” <J.Tate@massey.ac.nz>

MaxPlanck Jena 5 EvolutionaryBiology

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

The International Max Planck Research School (IMPRS) “The Exploration of Ecological Interactions with Molecular and Chemical Techniques” in Jena, Germany, invites applications for 5 PhD positions beginning in September 2018 - January 2019. The overarching research topic is the use of molecular, chemical and neurobiological techniques to experimentally explore ecological interactions under natural conditions. The main focus is on the relationship between plants, microbes and herbivores, and their environment, as well as the evolutionary and behavioral consequences of these interactions. We offer 14 exciting projects focusing on different organisms and approaches. The complete list of projects offered including project descriptions is available on our website (<http://imprs.ice.mpg.de/ext/index.php?id=420#header.logo>). We are looking for enthusiastic PhD students with strong interests in the above-described central topic. Applicants should have or be about to obtain a Masters or equivalent degree in one of the following fields: entomology, neurobiology, molecular biology, biochemistry, analytical chemistry, plant physiology, genetics, ecology, evolutionary biology, bioinformatics, and mathematics and computer science. Exceptional candidates with a Bachelor’s degree may also be considered. All our projects are highly integrative and require willingness to closely collaborate with researchers of different backgrounds. The Research School is a joint initiative of the Max Planck Institute for Chemical Ecology and the Friedrich Schiller University. We offer state-of-the-art equipment, an excellent research environment, supervision by a thesis committee and a structured training program including scientific courses, training in transferable and outreach skills and participation in research symposia. Successful candidates will receive a Max Planck support contract. There are no tuition fees and the working language is English. Application deadline is May 16th, 2018. For detailed information on the IMPRS, projects offered and appli-

cation requirements, please visit our website: <http://imprs.ice.mpg.de/>. Please apply online from March 28, 2018, at: <https://imprs-reg.ice.mpg.de/>.

Projects offered in 2018 Please find below a list of projects with evolutionary topics. All projects are highly integrative and require the collaboration between different research groups. Applicants can identify up to three projects of interest. It is possible to change project preferences during the recruitment in Jena.

Project 5: Specificity, phylogeny and fitness contributions of phytoplasma effector proteins Supervisors: Prof. Dr. Günter Theißen, Genetics, Matthias Schleiden Institute, Friedrich Schiller University Jena; Prof. Dr. Jonathan Gershenzon, Department of Biochemistry, Max Planck Institute for Chemical Ecology; Dr. Axel Mithöfer, Department of Bioorganic Chemistry, Max Planck Institute for Chemical Ecology

Project 9: Predators that eat toxic food Supervisors: Dr. Hannah Rowland, Research Group Predators and Prey, Max Planck Institute for Chemical Ecology; Dr. Christian Paetz, Research Group Biosynthesis/NMR, Max Planck Institute for Chemical Ecology

Project 10: The insect mustard oil bomb: A chemical weapon against predators and pathogens? Supervisors: Dr. Franziska Beran, Research Group Detoxification and Sequestration in Insects, Max Planck Institute for Chemical Ecology; Dr. Hannah Rowland, Research Group Predators and Prey, Max Planck Institute for Chemical Ecology

Project 13: Molecular basis of balanced color polymorphisms in grasshoppers Supervisor: Prof. Dr. Holger Schielzeth, Institute of Ecology and Evolution, Friedrich Schiller University Jena

Claudia Voelckel <imprs@ice.mpg.de>

MPIO Seewiesen EvolutionCognition

Announcement

PARROT COGNITION (TENERIFE)

MASTER PROJECTS / VOLUNTEER RESEARCH ASSISTANTS

Comparative Cognition Research Group, Max-Planck Institute for Ornithology, Tenerife, Spain

The Max-Planck Comparative Cognition Research

Group (CCRG) invites applications of Masters students and volunteer research assistants. The CCRG forms part of the collaboration between the Max-Planck Institute for Ornithology, Seewiesen, Germany, and the Loro Parque Fundación (LPF), Tenerife, Spain. We are currently running various comparative research projects on social and physical cognition in parrots. Interested candidates are encouraged to contact us to enquire about the ongoing projects. Successful applicants can expect to gain a solid insight in the field of Animal Cognition/Experimental Psychology and gain experience in working with psittacids in a dynamic, international research environment. The research is carried out on captive parrots of the LPF, which holds the largest parrot collection and gene reserve in the world (ca. 350 subspecies) for conservation and research purposes.

Logistics:

Voluntary research assistant position /Master Project start and end dates are flexible but preference will be given to students who can start in April/May 2018. The position requires a minimum of 4 months, but ideally 6 months, continuous commitment at the research station in Tenerife, Spain. Free accommodation in a shared student apartment can be provided. Successful applicants will be responsible for their own transportation expenses to and from the research station (Puerto de la Cruz, Tenerife, Spain).

Important skills/qualifications:

Successful candidates will have: * completed a degree in Biology or any related field * a strong interest in comparative cognition * high motivation and commitment to the project * reliability, efficiency and an ability to work independently * confidence to interact with animals * previous research experience * good verbal and written English skills * initiative to develop the project * good team work attitude and social skills (shared accommodation between 3 students)

To apply: Please send your CV and a cover letter reporting any relevant experience you have and motivation to participate in the project to Dr. Auguste von Bayern (avbayern@orn.mpg.de) or Dr. Anastasia Krasheninnikova (akrashe@orn.mpg.de). Contact details of 2 referees may be requested.

Anastasia Krasheninnikova <anastacia.k@web.de>

New Zealand 2 Evolutionary Ecology

Two fully-funded PhD Scholarships

Investigating native plants derived from whole-genome duplication events and understanding why they are successful

Project description: We are seeking two highly-motivated PhD students for a project that seeks to understand why plants with multiple sets of chromosomes (polyploidy) are so common in New Zealand and elsewhere. The three-year project is part of a new Royal Society of New Zealand Marsden Fund grant. Specifically, we want to determine the relative roles of genetic differentiation, genomic downsizing, trait innovation and novel ecological opportunities in the evolutionary success of many polyploid species. Our prediction is that polyploidy creates both costs and opportunities for plants which limit the type of environments they can occupy. The idea is to investigate plant lineages in New Zealand with well-documented and different levels of chromosome duplication. With the research team, the aim is obtain information on genome size, gene expression, phylogenetic relationships, ecophysiological and trait features, and undertake process-based niche modelling across ploidy levels in six representative lineages (e.g. *Asplenium*, *Poa*, *Plantago*, *Schizaelema*, *Leptinella*, *Veronica*).

This is an ideal PhD opportunity in evolutionary ecology and the students will gain experience in genomic analysis, comparative phylogenetics, trait analysis, and species distribution modelling, depending on their interests.

Project Supervisors: Professor Bill Lee, School of Biological Sciences, University of Auckland and Landcare Research, Dunedin, New Zealand; Dr Jen Tate, Massey University, Palmerston North; Dr Heidi Meudt and Dr Patrick Brownsey, Museum of New Zealand Te Papa Tongarewa, Wellington. The PhD students will also gain experience working with Professor Dirk Albach (Carl von Ossietzky-University Oldenburg, Germany) and Dr Andrew Tanentzap (University of Cambridge, UK).

Funding: Funding includes a tax-free stipend, full tuition fees, and operational expenses for travel, conference attendance and research expenses over the 3-year programme. Both international and domestic students are

eligible. One PhD (ecophysiology, species distribution modelling) will be run from the University of Auckland but will include time at Landcare Research in Dunedin, while the other (phylogenetics, genomics) will be based at Massey University, Palmerston North.

Requirements: Applicants should have completed a degree with a significant research component (e.g. MSc or BSc Honours), and have an excellent academic record. Applicants need to have a background either in plant ecology, ecophysiology, phylogenetics or computational biology.

Applicants should email their CV, academic transcripts, a cover letter stating why you are interested in the position and how your qualifications and experience make you a good fit for the proposed research, and the contact details for at least two referees to Prof. Bill Lee (wg.lee@auckland.ac.nz or leew@landcareresearch.co.nz). Applications close on 1st April 2018.

Angela J Brandt Ecologist/Modeller Manaaki Whenua
- Landcare Research T +64 3 470 7222 | M +64 21 121 5657

<http://angelajbrandt.wordpress.com>
www.landcareresearch.co.nz Manaaki Whenua -
Landcare Research

Angela Brandt <BrandtA@landcareresearch.co.nz>

Norway Comparative Genomic Regulation

PhD scholarship within comparative analysis of genome regulation

The successful candidate will be associated with the projects “TRANSDUCTION” (2018-2021) and “REWIRED” (2018-2021), recently funded by the Norwegian Research Council FRIPRO program. Both these projects are addressing fundamental knowledge gaps concerning genome evolution following whole genome duplication, using salmonid fishes as a model system. Specifically, our aim is to test if functional redundancy in a duplicated genome sparks evolution of novel adaptive functions, and the importance of transposable elements in the evolution of these novel adaptations.

A key element in the projects is collaboration with Rori Rohlf at San Francisco State University and use her computational framework (EVE) to identify genes under divergent selection pressure on gene regulation. The

candidate will therefore be expected to spend significant time in the Rohlf-lab during the project.

The main tasks will be to: - Annotate and build a catalogue of transposable elements in salmonid fish genomes - Integrate information on transposable elements (genomic positions and historical activity) with analyses of transcriptomics (RNA-Seq) and epigenomics (ChIP-Seq, ATAC-Seq) data in a comparative framework across 10 fish species. - Within the comparative framework, investigate the impact of transposable element activity on evolution of adaptive gene expression changes.

For more information about the project, please contact Simen RÅ©Åd Sandve (srsandve.org or simen.sandve@nmbu.no)

More information: <https://www.jobbnorge.no/en/-available-jobs/job/148999/phd-scholarship-within-comparative-analysis-of-genome-regulation-refno-18-01261> Rori <rrohlf@gmail.com>

Portugal Archaeogenetics

INVITATION TO JOIN A RESEARCH PROJECT
Call for a PhD candidate under the scope of ARCHAIC Project

We are looking for a highly motivated graduate student, who is interested in pursuing a PhD degree in the field of Archaeogenetics, Biology, Animal Science, Bioinformatics or related fields to join the team of a research project entitled “ARCHAIC - The archaeogenetics of Iberian cattle: investigating their origins, evolution and improvement” (PTDC/CVTÁLIV/2827/2014; POCL-01-0145-FEDER-016647).

The invited student will interact with an international team of scientists at CIBIO/InBIO-University of Porto in the Campus of Vairão, Portugal, at LARC-National Laboratory of Archaeosciences in Lisbon, Portugal, and at foreign participating institutions namely the Archaeological Research Laboratory of Stockholm University, under the supervision of Catarina Ginja < <https://cibio.up.pt/people/details/cginja> > (CIBIO-InBIO).

The application should include the following information:

1. Motivation letter with a short biography and research interests;
2. Curriculum vitae summarizing education, experience, other qualifying activity and a list of publications;
3. Copy of master degree and course grades; 4.

Names and contact information of two referees.

The application must be written in English and sent by e-mail to ARCHAIC@cibio.up.pt until *March 16, 2018*.

The invited student is expected to apply to the call for PhD Fellowships of Fundação para a Ciência e a Tecnologia - FCT, Portugal, open until March 28, 2018 and should comply with the necessary requirements. For details please check the call website:

<https://www.fct.pt/apoios/bolsas/concursos/-individuais2018.phtml.pt> *For more information about this call, please click here. < https://cibio.up.pt/upload/filemanager/CallPhD_ARCHAIC_2018.pdf >*

To know more about the ARCHAIC project click here < <https://cibio.up.pt/projects-1/page/494> >.

To know more about our research group, please click here. < <https://cibio.up.pt/research-groups-1/details/-archgen> >

Research Associate, IF2014 Fellow <http://cibio.up.pt/people/details/cginja> *CIBIO/InBIO **- Laboratório Associado* *Centro de Investigação em Biodiversidade e Recursos Genéticos* Universidade do Porto Campus Agrário de Vairão Rua Padre Armando Quintas n.º7 4485-661 Vairão, Portugal

E-mail: catarinaginja@cibio.up.pt Tel.: +351 252 660 411 Fax: +351 252 661 780

ARCHAIC project: Archaeogenetics of Iberian Cattle < <http://archaic.campus.ciencias.ulisboa.pt/Archaic/-home.html> >

Catarina Ginja <catarinaginja@gmail.com>

Requirements: The FCT criteria for scholarship selectivity gives a weight of 50% to the individual merit of the applicant (Individual evaluation). Therefore, only candidates with a very competitive curriculum are likely of being selected.

Preference for candidates with demonstrable experience in the area(s) of genetics, genomics, molecular evolution, bioinformatics and biotechnology.

Candidates should possess a Master's degree and English proficiency. Applicants should be Portuguese citizens or citizens of EU member states. Citizens of other countries may also apply, as long as they have legal resident status in Portugal at the time of the application. For further details about application requirements for this scholarship consult the Regulations: <https://www.fct.pt/apoios/bolsas/docs/RegulamentoBolsasFCT.pdf> Research project and laboratory: The PhD candidate will develop the awarded project in CIIMAR, Porto (Matosinhos), Portugal, under the Evolutionary Genomics and Bioinformatics group Head by Prof. Agostinho Antunes (<http://orcid.org/0000-0002-1328-1732> and <https://www.scopus.com/authid/detail.uri?authorId=7102537544>) in collaboration with several international institutions. Topic of research could range from Adaptive evolution (e.g. venom diversification, sensory, immunity, reproduction, development, etc), comparative genomics, selection signatures, symbiotic associations (e.g. animals-microorganisms symbioses, microbiomes, etc), bioinformatics, etc.

Candidates should send the CV and copies of their graduation and Master's degrees (including final grades) to Prof. Agostinho Antunes (aantunes@ciimar.up.pt) before 15th March 2018 (first come first served chance).

Agostinho Antunes <aantunes@ciimar.up.pt>

Portugal Evolutionary Genomics

PhD Students Proposals

Call for PhD candidates to apply for the FCT 2018 PhD Program competition - Portugal.

<https://www.fct.pt/apoios/bolsas/concursos/-individuais2018.phtml.en> The position is contingent on FCT approval.

Applicants: Primarily Portuguese citizens or citizens of the EU member states. Citizens of other countries may also apply, as long as they have legal resident status in Portugal at the time of the application.

QMUL London EvolutionChickBehaviour

A PhD position is available at the Evolution and Comparative Cognition laboratory at Queen Mary University of London (Dr Elisabetta Versace) to investigate the spontaneous behaviour and learning strategies of male and female chicks (*Gallus gallus*). Here is the link to the project on the School of Biology and Chemical Sciences website: <http://www.sbcs.qmul.ac.uk/postgraduate/-research/projects/display-title-527650-en.html> The project will be tailored on the interests and skills of the successful candidate, so candidates from different

backgrounds are expected to apply (e.g. biology, psychology, computer science). Informal inquiries welcome!
e.versace@qmul.ac.uk

Sincerely, Elisabetta Versace

Elisabetta Versace, PhD Lecturer in Psychology School of Biological and Chemical Sciences Queen Mary University of London Fogg Building, room 2.25 Email: e.versace@qmul.ac.uk Phone: + 44 (0) 2078828798

Twitter @so_evolutionary

e.versace@qmul.ac.uk

QMU London PhD BehaviouralDifferencesChicks

Dear All,

a PhD position is available at the Evolution and Comparative Cognition laboratory at Queen Mary University of London (supervisor Dr Elisabetta Versace) to investigate the spontaneous behaviour and learning strategies of male and female chicks (*Gallus gallus*). Here is the link to the project: <http://www.sbcs.qmul.ac.uk/postgraduate/-research/projects/display-title-527650-en.html> The project can be tailored on the interests and skills of the successful candidate, so we expect to receive applications from students of different backgrounds (e.g. biology, psychology, computer science). Informal inquiries welcome! e.versace@qmul.ac.uk

Thank you for circulating this information.

Sincerely, Elisabetta Versace

Elisabetta Versace, PhD Lecturer in Psychology School of Biological and Chemical Sciences Queen Mary University of London Fogg Building, room 2.25 Email: e.versace@qmul.ac.uk Phone: + 44 (0) 2078828798

Twitter @so_evolutionary

“e.versace@qmul.ac.uk” <e.versace@qmul.ac.uk>

StockholmNHM Palaeogenomics

SUBJECT: Graduate position: StockholmNHM.Palaeogenomics

ADVERTISEMENT TEXT:

PhD Student Position on Palaeogenomics of Prehistoric Climate Change

Swedish Museum of Natural History & Stockholm University

PROJECT DESCRIPTION

This PhD project will investigate how species are affected by climate change. To do this, we will use a palaeogenomic approach to analyse ancient DNA from prehistoric bones and teeth sampled across several well-known severe and rapid changes in climate that took place during the last ice age. The analyses will comprise several animal species in Eurasia. The specific aims of the project are to i) assess the degree to which past warm periods led to demographic bottlenecks, ii) examine to what extent climate-induced range contractions led to losses of unique genetic variation, and iii) use a comparative genomic approach to investigate whether species adapted genetically in response to rapid climate fluctuations.

For this project, good knowledge in population genetics, bioinformatics as well as experience of laborative DNA analysis are important qualifications. The PhD student will join the ancient DNA research group at the Swedish Museum of Natural History (for further details, see www.palaeogenetics.com/adna).

ENVIRONMENT The PhD student will be employed by Stockholm University (SU), but will be based at the Department of Bioinformatics and Genetics at the Swedish Museum of Natural History (SMNH). The museum is located in Stockholm, which by many is regarded as one of the most beautiful capitals in the world and is home to a vibrant scientific community with several leading research institutes as well as the National Genomics Infrastructure at the Science for Life Laboratory. The SMNH has a strong mission in natural history research, and its research division has more than 170 employees. The main supervisor for the PhD project will be Prof. Love Dalen at the SMNH. The project is funded by the Bolin Centre for Climate Research and the Department of Zoology at SU, and will be co-supervised by Prof.

Anders Gotherstrom at SU.

QUALIFICATIONS In order to meet the general entry requirements, the applicant must have completed a second-cycle degree, completed courses equivalent to at least 240 higher education credits, of which 60 credits must be in the second cycle, or have otherwise acquired equivalent knowledge in Sweden or elsewhere. In order to meet the specific entry requirements, the general syllabus for doctoral studies in the field of Systematics and Evolution stipulates that applicants must have completed a research degree (e.g. Master'Äs), or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level ("examensarbete") within systematics and evolution, ecology, population genetics, bioinformatics or a similar subject. Applicants who have in principle acquired the corresponding competence in Sweden, or abroad, are also qualified. The qualification requirements should preferably be met by the deadline for applications.

CONTACT For questions about the position and further information about the project, contact Prof. Love Dalen, Email: love.dalen@nrm.se

HOW TO APPLY Applications should be done using Stockholm University's online application system. Please follow the link below to obtain further information about how to write your application and how to access the online application system: <http://palaeogenetics.com/jobs> Closing date: 22 March 2018 Reference number: SU FV-0556-18

Love Dalén <Love.Dalen@nrm.se>

StockholmU EvolutionCognition

PhD position on Evolution of cognition in the guppy

PhD position available in Niclas Kolm's research group at Stockholm University. The group uses mainly the guppy (*Poecilia reticulata*) as a model to experimentally investigate the link between evolutionary changes in brain anatomy and behaviour. The aim of this PhD project is to investigate how individual cognitive ability and learning strategies are affected by rapid evolution of brain size and schooling behaviour. The existing artificial selection lines of large- and small-brained guppies and the recently developed selection lines of guppies with differences in schooling behaviour will form the base of the project. The main focus of the project is thus

to use existing and develop new ecologically relevant cognitive tests and behavioural assays to evaluate how rapid evolutionary changes in brain size and behaviour affect learning abilities and other behavioural aspects in both individual and collective contexts.

The work will be lab-oriented utilizing the Kolm lab guppy facilities with over 4000 aquaria and multiple set-ups for cognitive tests and behavioural assays of available selection lines in both 2D and 3D using advanced hard- and software to track individual behaviour. You will be part of a dynamic international team of PhD students and postdocs. The project will require hard work but at the same time provide excellent opportunities for personal initiatives and development towards a successful academic career. An important task will be to collect and analyse complex data in a way that controls for the setups of replicated artificial selection designs. Worth noting is that Stockholm University offers extremely good conditions for this type of 4 year fully funded PhD position.

Contact For more information, please contact Professor Niclas Kolm, niclas.kolm@zoologi.su.se.

Application Link to Stockholm University website on this PhD position and how to apply (deadline 9th April 2018):

<https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=4874 &rmlang=UK>

Niclas Kolm

Niclas Kolm

Professor, Head of Ethology division

Department of Zoology

Stockholm University

Svante Arrhenius väg 18B

10691 Stockholm, Sweden

Email: niclas.kolm@zoologi.su.se

Tel: 46 (0)8 164050

Mobile: 46 (0)730 980809

Website: <http://www.zoologi.su.se/about/-staff/person.php?suuid=nkolm> Niclas Kolm
<niclas.kolm@zoologi.su.se>

StockholmU LifeHistoryEvolution

PhD position on Life history evolution across climate clines in butterflies We are inviting applications for a PhD position in the research group of Karl Gotthard that is focusing on the evolution of life history and plasticity in seasonal environments, using primarily natural populations of butterflies as model organisms.

The new PhD will work within the project 'Life history evolution across climate clines' and will focus on the evolution of life cycle timing in situations where insect species show shifts in the number of annual generations, i.e. when there are shifts in voltinism. The phenomenon of voltinism shifts is relatively common in insects and means that a given species shifts from having two full generations per year in southern or low altitude locations, to have only one annual generation in northern or high altitude locations. Selection is likely to change significantly across voltinism shifts as they signify a dramatic change in optimal life history strategy. In particular the new project aims at exploring life cycle adaptations and potential voltinism shifts in the expanding range margins of butterfly species that are presently expanding their distributions northwards. At the northern range limits these expanding species are expected to experience strong selection for changes in how photoperiod regulates life cycle timing and voltinism. The project aims at testing the general prediction from life history theory that there are footprints of selection for a change in life cycle regulation resulting in a shift from the ancestral state of having two generations per year to having only one annual generation. In this way the project will provide novel insights into ecological consequences of the interaction between the two most prominent effects of climate change on natural populations: northward range expansions and selection for changes in seasonal life cycle regulation.

The project will contain aspects of both field and laboratory work to study the ecology, genetics and physiology of life cycle timing in temperate butterflies. The prospective student will sample replicated populations and do controlled laboratory studies of how phenotypic adaptations and associated genetic variation is changing across shifts in voltinism. The genetics will be studied by quantitative genetic methods and genomics, while the physiological manifestations of the different timing adaptations will be investigated using respirometry

and cold tolerance assays. Finally, we plan to do use reciprocal transplant experiments in outdoor cages to test the adaptive significance of local difference in these adaptations.

The PhD will be part of the Division of Ecology and it is funded by grants from the Bolin Centre for Climate Research at Stockholm University and the Swedish Research Council (VR).

Stockholm University offers very good conditions for PhD positions, that are 4 year fully funded positions.

We are looking for candidates with a strong interest in evolutionary ecology, plasticity and life history theory, with excellent analytical ability and experience with quantitative analyses of life history traits and of other traits of interest. Experience in working with insects in the lab and in the field, as well as having a valid drivers license, is especially meriting.

Contact For more information please contact Dr. Karl Gotthard karl.gotthard@zoologi.su.se

Application Below is a link to the Stockholm University website where you find instructions about how to apply (deadline April 15).

<https://www.su.se/english/about/working-at-su/phd> Karl Gotthard Department of Zoology Stockholm University 106 91 Stockholm Sweden <https://www.su.se/english/profiles/gotth-1.183261> Carl Gotthard <Karl.Gotthard@zoologi.su.se>

StockholmU WinterEvolutionaryEcology

PhD project on Winter evolutionary ecology in butterflies

The Department of Zoology invites applications for a four-year PhD position as part of the project 'The effects of microclimate variability on insect overwintering biology' funded through grants from the Bolin Centre for Climate Research and the Research Council Formas.

Diapause is a resting stage characterized by developmental arrest and suppressed metabolism that occurs commonly in insects. Its mechanistic underpinnings are poorly understood, as are physiological commonalities among insects in how diapause is regulated. This is surprising since diapause is common and an important part of the life-cycle in most insects in seasonal environments. Models of insect phenology are critical to

correctly manage pest insects, but these often suffer from unclear diapause physiology components and inaccurate microhabitat climate models, which leads to overall poor model resolution. Ongoing climate change is affecting winter climate more strongly than summer climate, which exacerbates the lack of information on diapause development and winter microclimatology.

The overarching aim of the PhD project is to understand how spatial and temporal variation in microclimate affects the life-cycle regulation of butterflies in Sweden. The student will investigate seasonal microclimatic variability in overwintering habitats with the aim to link large scale climate models to micro-scales - scales that actually matter for overwintering insects. The student will also combine integrated physiological models on diapause termination with microclimate models to measure the energetic cost of diapause with the aim to estimate the effect of winter warming on insect population ecology and range dynamics.

The project will combine several approaches: (i) Fields surveys describing the spatial and temporal microclimatic patterns in overwintering landscapes that are combined with sophisticated statistical microclimate models. (ii) In-situ field experiments where summer and winter components of life-cycles are investigated by tracking butterfly performance in the field. (iii) Detailed climate-chamber and laboratory experiments where field data is used to design informative rearing regimes aimed at elucidating consequences of thermal variation on winter development and energetics.

Contact For more information, please contact project leader Philipp Lehmann, telephone: +46 73 907 88 90, philipp.lehmann@zoologi.su.se, or Karl Gotthard, telephone: +46 8 16 40 48, karl.gotthard@zoologi.su.se.

Application Link to Stockholm University website on this PhD position and how to apply (deadline 31st of March 2018): <https://www.su.se/english/-about/working-at-su/phd?rmpage=job&rmjob=4843&rmlang=UK> Philipp Lehmann

Researcher Department of Zoology Stockholm University tel: +468164089 email: philipp.lehmann@zoologi.su.se orcid: <http://orcid.org/0000-0001-8344-6830> homepage: <https://lehmannzoology.wordpress.com/> Philipp Lehmann <philipp.lehmann@zoologi.su.se>

U Aberdeen Experimental Evolution Microbes

Funded PhD studentship in microbial evolution at the University of Aberdeen (Scotland, UK): “Experimental evolution of Thaumarchaeota”

The fundamental aim of this project is to determine the process of adaptive diversification and associated trade-offs in fitness, by studying microbial evolution experimentally.

A 4-year PhD studentship in microbial evolution, starting in May 2018 at the earliest, is now open for application at the University of Aberdeen, Scotland, UK. The deadline for applications is April 12th 2018 and this studentship is available to students of any nationality (providing funding for tuition fees and stipend). The PhD project is funded by the Royal Society and will target key evolutionary questions with a special focus on Thaumarchaeota to align with the research thematic of the University of Aberdeen Nitrification Group.

Using microbes to test theory in evolutionary biology has led to major scientific advances. In particular, microbial experimental evolution has allowed analysis of both microbial adaptation (genomic and phenotypic changes) and diversification (phenotypic evolution and lineage-splitting) using controlled environments, through increased understanding of the nature and frequency of genomic substitutions, their effects on microbial fitness and the mechanisms by which diversity is created and maintained in microbial populations. These concepts were established from studies of bacteria, fungi, viruses and phage, focussing mainly on a few bacterial model organisms (1, 2). However, an entire domain of life, the Archaea (3), has largely been ignored by evolutionary biologists, despite their widespread distribution in natural environments, high abundance and essential contribution to global ecosystem functioning that sustains the planet. A priori, no clear reasons for different evolutionary processes between archaea and bacteria can be advanced, but their ancient evolutionary divergence (despite the existence of lateral gene transfer between domains) suggests that the relevance of established microbial models of adaptation and diversification should be tested on these organisms if they are to be considered universal. Indeed, despite the global importance and diversity of archaea, our understanding of the ecological and evolutionary processes generating their high diver-

sity is scarce compared to that of eukaryotes and, to a lesser extent, bacteria. eaaf3883.

This project will focus on members of a key microbial phylum, the Thaumarchaeota (4, 5), which are abundant and ubiquitous and perform a critical ecosystem function, ammonia oxidation. The distribution of natural microbial communities is influenced by environmental characteristics, and pH is the major abiotic factor influencing extant thaumarchaeotal niche specialisation (4), and has also influenced their diversification and patterns of lineage formation through deep evolutionary time (5).

This project will involve re-isolation of a thaumarchaeotal strain (6) followed by the study the evolution of these microbes experimentally. Experimental evolution will be performed in automated mini-bioreactors by imposing environmental changes under controlled conditions and the evolutionary mechanisms of adaptation and diversification as well as the existence of trade-offs will be determined using genomic and fitness changes over time.

The PhD student will join a dynamic team of researchers led by Dr Cécile Gubry-Rangin (<https://www.abdn.ac.uk/ibes/people/profiles/c.rangin>) and will benefit from the presence of strong groups in the department working on related topics as well as being embedded in a strong network of international collaborations. The University of Aberdeen provides an excellent scientific environment, state-of-the-art technological support facilities and diverse training opportunities for all aspects of research and for transferable academic and generic skills.

Candidate should have (or expected to achieve) a minimum of 2:1 Honours degree, ideally (but not required) an MSc in evolution, ecology or related, strong theoretical skills and enthusiasm for learning and developing microbial experimental evolution.

Application Process: Formal application should be made as described on <https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=96539> . References:

1. Barrick JE, Yu DS, Yoon SH, Jeong H, Oh TK, Schneider D, Lenski RE, Kim JF. (2009) Genome evolution and adaptation in a long-term experiment with *Escherichia coli*. *Nature* 461(7268):1243-7
2. Rainey PB, Travisano M. (1998) Adaptive radiation in a heterogeneous environment. *Nature* 394(6688):69-72.
3. Spang A, Caceres EF, Ettrema TJG. (2017) Genomic exploration of the diversity, ecology, and evolution of the archaeal domain of life. *Science* 357(6351). pii:

— / —

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>

UAucklandNZ EvolBirdSong

One PhD position available for new project on the evolutionary origins of song learning in birds. This project is a collaboration between Dr. Kristal Cain (kecain.weebly.com) at the University of Auckland in New Zealand, and Dr Michelle Hall (michellehall.wordpress.com) at The University of Melbourne in Australia. Both domestic and international applications are encouraged.

Vocal learning in birds is of great interdisciplinary importance and an excellent model for human language. This research relies on a clear understanding of the evolutionary origins of vocal learning, but recent reports have undermined previous assumptions, leading to a hotly contested debate about the evolution of vocal learning. Vocal development in one group of birds, the New Zealand wrens (*Acanthisitta*), is critical for resolving this debate, but is currently unknown and unstudied. The project will focus on tiitipounamu/rifleman and combine in-depth behavioural analyses with new acoustic tools to determine whether vocalisations are learned or innate in these endemic birds. We are also interested in sex differences in vocal acquisition patterns.

This project has a strong field focus and will require substantial time in remote areas. There is flexibility for keen students to guide the direction of the research within the framework of the overall project. The PhD project is anticipated to start mid-2018, with fieldwork commencing in August. Informal inquiries are welcome.

Preferred selection criteria

- Strong previous academic record
- Enthusiasm and interest in the broad concepts and questions motivating the research
- Interest in undertaking field-based avian research, especially in collecting acoustic data
- Enjoyment of outdoor fieldwork and confidence in working in remote locations that can experience extreme weather.

- Excellent interpersonal, oral and written communication skills
- Ability to learn/use R (statistical programming language), new packages for analysis (e.g. warbleR), and new software (e.g. Sound Analysis Pro)
- Experience with bird banding/ringing, nest searching, and acoustic techniques is helpful

To apply, please send an e-mail briefly explaining your research interests and career goals, a CV, a copy of academic transcripts, and contact information for two references to Dr. KE Cain (k.cain@auckland.ac.nz). Informal enquires are also welcome.

Application and funding details: This project supported by the Marsden Fund of The Royal Society of New Zealand (broadly equivalent of US NSF). Funding includes a tax-free stipend, full tuition fees, and operational expenses for travel, conference attendance and research expenses over the 3-year programme.

Requirements: Applicants should have completed a degree with a significant research component (e.g. MSc or BSc Honours), and have an excellent academic record. Students will need to qualify for a U Auckland scholarship and admission to U Auckland (see <https://www.auckland.ac.nz/en/for/future-postgraduates>). Please also note the English language proficiency requirements.

APPLICATIONS CLOSE ON 1ST APRIL 2018.

We encourage all qualified applicants to apply. Auckland is a diverse and welcoming city and we are committed to increasing diversity in biology. We particularly encourage Maori/Pacifica students to apply; tūtipounamu are endemic songbirds and taonga, adding special significance and kaitiakitanga to our proposed research. Our project celebrates their unique status - the phylogeny/whakapapa of this species is critical to our project and for understanding the true origins of vocal learning worldwide. –

Kristal Cain - Lecturer School of Biological Sciences
University of Auckland kecain.weebly.com +64 9 923 5815

k.cain@auckland.ac.nz k.cain@auckland.ac.nz

UBielefeld RaptorMalariaGenomics

Short-term and long-term consequences of avian malaria-like infection

A PhD position in behavioural ecology is available at the Faculty of Biology at Bielefeld University, in the Department of Animal Behaviour (with Dr. Nayden Chakarov, see <http://www.uni-bielefeld.de/biologie/animalbehaviour/nchakarov>). The position runs for three years from early 2018 to 2021 and is funded by the German Research Foundation (DFG). The PhD student will be part of the buzzard research team (together with the group of Prof. Dr. Oliver Krüger) and of a large PhD cohort, which is supported by a DFG-funded collaborative research centre NC3 (full details at www.uni-bielefeld.de/biologie/crc212).

The PhD project will combine field work, lab work and genomics. We'll explore physiological causes and consequences of a very common blood parasite infection in a common buzzard population (*Leucocytozoon* in *Buteo buteo*). The student will conduct experiments in the field, produce transcriptomic data and analyse it in combination with fitness correlates. The long-term fitness consequences for buzzards will be monitored using lifelong wing-tags, and survival and recruitment data will be collected. So far, over 2500 individual buzzards have already been fitted with lifelong wing tags and the resulting data set will be used. The goal is to understand the extent and mechanisms of resistance and tolerance to the parasite in these hosts.

Main responsibilities

- Research tasks (90%) - Conducting field work on a buzzard population, including chick-ringing and treatment from late March to early July each year; RNA extraction and library preparation; Transcriptomic and statistical analyses; Writing scientific publications
- Organisational tasks in the research group and collaborative efforts (10%)

Applicant's profile

We seek a bright and highly motivated student with a university degree in a relevant discipline with specialization in either behavioural ecology, ornithology, population ecology and/or bioinformatics, and a strong eagerness to delve into the other; interest to develop scientific capabilities and questions; experience with field work, preferably in birds of prey; experience with molecular lab work; interest in behavioural and life history, immunological and parasitological questions; coding experience, preferably with Unix command-line, omics-techniques, and/or R; ability to work both independently and as part of a team; excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage: papers in peer-reviewed international journals; experience in tree-climbing with rope techniques;

experience with large-scale research projects.

Remuneration

Salary will be paid according to Remuneration level 13 (65%) of the Wage Agreement for Public Service in the Federal States (TV-L). Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its employees.

Application procedure

To apply, please provide: (i) a letter of motivation including a statement of your research interests and skills and experience relevant to the position, as well as specific ideas and plans related the project outline; (ii) a CV including publication list; (iii) names and contact details of two referees willing to write confidential letters of recommendation. All materials should be emailed as a single PDF file to: nayden.chakarov@uni-bielefeld.de. The application deadline is March 15th 2018 and interviews will take place shortly thereafter. After the decision, the position should start as soon as possible. For further information on the project and the department, please contact Nayden Chakarov nayden.chakarov@uni-bielefeld.de with any informal inquiries.

Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor pursuits. It offers a high standard of living and is well connected to most major European cities. Bielefeld University has received a number of awards for its achievements in the provision of equal opportunity and has been recognized as a family friendly university. The University welcomes applications from women. This is particularly true with regard both to academic and technical posts as well as positions in Information Technology and Trades and Craft. Applications are handled according to the provisions of the state equal opportunity statutes. Applications from suitably qualified handicapped and severely handicapped persons are explicitly encouraged.

Nayden Chakarov <nayden.chakarov@uni-bielefeld.de>

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.

— / —

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>

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

— / —

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>

ULausanne Evolutionary Genomics Neurogenetics

Graduate positions are available within the lab of Roman Arguello at University of Lausanne's (UNIL) Department of Ecology and Evolution.

We are a newly formed lab interested in understanding the genetic and neural bases of sensory evolution. We take a very interdisciplinary approach that bridges computational/comparative genomics with neurogenetics. Our model organisms are diverse *Drosophila* species from around the globe, and we are particularly interested in the evolution of neural circuits and in the evolutionary processes related to the rapid changes underlying olfaction and temperature preference.

The specific focus for these positions will be on olfactory evolution. The projects will relate repeated gains/losses in olfactory receptors to the evolution of their protein sequences, to their neural circuits, and to behavior. This work will test hypotheses about how the olfactory system evolves, and to what extent these changes are repeatable. Due to the cross-disciplinary nature of the research, there is a range of opportunities for contributing to the projects depending on particular interests and strengths (i.e. comparative/population genomics, neurobiology, generation of transgenic tools for new species).

Qualifications: - Undergraduate degree or master's degree in the biological sciences with a focus on evolutionary biology, genetics, neurobiology, or molecular biology - some experience with (or willingness to learn) basic

molecular biology techniques - some experience with (or willingness to learn) computer programming/scripting (i.e. R, Python, Perl, Unix) - soft skills: ability to be self-motivated and to work independently as well as within a small group, good communication skills, comfortable with public presentations, ability to clearly document work This is a 100% position for an initial duration of one year, renewable up to 3 years if the contract starts on July 1st 2018.

The Department of Ecology and Evolution is a lively, fun, productive, and highly diverse group. While UNIL is a French-speaking university, the working language of the Department and the lab is English. For more information about the Department of Ecology and Evolution please see its page here: <https://www.unil.ch/-dee/en/home.html> Lausanne is a scenic medium-sized city situated on the edge of Lake Geneva. Life here is good. Its central location within Europe makes traveling by train and plane convenient. And for outdoor enthusiasts, Lausanne sits at the base of Alps and Jura which offer year-round escape and fun.

For more information about the lab and projects, or for further questions, please visit: arguellolab.org or email Roman Arguello at: jacob.arguello@unil.ch Formal applications need to be done through HR and must include a cover letter detailing your research interests and background, a CV, and the names of references (2-3). Applications should both be uploaded through the University of Lausanne platform (via the link below), and sent as a single pdf to jacob.arguello@unil.ch.

Application link: <https://bit.ly/2GxDV9l> University equality policy: The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

“jacob.arguello@unil.ch” <jacob.arguello@unil.ch>

UMassachusetts Lowell EvolutionVertJaw

two post-doc positions

Mass Lowell: Phd positions in Development and Evolution of the Vertebrate Jaw

The Fish lab is recruiting Phd students to work on the development and evolution the vertebrate jaw. We take an integrative approach to understand molecular and morphological evolution. Collaborative relation-

ships within our department allow for use of functional and genomic approaches as well. For more information, visit our website: <https://fishlab.weebly.com/> or contact jennifer_fish@uml.edu

Jennifer L. Fish, Ph.D Assistant Professor Department of Biological Sciences University of Massachusetts Lowell
“Fish, Jennifer L” <Jennifer.Fish@uml.edu>

UMuenster MolecEvolutionNasonia

Graduate position: UMuenster.MolecEvolutionNasonia

1 PhD position within the Research Training Group “Evolutionary Processes in Adaptation and Disease” (EvoPAD, GRK 2220) at the University of Münster, Germany

Start: As soon as possible. 3-year position (salary level TV-L E13, 65%).

The project is on “genotype to phenotype” - linking the evolution of the mitochondrial OXPHOS system, mitochondrial capacity, metabolic rates and hybrid incompatibility in the parasitoid wasp *Nasonia*.

The DFG-funded Research Training Group “Evolutionary Processes in Adaptation and Disease” (EvoPAD, GRK 2220) unites biological, medical, and philosophical research. The core idea is to use the theory of evolution to understand processes leading to adaptation and/or disease. PhD students work on advancing evolutionary theory and, in turn, apply modern evolutionary approaches to medical questions. EvoPAD doctoral researchers perform cutting-edge research in an interdisciplinary environment. Our multidisciplinary qualification program is tailored to individual career tracks and offers opportunities for international cooperation, summer schools, and courses covering evolutionary and population genetics, bioinformatics, experimental design, philosophy of science, and bioethics. EvoPAD is coordinated within the stimulating city of Münster and offers a family-friendly and international atmosphere.

Project details: The successful candidate will work on subproject B7, supervised by Prof Dr Jürgen Gadau at the Institute for Evolution and Biodiversity (<http://www.uni-muenster.de/Evolution/molevolsoebio/>). The project aims to understand the genomic, genetic and physiological basis of nuclear cytoplasmic incompatibilities, specifically concerning mitochondria. Well-functioning mitochondria are essential for the survival

and reproduction of all eukaryotes, including humans. To make a functioning mitochondrion, both nuclear and mitochondrial genes have to interact harmoniously. In general, mitochondrial genomes evolve faster, posing a potential problem due to nuclear cytoplasmic incompatibilities. In humans, mitochondrial mutations cause the most common human genetic diseases. Additionally, nuclear-cytoplasmic incompatibilities contribute to early postzygotic isolation between incipient species.

This project uses known hybrid incompatibilities in a four-species parasitoid wasp system to reveal and understand the genetic architecture of the observed nuclear-cytoplasmic incompatibilities in F2 male hybrids. This incompatibility comes in degrees ranging from none to 90% lethality in the most distant crosses. It is also known that rearing temperature influences the effect of this hybrid incompatibility (e.g., no offspring survive at 15°C and 31°C, but >30% survive at 25°C for one cross). Hence, we will investigate the interaction of temperature, nuclear-cytoplasmic incompatibilities and mitochondrial evolution. This should help us to generally identify and understand the gene regulatory networks that allow the nuclear and mitochondrial encoded genes to interact appropriately.

For further information visit: www.uni-muenster.de/-EvoPAD/application/ Applicant requirements: Applicants should have an outstanding master's or equivalent degree in biology or related fields, and they should have proven qualifications with particular relevance to EvoPAD. Applicants must be able to formulate and solve research problems and effectively interpret research results. They should also show a willingness to interact with colleagues in an interdisciplinary setting and be motivated to manage a PhD project and to participate in our multidisciplinary qualification program. Applicants must also be fluent in written and spoken English.

How to apply: The application should include: (1) a CV, including information about former academic education and degrees, professional experience, publications, fellowships/awards, conference contributions, languages, and further relevant skills and abilities; (2) a cover letter, stating the candidate's expectation from EvoPAD and motivation to join the project; (3) the candidate's master's thesis abstract; and (4) contact details of at least two referees.

The University of Münster is an equal opportunity employer and is committed to increasing the proportion of women academics. Consequently, we actively encourage applications by women. Female candidates with equivalent qualifications and academic achievements will be preferentially considered within the framework of the legal possibilities. We also welcome applications from

candidates with severe disabilities. Disabled candidates with equivalent qualifications will be preferentially considered.

Applications should be sent by e-mail as one PDF file (max. 5 MB)

— / —

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>

UOslo 2 ancientDNA Conservation

PhD position available in sedimentary ancient DNA

Applications are invited for a position as PhD Research Fellowship in sedimentary ancient DNA available at the Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biosciences, University of Oslo.

Project description

Sedimentary ancient DNA (sedaDNA) preserved in soil and sediments has become a valuable tool to assess biodiversity changes through time. Importantly, it allows detection of organisms even in the absence of fossil evidence and its provenance is primarily local in origin. In this project, we will use sedaDNA to trace the historic uses of plants and animals, study human-assisted dispersal and evaluate the impact of past human civilization on local ecosystems. We will be working with material from a variety of locations, including the Caucasus and Central Asia. Methodology will include metabarcoding combined with high-throughput sequencing, as well as amplicon sequencing of specific taxa of interest.

The fellowship will be for a period of 3 years, with the possibility of a fourth year with 25% compulsory work (e.g. teaching responsibilities at the department) contingent on the qualifications of the candidate and the teaching needs of the department.

Requirements

Applicants must hold a master-degree or equivalent, or must have submitted their master's thesis for assessment prior to the application deadline, within the fields of evolutionary biology, systematics, molecular ecology or a similar subject. Experience with DNA laboratory methods, high-throughput sequencing, and bioinformatics are considered important qualifications. We seek a

highly motivated, enthusiastic person with the ambition to gain insight and publish papers in leading, international journals, and in possession of good interpersonal skills.

* It is a condition of employment that the master's degree has been awarded. * the average grade point for courses included in the Master's degree must be B or better in the Norwegian educational system * the Master's thesis must have the grade B or better in the Norwegian educational system * the average grade point for courses included in the Bachelor's degree must be C or better in the Norwegian educational system * Candidates are expected to be in the upper segment of their class. * Candidates without a Master's degree have until 30 June, 2018 to complete the final exam

The Faculty of Mathematics and Natural Sciences has a strategic ambition of being a leading research faculty. Candidates for these fellowships will be selected in accordance with this, and expected to be in the upper segment of their class with respect to academic credentials.

All Ph.D. candidates must demonstrate high English language skills. International applicants must document these skills prior to admission to the PhD programme (please see the announcement website for details and exemptions).

The fellowship requires admission to the PhD programme at the Faculty of Mathematics and Natural Sciences. The application to the PhD programme must be submitted to the department no later than two months after taking up the position.

Salary and welfare

* Salary NOK 436 900 'V 490 900 per annum depending on qualifications and seniority as PhD Research Fellow, (position code 1017) * Attractive welfare benefits <<http://www.uio.no/english/for-employees/employment/welfare/index.html>> and a generous pension agreement, in addition to Oslo's family-friendly environment with its rich opportunities for culture and outdoor activities

The application must include the following:

* Application letter including a statement of interest, briefly summarizing your scientific work and interests and describing how you fit the description of the person we seek * CV (summarizing education, positions pedagogical experience, administrative experience and other qualifying activity) * Copies of educational certificates, transcripts of records and letters of recommendation * Documentation of English proficiency * List of publications and unpublished work, and up to 3 academic works that the applicant wishes to be considered by the

evaluation committee * Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number)

Foreign applicants are advised to attach an explanation of their University's grading system. Please note that all documents should be in English (or a Scandinavian language).

The application with attachments must be delivered in our electronic recruiting system. Further details and instructions on how to apply can

— / —

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>

UOtago NewZealand EvolutionaryGenomics

Evolution of the New Zealand bird fauna

A PhD position in evolutionary genomics is available to study aspects of the evolution of New Zealand's unique bird fauna with Dr Michael Knapp at the University of Otago, Dunedin, New Zealand.

New Zealand's isolation and mammal predator free environment has led to the evolution of a unique bird fauna. It includes model species to study the evolution of island gigantism, flightlessness and alpine adaptations, to name just a few and is therefore uniquely suited to shed light on the ecological and molecular processes that underlie such evolutionary adaptations.

This PhD project is part of our Royal Society funded research programme, which uses genomic data to address key questions of bird evolution and conservation in New Zealand's unique environment. It offers the flexibility for the PhD student to decide on the direction of the PhD studies within the framework of our research programme. Possible questions include for example the response of the New Zealand bird fauna to past and predicted future climate change, and the evolutionary basis of island gigantism and flightlessness. The ideal PhD student will have skills in molecular ecology/population genetics and/or bioinformatics and genome data analyses. The University of Otago is one of the most research-intensive Universities in New Zealand with a world-class reputation in the life sciences. It provides an environment

that allows its students to undertake internationally recognised research, in a diverse and vibrant postgraduate environment and has been ranked as one of the 15 most beautiful campuses in the world. The PhD student will be hosted by the Department of Anatomy, a diverse and research-oriented department with expertise ranging from genomics to biomedical sciences.

For details and instructions on how to apply, please <http://www.otago.ac.nz/anatomy/study/-postgraduate/opportunities/otago680718.html>. The project is listed under “Evolution of the New Zealand bird fauna”.

For further questions please contact Dr. Michael Knapp (michael.knapp@otago.ac.nz).

Please apply by 22/April/2018 (New Zealand time).

Dr Michael Knapp Rutherford Discovery Fellow Senior Lecturer in Biological Anthropology Department of Anatomy University of Otago Dunedin New Zealand

michael.knapp@otago.ac.nz

UPrague ArabidopsisAdaptation

PhD-position Ecophysiology of adaption to alpine environments in *Arabidopsis arenosa*

The position is available as of 1st April 2018

The PhD project is embedded in the three-years' FWF-project “Disentangling evolutionary adaptation from transient acclimation to alpine environments in *Arabidopsis arenosa*” and will be conducted under the supervision of Profs. Gilbert NEUNER, Ilse KRANNER, Peter SCHÄNSWETTER and Dr. Filip KOLÁŘ (University of Prague; genomics, RNAseq) in close collaboration with Drs. Erwann ARC (metabolomics) and Karl HÄLBER (University of Vienna; ecology). The PhD project focuses on the eco-physiology of photosynthesis and stress physiology of lowland populations and independently evolved alpine populations of *Arabidopsis arenosa* from different mountain ranges. It will also offer the possibility to integrate the results in a wider framework of genomic, transcriptomic & metabolomic investigations carried out under related projects that focus on the same species. We are looking for a highly motivated and enthusiastic young scientist to join our international research team. The gross salary is 37,680 per year.

The successful candidate will be tasked with - planning

and conducting field work in alpine sites together with other team members; - assessment of functional (eco-physiological) and structural leaf traits (lab work in Innsbruck and approximately two months of field work per year); - statistical data analyses; - dissemination of the results through publications in scientific journals and presentations at international conferences.

Applicants must - hold a MSc degree in plant sciences or a related field; - have an excellent knowledge of plant physiology; previous experience with physiological ecology, functional ecology or alpine ecology are desirable; - be able to conduct fieldwork in remote areas; - be proficient in English, both written and orally; - have excellent social skills; - be able to work in a team as well as independently; - provide the following documentation (all in one file): - Cover letter stating the motivation - Curriculum vitae including copies of all university degrees received - Letter of recommendation by the supervisor of the Master thesis

Please send your application and enquiries for further information to A.Univ.-Prof. Mag. Dr. Gilbert NEUNER (Gilbert.neuner@uibk.ac.at).

“Neuner, Gilbert” <Gilbert.Neuner@uibk.ac.at>

USunshineCoast Aust EvolutionaryRobotics

PhD Position in Evolutionary biomechanics, University of the Sunshine Coast, Australia.

The Clemente Lab at the University of the Sunshine Coast, Australia is seeking outstanding applicants for fully-funded PhD scholarships.

Our research focuses on the relationship between form, function and ecology of living and extinct animals. This project aims to explore how well evolution can perform by comparing biological systems, with robotic (and computational) systems which mimic them.

The PhD project will contribute to research that explores the limits to natural evolution. The successful candidate will do this by: 1) Measuring natural variation in running and climbing biomechanics in three species of lizard which vary in body size. 2) Constructing small autonomous climbing robots, recreating the technique used for each lizard species. Then expand the control space with small changes in biomechanics, to determine how well each species is optimised for climbing performance.

Essential qualities for candidates include: - strong computational and analytical skills in biomechanics - experience using biomechanical assessment tools (e.g. high speed video, force plates)

Preferred qualities for candidates include: - interpersonal skills to work effectively with research animals, team members, and project collaborators. - excellent critical thinking skills, ability to work independently - research experience and practical knowledge of research principles is required whether through previous internship, work experience, or coursework.

- interest or previous experience in electronics/microprocessors.

- interest in evolutionary theory

The Clemente Laboratory (<https://www.usc.edu.au/explore/structure/faculty-of-science-health-education-and-engineering/staff/dr-christofer-clemente>) is part of the Animal Ecology Lab within the University of Sunshine Coast. We are located on the Sunshine Coast, approximately an hour north of Brisbane Queensland on the Sippy Downs campus.

Course fees and a living stipend (currently \$26,300 AUD per annum, tax free) will be included as part of the scholarship.

The opportunity is open to both Australian/New Zealand nationals and international candidates, however exceptional international candidates will be considered (with top-up scholarships available to cover international tuition fees).

For queries or if you are interested in applying please contact Christofer Clemente, PhD, School of Science and Engineering, cclement@usc.edu.au with your CV.

USC, Locked Bag 4, Maroochydore DC, Queensland, 4558 Australia. CRICOS Provider No: 01595D Please consider the environment before printing this email.

“cclement@usc.edu.au” <cclement@usc.edu.au>

UWageningen HyperparasitoidEvolution

PhD position - The enemy of your enemy's enemy: multi-trophic interactions in hyperparasitoid ecology

Application deadline: 16 April 2018

Hyperparasitoids are fascinating insects that lay their eggs in larvae or pupae of primary parasitoids. In our

curiosity driven research programme, we identified that some hyperparasitoids find their parasitoid host by using plant odours derived from a complex multi-trophic interaction chain. The hyperparasitoids use plant odours induced by feeding of parasitized herbivores to locate the parasitoid larvae that are concealed in the herbivore body. The main aim of this PhD project is to mechanistically understand the interaction chain involved in hyperparasitoid host location and the role of indirect interaction chains in community organisation across four trophic levels. In the project you will aim to i) unravel plant responses to parasitized aphids and caterpillars that allow associated hyperparasitoids to locate their host; ii) identify the physiological changes in aphids and caterpillars after parasitism; and iii) establish a causal relationship of which mechanisms in the multi-trophic interaction chain affect hyperparasitoid host location and community composition in the field. You will use molecular techniques such as RNA-seq and CRISPR-Cas9-mediated targeted gene mutagenesis, insect behavioural observations, as well as field studies. Within the project you will be closely collaborating with a technician and post-doc as well as researchers at international institutes with expertise in molecular biology, ecology, entomology and plant sciences.

Our ideal candidate has a strong background in molecular ecology, behavioural ecology and/or entomology. Some experience with molecular techniques such as RNA-seq, CRISPR-Cas9 and/or bioinformatics will be considered as advantage. You should be curious for fundamental sciences and enjoy to combine molecular biology with field ecology. We are looking for a highly motivated candidate who likes to work in a multidisciplinary team in a collaborative spirit. Proficiency in the English language is a prerequisite.

We offer a full-time position (38 hours), initially for 1 year after which a go/no go decision will be taken on extension with another three years. Gross salary per month € 2222,- in the first year rising to € 2840,- per month in the fourth year, for a fulltime appointment. The candidate will be based at the Laboratory of Entomology Wageningen University, the Netherlands, in the research team of Dr. Erik H. Poelman. Our team studies community ecology of plant-insect interactions and consists of ecologists, entomologists, molecular biologists and computational modellers. At the Laboratory of Entomology we aim at an interdisciplinary approach from cellular to community level to unravel biological phenomena underlying the functioning of plant-insect communities, insect vectored diseases, insect neurobiology and insects as food and feed. The Laboratory of Entomology is part of the Plant Sciences Group of the Wageningen University and Research Centre. For

further information about working at Wageningen UR, take a look at www.jobsat.wur.nl Information on the research project: Dr. Erik H. Poelman, +31(0)317 485433, erik.poelman@wur.nl

For this position you can only apply on line: <https://www.wur.nl/en/Jobs/Vacancies/Show/PhD-position-The-enemy-of-your-enemys-enemy-multi-trophic-interactions-in-hyperparasitoid-ecology.htm>
Don't email directly to the people mentioned above but use the website to apply.

"Poelman, Erik" <erik.poelman@wur.nl>

UWesternAustralia SeagrassAdaptation

Graduate positions: The University of Western Australia, Perth: Seagrass ecophysiology and gene expression

Two PhD positions are available to study 'Seagrass adaptation and acclimation responses to extreme climatic events' in the Kendrick Lab (<https://seagrassresearch.net>). Research in the Kendrick lab focuses on ecology, genetics, and restoration of benthic habitat-forming species, particularly seagrasses.

PROJECT DESCRIPTION

Seagrasses evolved around 100 million years ago and have persisted in the oceans through many significant climatic events, including sea level oscillations and temperature changes. The low levels of morphologic and phylogenetic differentiation within genera suggest they are incredibly resilient, and that phenotypic plasticity may play a significant role in acclimation and/or adaptation to changing environments. The recent increase in frequency and intensity of extreme climatic events can cause rapid ecosystem change, likely to be greater than that caused by a gradually changing climate. These extreme events can act as strong and acute agents of selection, generating widespread mortality and collapse of ecosystems. Understanding how seagrasses respond to change will be a critical component of their management in the future.

Research for these projects will take place in the World Heritage Area of Shark Bay, where some of the largest temperate seagrass meadows in the world occur. These projects will take interdisciplinary approaches that incorporate whole plant growth, ecophysiology and gene expression responses to explore interactions of multi-

ple stressors to extreme events under predicted climate change scenarios. The PhD applicants will play a major role in growth, physiology and gene expression studies in *Posidonia australis*.

Project supervisors: Professor Gary Kendrick and Dr Elizabeth Sinclair, School of Biological Sciences and Oceans Institute, The University of Western Australia, Dr Martin Breed, School of Biological Science, University of Adelaide and Dr Siegy Krauss, Department of Biodiversity, Conservation, and Attractions, Western Australia. Both positions will be based in Perth at The University of Western Australia.

QUALIFICATIONS

We are seeking two highly-motivated candidates with a strong background in evolutionary biology, plant physiology, marine biology, statistics, genomics, and/or bioinformatics. Applicants must have a first class Honours or Masters degree in a related field, be able to conduct fieldwork in remote areas, be proficient in written and oral English, have excellent communication skills, and be able to work independently as well as collaborate effectively as part of a team. Applicants with diving qualifications are preferred.

CONTACT

Prospective applicants should contact Prof Gary Kendrick, gary.kendrick@uwa.edu.au or Dr Elizabeth Sinclair, elizabeth.sinclair@uwa.edu.au outlining interests and suitability prior to completing the application process.

HOW TO APPLY

Prospective applicants will be expected to apply for scholarship funding through the University of Western Australia for a mid-year (July 2018) start. Applications are open now and close on Friday 6 April 2018 <http://www.science.uwa.edu.au/future-students/-postgrad/opportunities/biological> Elizabeth Sinclair <Elizabeth.Sinclair@uwa.edu.au>

UZurich PlantAdaptation

A PhD position funded by the Swiss National Science Foundation is available (to be filled as soon as possible) in the group of Prof. Schiestl at the Department of Systematic and Evolutionary Botany, University of Zurich, for a period of four years. The position is to study the ecological and molecular bases of plant adaptation to biotic and abiotic habitat parameters. In the project, experimental evolution using fast cycling Brassica plants will be used to investigate real-time adaptation to these habitat parameters. The traits modulating adaptations as well as their molecular bases will be studied using selection analysis, phenotyping, as well as molecular and bioinformatics tools. You should have a Master degree in any field of biology and a thorough interest in evolution-

ary biology. Prior experience with plants and/or insects is an advantage. Proficiency in English both orally and written is a must. The successful candidates will work in an exciting research environment focussing on patterns and process of plant evolution. Our department is located in the botanical gardens and houses modern molecular and ecological labs, including greenhouses and climate chambers for plant cultivation. The University of Zurich has a very broad coverage of organismal and molecular biology, and several research groups work on evolutionary topics (www.lifescience-zurich.ch). The city also offers excellent quality of life through cultural programs and infrastructure, as well as an attractive surrounding. If you are interested in the job, please send me by e-mail (florian.schiestl@systbot.uzh.ch) a letter describing your motivation, C.V., copy of degrees, publications (manuscripts), and e-mail addresses of two academic referees, by 30th of April 2018. If you have any further questions, don't hesitate to contact me.

“florian.schiestl@systbot.uzh.ch”
<florian.schiestl@systbot.uzh.ch>

Jobs

ArizonaStateU InsectCollectionCollection	48	UCalifornia Berkeley ResAssist TreeAdaptation ...	56
ClaremontColleges BiologyLabCoordinator	48	UConnecticut 2 ResTech EvolutionaryImmunology	56
DukeU GeneticsEvol TeachingPosition	49	UDebrecen EvolutionaryBiol	57
Embark CanineGenomics	49	UGlasgow ViralEvolution	57
HopkinsMarineStation StanfordU TeachingEvolution	50	UHelsinki Bioinformatician	57
Idaho FishGenetics	50	UKansas 1yr EvolutionaryGenetics	58
London BetaBugs DirectorOfEvolution	50	UNAM Mexico EvolutionaryFunctionalGenomics ..	58
Lyon GroupLeader AnimalEvolution	51	uOttawa QuantitativeBiology	59
MichiganStateU FieldTech GrassAdaptation	51	UPennsylvania ResProf PDF HumanGenomics	59
MNHN Paris SpeciationEvolutionCytogenomic	51	URhodeIsland ResTech Genomics	60
PaceU TeachingEvolution	52	URichmond 1yr EvolutionBiology	60
RBG Kew PlantsFungi EarlyCareerResFellowships	52	UScranton EvolutionaryBiol	61
RutgersU TeachingEvolution	53	UTennesseeKnoxville HerbariumCollectionsManager	62
SanFranciscoStateU DirectorGenomicsFacility	53	Worcester MA VisitingProf Evolution	63
SGN Frankfurt BiodiversityGenomics	54		
UAntwerp EvolEcolEnvOmics	55		

ArizonaStateU InsectCollectionCollection

The Arizona State University Hasbrouck Insect Collection is offering a three-year Collection Specialist (Research Technician) position for the project “Building a specimen-based Biologia Centrali-Americana for weevils: Improved access to the Charles W. and Lois B. O’Brien Collection”. The project will enhance physical and on-line data access to an exceptional research collection - including nearly 1,000,000 weevil and 250,000 planthopper specimens - currently being accessioned at ASU. This process involves a comprehensive reorganization of the O’Brien Collection into a new storage infrastructure. In addition, specimens of select Central American weevil subfamilies will be digitized and imaged to generate Symbiota Collections of Arthropods Network (SCAN) checklists.

More information, and instructions to apply, are found here:

1. Go to: <https://cfo.asu.edu/applicant> 2. Then: “External staff job opportunities” 3. Search for position ID: 40290BR

Or direct link: https://sjobs.brassring.com/-/TGnewUI/Search/Home/Home?part-nerid%620&siteidT94#jobDetails392901_5494

The application window is open until April 03, 2018. Prospective applicants are welcome to contact nico.franz@asu.edu for further (specific) information.

Submitted by:

Nico M. Franz, Ph.D.

School of Life Sciences, PO Box 874108

Arizona State University, Tempe, AZ 85287-4108

E-mail: nico.franz@asu.edu

Twitter: @taxonbytes

“nico.franz@asu.edu” <nico.franz@asu.edu>

ClaremontColleges BiologyLabCoordinator

The W.M. Keck Science Department of Claremont McKenna College, Pitzer College and Scripps College invites applications for full-time Biology Lab Coordinator. The department, which houses a wide spectrum of faculty members from the physical and life sciences, for three of the five undergraduate Claremont Colleges, offers innovative and interdisciplinary programs in the natural sciences.

This position is responsible for the set-up and preparation of the laboratory curriculum for the department’s Introductory Biology laboratories and teaching a number of introductory lab sections as specified each semester. Responsibilities also include updating laboratory curricula to match best practices in biology education. This position may teach other biology courses on an as needed basis. A Ph.D. in Biology, Biological Education, or related interdisciplinary field is required. Prior experience teaching and/or designing inquiry-based labs in the biological sciences is preferred.

In a continuing effort to enrich its academic environment and provide equal educational and employment opportunities, the Claremont Colleges actively encourage applications from women and members of historically underrepresented groups in higher education. The Claremont Colleges are an equal opportunity employer.

Please apply online at https://theclaremontcolleges.wd1.myworkdayjobs.com/-en-US/CMC_Staff/job/Claremont/Biology-Lab-Coordinator_REQ-243-1

Sarah Gilman Associate Professor Biology

W.M. Keck Science Department, of Claremont McKenna, Pitzer, and Scripps Colleges 925 N. Mills Avenue Claremont, CA 91711

<http://faculty.jsd.claremont.edu/sgilman>
sgilman@kecksci.claremont.edu 909-607-0715

“Gilman, Sarah” <SGilman@kecksci.claremont.edu>

DukeU GeneticsEvol TeachingPosition

Lecturer in Introductory Genetics and Evolution in the Department of Biology at Duke University.

Position Description: The Department of Biology at Duke University invites applications for a non-tenure-track faculty position at the Lecturer level, to start in July or August 2018. This position is responsible for developing and coordinating the laboratory exercises for Biology 202L Genetics and Evolution: Introduction to genetics and evolution. The hire will also supervise a team of teaching assistants, teach at least one laboratory section personally, oversee the course management site, and assist with assessments both in the lecture and laboratory portions of the course. Topics covered include Mendelian inheritance, quantitative genetics, genetic mapping, evidence for evolution, natural selection, genetic drift, kin selection, speciation, molecular evolution, and phylogenetic analysis. Relevance to evolution of infectious disease, human hereditary disorders, and social implications of genetic knowledge are also discussed. The course serves approximately 600 students per year over two semesters.

Applicants should have a Ph.D. degree in biological science and strong experience in teaching at the collegiate level. Experience with active learning and other evidence-based pedagogies preferred. The application should be pdf files that include a cover letter, curriculum vitae, a one-page teaching statement, and letters of recommendation from three referees are required. Applications and recommendation letters should be submitted electronically to Academic Jobs Online (<https://academicjobsonline.org/ajo/jobs/10942>). Applications received on or before May 15, 2018 will be given full consideration.

Duke University is an Affirmative Action/Equal Opportunity Employer committed to providing employment opportunity without regard to an individual's age, color, disability, genetic information, sex, gender, gender identity, gender expression, national origin, race, religion, sexual orientation, or veteran status.

Duke aspires to create a community built on collaboration, innovation, creativity, and belonging. Our collective success depends on the robust exchange of ideas'Xan exchange that is best when the rich diversity of our per-

spectives, backgrounds, and experiences flourishes. To achieve this exchange, it is essential that all members of the community feel secure and welcome, that the contributions of all individuals are respected, and that all voices are heard. All members of our community have a responsibility to uphold these values.

Mohamed Noor <noon@duke.edu>

Embark CanineGenomics

Embark Veterinary is looking to expand their science team. Now accepting applications for Population Geneticists, Bioinformatics Scientists and Software Engineers.

Embark is a fast-growing, VC-backed startup launched in 2016 to bring high throughput genetic testing to dogs. Embark scientists are developing the next generation of breeding tools, novel genetic tests, and evolutionary research in dogs with the goal of accelerating canine genetic science and a long-term vision of ending preventable diseases in pets.

Embark's science team consists of leaders in the canine genomics research community and expert veterinary geneticists, computational biologists and population geneticists. The company is a research partner of the Cornell University College of Veterinary Medicine, with a science headquarters in Ithaca, NY and a company headquarters in Boston, MA. We are looking to hire top-notch scientists and engineers in both locations to further improve our core product and expand our research and development capabilities. Areas of interest include:

Ancestry Deconvolution

Trait and Disease Mapping

Population Genetic Inferences of Selection, Demographic History, and Inbreeding

Structural Variation

Genomic Selection

Embark's proprietary database of tens of thousands of dogs is already the largest in the world, leading to exciting new genomic discoveries in many areas of canine genomics. We're looking for colleagues to build the engine driving a million-dog database to discover and prevent cancer, hip dysplasia, cardiac disease and inbreeding depression in dogs.

Embark has doubled their database size in the last six

months and expects to double it again in the next six months. We have raised over \$6M in funding and offer competitive base salary and equity and dog-friendly benefits including health, dental, vision, life and disability insurance, open PTO policy, and pet insurance. Scientists with strong computational and communication skills at all levels of experience are encouraged to apply. Embark Veterinary is an equal opportunity employer. We do not discriminate on the basis of sex, disability, ethnicity, race, religion, sexual orientation, or gender identity.

To apply, send a brief cover letter and CV or resume to Dr. Aaron Sams (asams {at} embarkvet.com).

Aaron Sams <asams@embarkvet.com>

Adam Boyko <adam@embarkvet.com>

HopkinsMarineStation StanfordU TeachingEvolution

Hopkins Marine Station of Stanford University is searching for a Lecturer who will use their expertise in zoology, botany, and general natural history to help the station take advantage of its long history and unique location on Monterey Bay. The Lecturer will (1) teach a summer field course centered on the local kelp-forest/rocky reef ecosystem, (2) teach other courses during the academic year, (3) use their expertise in natural history and field research to facilitate exploration of the local coastal waters and their use in education, and (4) assist in the development and promotion of graduate and undergraduate courses and curricula. A PhD in the natural sciences is required, as well as scientific diving certification (AAUS or equivalent). Experience in teaching inquiry-based courses, especially those involving fieldwork, is highly desirable. The qualified applicant will also have good interpersonal and communication skills.

This position is a full time (12 month) appointment at 100%. Send a cover letter, CV, a statement of teaching philosophy and plans, and names and addresses of three references to Beth Sheets at Hopkins Marine Station, 120 Ocean View Blvd., Pacific Grove, California, 93950, or by email (esheets@stanford.edu). Applications will be reviewed starting April 16, 2018. The final candidate will need to successfully pass a background check to be considered for this position.

Stanford is an equal opportunity employer and all applicants will receive consideration without regard to race,

color, religion, sex, sexual orientation, gender identity, national origin, disability, veteran status, and any other characteristic protected by law.

Beth Sheets <esheets@stanford.edu>

Idaho FishGenetics

Fisheries Geneticist Closing Date: March 30, 2018
<http://www.critfc.org/blog/jobs/fisheries-geneticist-2/>
 The Columbia River Inter-Tribal Fish Commission (CRITFC) is seeking Fisheries Geneticists with experience in population genomics, association mapping, and mixed stock analyses. Positions are part of the Fishery Science Department, but will be located with the genetics group at the Hagerman Fish Culture Experiment Station in Hagerman, ID. This research group is involved in testing conservation, evolution, and ecological theories related to salmonids and other fishes. The employee will work under the Lead Geneticist, in association with CRITFC geneticists and technicians, as well as staff of the Fishery Science Department in Portland, OR. Efforts will focus on applying empirical genetics/genomics data to address questions related to conservation and recovery of steelhead, Chinook, sockeye, and coho salmon, white sturgeon, Pacific lamprey, and other fishes of the Columbia River Basin.

Position Details: <http://www.critfc.org/blog/jobs/-fisheries-geneticist-2/> - Starting Salary: \$57,098 - \$88,974 (CRITFC equivalent to GS11/12) - Department: Fishery Science, Genetics - Classification: Full-time, Regular, Exempt - Location: Hagerman, Idaho

Shawn Narum <nars@critfc.org>

London BetaBugs DirectorOfEvolution

Beta Bugs - aiding a sustainable future by improving insect farming.

At Beta Bugs we're accelerating insect evolution through biotechnology and high throughput breeding. We're laying the foundation of a new, sustainable and rapidly growing bioindustry - be it for food, feed, waste processing or fuel.

We're now hiring a Director of Evolution to take Beta Bugs to the next level. You'll be directly responsible for shaping and rapidly implementing our technologies and will work closely with our Head of Husbandry to develop and maintain our insect lines. This is a one-off opportunity to implement a world-first programme which will be the cornerstone of a rapidly emerging insect farming industry.

You'll have a background in the biological sciences, having specialized in evolutionary biology and/or functional genetics at PhD Level or beyond, with a focus on arthropods (insects preferred). You'll need molecular biology, sequencing and bioinformatics skills, along with hands-on experience of trait generation, selection and maintenance. Experience with transgenic modification and/or breeding for industry requirements is also a plus.

The ideal candidate would be available for an April start, even if on a part-time basis, and then gradually phasing in as full-time. We're currently based within London and as such you'd need right to work within the UK - we cannot currently assist with visa applications.

If you're keen send Thomas a CV and covering letter to thomas@betabugs.uk.

skeletonmanemail@gmail.com

Lyon GroupLeader AnimalEvolution

The Institut de Génomique Fonctionnelle de Lyon (IGFL) has an opening for a new independent group leader. The IGFL has a unique scientific profile and fosters an outstanding international environment. Teams address basic research questions at the interfaces of evolution, physiology and development using functional genomics, bioinformatics, genetics and comparative approaches. The IGFL has a strong focus on integrative, organism-level research using a diversity of model and non-model organisms.

More information at: <https://www.nature.com/naturejobs/science/jobs/636517-research-group-leader-opening> The deadline for applications is April 2nd.

Michalis Averof <michalis.averof@icloud.com>

MichiganStateU FieldTech GrassAdaptation

The Lowry Lab and the Great Lakes Bioenergy Research Center at Michigan State University is seeking to hire a research technician available to work on a large collaborative project studying adaptation in the bioenergy feedstock switchgrass. The research will utilize new genetic mapping populations to identify genomic regions responsible for adaptation between northern upland and southern lowland ecotypes of switchgrass. These mapping populations have been planted at an unprecedented geographical scale, spanning ten common garden field sites distributed over 17 degrees of latitude, making them ideal for studies of regional adaptations. The technician will be primarily responsible for maintaining and gathering data from the switchgrass common garden located at MSU's Kellogg Biological Station (KBS). However, the technician will also travel to field sites in Austin, TX, Columbia, MO, and Lincoln, NE. The research will often involve all-day physical activity outdoors. The technician will be expected to organize data collection efforts and coordinate these efforts with the larger team across the central United States. For more information please contact David Lowry at dlowry@msu.edu. This is a limited term position funded for one year from date of hire with possible extension contingent upon funding renewal.

Please apply for the job at the following website: <http://careers.msu.edu/cw/en-us/job/498731/-research-technologist-i> David B. Lowry Assistant Professor Plant Biology Department Michigan State University Plant Biology Laboratories Room 268 517-432-4882 <http://davidbryantlowry.wordpress.com/> David Lowry <davidbryantlowry@gmail.com>

MNHN Paris SpeciationEvolutionCytogenomic

The "Institut de Systématique Evolution et Biodiversité" (UMR 7205 ISYEB) of the Museum National d'Histoire naturelle (Paris, France) invites applications for a position as Professor in «—Speciation, Evolution and

Cytogenomic—> (closing date: 4 April 2018).

The successful applicant is expected to develop cytogenomic tools in order to study speciation mechanisms and evolution in several groups of vertebrates (mammals, birds; 50% of his activity). Among others, the candidate is requested to have a strong expertise in cytogenetics and cytogenomics. He will have to develop evolutionary centered researches on various non-model vertebrate species and will be in charge of a collection of cryopreserved living cells. We seek an enthusiast researcher able to develop and manage new researches in cytogenomics in relationships with developing genomics exploration of biodiversity. The candidate will have to demonstrate his ability to work in close collaboration with other researchers specialized in the fields of systematics, evolutionary biology, phylogeography, population genetics and conservation. The successful applicant is expected to be able to obtain independent funding and to supervise PhD and Master students.

Previous experience in teaching and team management would be useful as the Professor will have to develop and coordinates the cytogenetic team and to teach cytogenetics (10% of his activity).

The applicant will have to valorize and develop the collection of cryopreserved cells of the Museum National d'Histoire naturelle (40% of its activity).

For additional details see the full job position (in French) here: http://www.mnhn.fr/sites/mnhn.fr/files/atoms/files/galaxie_profil_pr_2018_isyeb_cytogenomique.pdf –

NICOLAS-COLIN Violaine

Curator of Rodents and Shrews

Museum National d'Histoire Naturelle Département de Systématique et Evolution UMR CNRS 7205 CP51, 55 rue Buffon 75005 Paris France ATTENTION CHANGEMENT DE NUMERO!!! Tel: 01 40 79 48 52 Fax: 01 40 79 30 63 Mailto: vnicolas@mnhn.fr *Website *: <http://violainenicolas.free.fr> For any request or to follow up requests and loans concerning the collections of MNHN, please use the following address : <http://colhelper.mnhn.fr/> Violaine Nicolas <vnicolas@mnhn.fr>

PaceU TeachingEvolution

Seeking early career, Ph.D.-holding educators and/or post-doctoral fellows to teach introductory biology lecture and laboratory courses for undergraduate STEM majors at Pace University in lower Manhattan. Applicants should be able to demonstrate that they have either taught undergraduate courses while employing best-practices to engage their students in learning or participated in teaching and learning professional-development activities. Applicants will also be expected to demonstrate that they are (or are open to learning how to be) thoughtful and deliberate about undergraduate course development and measuring student performance using both summative and formative assessments that are aligned to course outcomes. We are seeking applicants who are interested in developing their skills for future careers in undergraduate biology education.

Interested candidates should forward a CV, a 2-page statement of teaching philosophy that highlights the criteria described above, and the contact information for two references to Dr. Marcy Kelly, Assistant Chair and Professor of Biology, at mkelly2@pace.edu by Monday, April 30, 2018.

“Crispo, Erika” <ecrispo@pace.edu>

RBG Kew PlantsFungi EarlyCareerResFellowships

Early Career Research Fellowships in various areas of plants and fungi research Royal Botanic Gardens, Kew
An opportunity has arisen for 12 new research fellowships in specified areas across science departments at the Royal Botanic Gardens, Kew.

You will be an outstanding early career scientist with a PhD in a relevant subject area (awarded within the past eight years) and, ideally, some postdoctoral experience. You will have a proven aptitude for delivering excellent science publications and demonstrated potential to raise research income. You will be an outstanding and enthusiastic communicator who is ready to engage with students, peers and the general public.

Fellowships are offered for three years, with a potential extension to five years dependent on performance.

The salary will be up to \$33,132 per annum, depending on skills and experience.

Closing Date: April 8th, 2018

Further information: <https://careers.kew.org/vacancy/early-career-research-fellowships-344760.html> Dr. Ester Gaya Senior Research Leader | Comparative Fungal Biology Jodrell laboratory Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, UK Tel.:+44(0)208 332 5381 Fax:+44(0)208 332 5310 www.kew.org Email: EGaya@kew.org/ ester.gaya@gmail.com

Ester Gaya <E.Gaya@kew.org>

RutgersU TeachingEvolution

Position Information: Recruitment/Posting Title Teaching Instructor

Department FASN - Biological Sciences

Salary Open

Posting Summary The Department of Biological Sciences, Rutgers University-Newark (RU-N) seeks to hire a full-time, non-tenure track member at the rank of Teaching Instructor. The candidate is expected to have a Ph.D. degree in Biology and should be able to demonstrate excellence at lecture and laboratory course instruction and development. The successful applicant will be expected to develop at least one introductory biology major course, teach a more advanced lecture/lab course, and participate in additional undergraduate teaching.

Qualifications Minimum Education and Experience Ph.D. in Biology

Posting Details Posting Number 18FA0056

Posting Open Date 02/12/2018 Posting Close Date 03/05/2018

Special Instructions to Applicants Please provide the following; 1. Cover letter; 2. Curriculum Vitae; 3. Two letters of recommendation; 4. Statement of Teaching Philosophy; 5. Research Statement; 6. Example(s) of course syllabi

Quick Link to Posting <http://jobs.rutgers.edu/postings/60104> Campus Rutgers University-Newark Home Location Campus Rutgers University-Newark

Affirmative Action/Equal Employment Opportunity

Statement It is university policy to provide equal employment opportunity to all its employees and applicants for employment regardless of their race, creed, color, national origin, age, ancestry, nationality, marital or domestic partnership or civil union status, sex, pregnancy, gender identity or expression, disability status, liability for military service, protected veteran status, affectional or sexual orientation, atypical cellular or blood trait, genetic information (including the refusal to submit to genetic testing), or any other category protected by law. As an institution, we value diversity of background and opinion, and prohibit discrimination or harassment on the basis of any legally protected class in the areas of hiring, recruitment, promotion, transfer, demotion, training, compensation, pay, fringe benefits, layoff, termination or any other terms and conditions of employment. For additional information please see the Non-Discrimination Statement at the following web address: <http://uhr.rutgers.edu/non-discrimination-statement> Jessica Ware <jware42@newark.rutgers.edu>

SanFranciscoStateU DirectorGenomicsFacility

The Department of Biology in the College of Science & Engineering at San Francisco State University is searching for a Director for the Genomics/Transcriptomics Analysis Core (GTAC) Facility, effective immediately.

The Director will independently carry out multiple tasks in the areas of scientific research, grant program administration, and work related to the day-to-day operation of the GTAC Facility in the Department of Biology and provide support to the Gene Lab facility at the Estuary & Ocean Science (EOS) Center at the Romberg Tiburon Campus. Duties will include training new users in the proper use and care of research equipment, developing and conducting research experiments with facility users, providing scientific and technical assistance to facility users with their research projects, and aiding in the writing of equipment grants and in the development of research grants. The successful candidate will also be responsible for maintaining lab equipment, carrying out the administrative duties of the facility, and supervising facility personnel, including student assistants and research technicians.

The mission of the Department of Biology is to provide an outstanding education, at the graduate and undergraduate levels, preparing the next generation of leaders

in the field and ensuring the nation's future with a science-literate, educated public. We are committed to serving the needs of a student population with diverse backgrounds and goals, a geographic region rich in ecological complexity, and a community operating at the forefront of basic science, biotechnology and medicine.

Anticipated hiring range for this full-time position is \$6,082 - \$6,758 per month, commensurate with experience. SF State offers a competitive compensation package that includes Medical, Dental, Vision, Pension, 401k, Healthcare Savings Account, Life Insurance, Disability Insurance, Vacation and Sick Leave as well as State Holidays and a dynamic Fee Waiver program.

To apply, please submit an application for job #9776 at https://hr.sfsu.edu/Employment_HRMS/-employment/jobs. This position is open until filled.

Dr. Gretchen Le Buhn lebuhn@sfsu.edu

Director Great Sunflower Project
www.GreatSunflower.org Professor Biology San
 Francisco State University

Gretchen LeBuhn <lebuhn@sfsu.edu>

SGN Frankfurt Biodiversity Genomics

Sehr geehrte Damen und Herren,

anbei finden Sie eine Stellenausschreibung mit der Bitte um Veröffentlichung auf Ihrem Jobportal.

Vielen Dank!

Job offer ref. #12-18003

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.

In this LOEWE-TBG project, we want to assess, how

anthropogenic substances influence the mutation rate of metazoan organisms. Based on an existing genome-wide mutation rate test, we thus want to develop and introduce new ecotoxicological assessment methods that will be eventually internationally established within the ISO framework. Furthermore, the project will significantly increase our knowledge on the mutation process as such. It is planned to work with several ecotoxicological model species such as *Chironomus riparius*, *Daphnia galeata*, *Eisenia fetida* and *Folsomia candida*.

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

Evolutionary Biologist Ecotoxicologist/Bioinformatician (100%)

Your tasks: -Performing, respectively coordinating ecotoxicological experiments with partners - Improving existing bioinformatics workflow - Analysing individual reseq data - Publishing the results

Your profile: - Population genomic experience with individual resequencing data (mapping to reference genome, genotype calling, awareness of data quality issues etc.) - Experience with ecological/ecotoxicological experiments - Programming and/or scripting experience to adjust/improve existing bioinformatic pipelines - Ability to work in close collaboration with several partners - Excellent communication skills

What is awaiting you? - An interesting task in a dynamic team of researchers in an internationally research institution - The opportunity to gain experience in the above-mentioned research field - The occasion to build a network with scientists in interdisciplinary fields - Flexible working hours - annual special payment - company pension scheme - Senckenberg ID card for free entry in museums in Frankfurt - 30 days holidays 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 be limited until December 31st, 2021. 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. # 12-18003) before April 15th, 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

recruiting <recruiting@senckenberg.de>

UAntwerp EvolEcolEnvOmics

Research professor, area of Evolutionary, Ecological and Environmental Omics - 2018ZAPFWETEX015

Deadline for application: 25 March 2018 <https://www.uantwerpen.be/en/jobs/vacancies/ap/-2018zapfwetex015/> As part of its dynamic research policy and supported by the possibilities offered by the Flemish Government through the resources of the Special Research Fund (BOF), the Faculty of Science is seeking to fill a full-time vacancy in the Department of Biology for a

Research professor (TTZAPBOF) in the area of Evolutionary, Ecological and Environmental Omics

The molecular instrumentation of an organism determines its capacity to handle natural and anthropogenic challenges, and is continuously under selective pressure. Knowledge concerning the molecular and cellular events is therefore vital to understand the evolutionary processes and constraints leading to adaptation to natural and anthropogenic stressors in vertebrate and invertebrate species, as well as the factors that make the difference between success and failure on the organismal and population level. The latest technological developments create exciting opportunities to identify these molecular pathways and adaptations through (epi)genomics, transcriptomics and proteomics.

These approaches allow to search for patterns of genetic variation, signatures of selection and to unravel the molecular processes that control adaptation and physiological fitness. These processes can only be understood when applying an integrated approach that is embedded in a physiological, evolutionary and environmental context. The research profile complements the present expertise in the Department of Biology, which strongly focuses on the evolutionary, ecophysiological and ecotoxicological processes of adaptation.

We seek to hire an ambitious researcher with a strong and preferably combined background in the fields of evolutionary biology, environmental physiology and toxicology, applying “omic” approaches to study evolutionary, genetic and demographic processes in natural popula-

tions and/or model species in relation to environmental stress. The candidate is expected to develop strong collaborative and complementary links with available expertise and to strengthen the department’s research capacity within these domains. The research should lead to novel fundamental insights in the study of adaptation of natural vertebrate and/or invertebrate populations in response to natural or anthropogenic stressors (e.g. global change, environmental pollution).

Job description

The assignment consists of lecturing duties, scientific research and academic service to society. During a period, limited to five years (duration of the temporary appointment in tenure track), scientific research will be the main activity.

- You will expand the scientific research in the area of evolutionary, ecological and environmental omics as outlines above.
- You will acquire and manage external funding (national and international).
- You will supervise doctoral students.
- You will offer scientific services: among others you take part in further developing and managing the omics based analytical platforms.
- You will be assigned limited lecturing duties within the domain not exceeding 30 contact hours per semester.

Profile and requirements

- You hold a doctorate degree (PhD) in Biology or a related discipline.
- You have a minimum of 2 year experience on Postdoctoral level at the closing date of the vacancy.
- You have an international academic CV and perform qualitatively outstanding academic research in the broader field according to the domain involved.
- You have experience in grant application and project management.
- The focus in your teaching corresponds to the educational vision of the university.
- Your academic qualities comply with the requirements stipulated in the university’s policy.
- You have leadership skills (or the potential to develop them).
- You are quality-oriented, conscientious, creative and cooperative.
- You can meet the statutory language requirements for both the knowledge of the teaching language and the administrative language, Dutch. The University of Antwerp provides the necessary support.

We offer

- a full-time position as a lecturer in a temporary appointment in the tenure track for a term of five years. This position will lead to an immediate permanent appointment as a senior lecturer if the performance is assessed favourably on the basis of previously fixed and publicly announced evaluation criteria;
- in case of equal qualifications, priority will be given to candidates of the underrepresented gender within the domain of science.

This priority is not automatically and unconditionally; as

— / —

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>

UCalifornia Berkeley ResAssist TreeAdaptation

Richard Dodd's Research Group in the Dept. of Environmental Science Policy and Management at the University of California, Berkeley is seeking applicants for a plant molecular biology research specialist position. This will be a 3-year appointment to work with Professor Dodd on the application of gene editing technology to address adaptation of trees to climatic stress. Applications should be submitted to <https://aprecruit.berkeley.edu/apply/JPF01654> by March 13. Questions regarding the position can be addressed to Prof. Richard Dodd, dodd@berkeley.edu.

Richard DODD <dodd@berkeley.edu>

UConnecticut 2 ResTech EvolutionaryImmunology

Two Research Technician positions are available in Dr. Daniel Bolnick's research group in the Department of Ecology and Evolution at the University of Connecticut (<https://bolnicklab.wordpress.com>).

Tasks: The technicians will be funded by a National Institutes of Health grant to study evolutionary immunology and genetics of a vertebrate host's resistance to a helminth parasite, and parasite evasion of host immunity. Previous work by the Bolnick lab identified naturally evolved variation in stickleback fishes' resistance to a severe cestode parasite (Weber et al 2017 American Naturalist; Weber et al 2017 Proceedings of the National Academy of Sciences). The technicians will contribute to this research by assisting with fish care, experimental infection and immune challenge assays,

molecular genetics lab work, transgenic experiments, cell culture, and immune assays. The technicians will also assist with maintaining a stocked and organized laboratory. Some field research on Vancouver Island, British Columbia, will also be an option. These research tasks will be partitioned between two technicians according to their areas of interest and expertise.

Duration: The positions are annual contracts that can be extended for up to four years subject to annual performance reviews. The technicians should be able to start in summer or fall 2018, exact dates to be negotiated with the PI.

Compensation: Starting salary will be between \$30-\$35,000 depending on experience, plus health benefits.

Qualifications: Applicants must have a BS, BA, or MA degree in biology or a closely related field. Prior experience with molecular genetics, immunology, and/or fish care is a plus. Previous research experience and work records should demonstrated a commitment to research, good work ethic, lab skills, and organizational ability.

Applications should electronically submit a single pdf file containing the following, in order: 1) Coverletter, including a summary of research experience and career goals 2) CV 3) List of three references, with contact information (email, telephone, and mailing address). We will request letters directly from these references, after identifying top candidates.

The application file should be emailed to Dr. Daniel Bolnick (daniel.bolnick@uconn.edu). Include the subject line "Research Technician Application: <YOUR NAME>". Applications must be received by April 2, 2018 for full consideration, though the position is open until filled.

For questions about this position, please email Dr. Bolnick (daniel.bolnick@uconn.edu). For information about the Bolnick Lab (presently at the University of Texas, moving to Connecticut this summer), visit the lab website (<https://bolnicklab.wordpress.com>), lab photostream (<https://www.flickr.com/photos/98765823@N08/albums>), and Dr. Bolnick's Google Scholar page (<https://scholar.google.com/citations?user=cfwxm0AAAAAJ&hl=en>).

The University of Connecticut is an Equal Opportunity Employer. Applicants with questions about disability services can privately discuss their application with the University of Texas Disability Services Office (<http://sites.utexas.edu/disability/>). The Bolnick Lab is simultaneously searching for postdoctoral researchers. With multiple positions open, this advertisement may be of interest to dual career couples.

Dr. Daniel I. Bolnick

Editor-In-Chief, The American Naturalist Professor, Department of Integrative Biology, University of Texas

Mailing Address: One University Station C0990, University of Texas at Austin, Austin, TX 78712

512-471-2824 Preferred email: danbolnick@austin.utexas.edu

Lab website: <https://bolnicklab.wordpress.com> "Bolnick, Daniel I" <danbolnick@austin.utexas.edu>

UDebreceen EvolutionaryBiol

Dear All,

The Department of Evolutionary Zoology at the University of Debrecen, Hungary (<http://zoology.unideb.hu>) will have a new job opening in October 2018. We are seeking promising candidates to apply.

What we are looking for:

- a dedicated and highly motivated researcher working in any field of zoology and/or evolutionary biology - strong international research experience either at the PhD student or postdoc level - fluent to teach in Hungarian and in English

What we can offer:

- a permanent position (after a one-year probation period) - a vibrant and diverse research community - a rapidly developing, liveable city

For further information please contact Prof. Zoltan Barta, Head of the Department, at barta.zoltan@science.unideb.hu. Please send your CV, list of publications and a short (max one page) statement of your proposed research programme.

Sincerely yours, Zoltan Barta

Zoltan Barta MTA-DE Behavioural Ecology Research Group Department of Evolutionary Zoology, University of Debrecen, Debrecen, Egyetem ter 1., 4032, Hungary Phone: +36 52 316 666 ext. 62334 | Fax: +36 52 512 941 E-mail: barta.zoltan@science.unideb.hu | <http://web.unideb.hu/~zbarta/> Zoltan Barta <barta.zoltan@science.unideb.hu>

UGlasgow ViralEvolution

We've a bioinformatician/computational biologist post to offer at to join our virology-focussed bioinformatics team and enhance the research activities of the MRC-University of Glasgow Centre for Virus Research (CVR) (<http://www.cvr.ac.uk/>).

The postholder will work with us to support researchers and carry out independent computer-based research. This will involve performing data analysis and developing novel analytical approaches for viruses, virus-host interaction data sets and the study of viral evolution. Candidates with a background in bioinformatics, computational, systems or evolutionary biology, computer science, biostatistics and/or machine learning are encouraged to apply. We welcome applications from early career bioinformaticians.

The position is funded until 31 March 2021 in the first instance. Salary will be on the University's Research and Teaching Grade, level 6/7 depending on experience, 28,098 - 31,604/34,520 - 38,833 per annum. Informal enquires should be directed to Prof David Robertson, david.l.robertson@glasgow.ac.uk. Interested applicants should apply on-line at <http://www.glasgow.ac.uk/jobs> and seek reference no. 018901 by 11th March 2018.

[University of Glasgow: The Times Scottish University of the Year 2018]

David Robertson <David.L.Robertson@glasgow.ac.uk>

UHelsinki Bioinformatician

Bioinformatician

University of Helsinki, Finland

The Organismal and Evolutionary Biology Research Programme at the University of Helsinki has an open Bioinformatics position. The bioinformatician will join the research groups of Dr Marjo Saastamoinen (<http://www.helsinki.fi/life-history-evolution>) and Prof. Anna-Liisa Laine (<https://allaine.it.helsinki.fi/>).

The position will be focused on the genomics analyses carried out within the Glanville fritillary (*Melitaea*

cinxia) butterfly genome sequencing project and the ribwort plantain (*Plantago lanceolata*) genome and transcriptome projects. The successful applicant has completed MSc or PhD in relevant field, and has previous experience with the analysis of next generation sequencing data.

The position can be filled immediately but no later than 1st of June 2018 for a fixed term until the end of June 2019.

Closing Date: March 25th 2018.

Further information: <https://www.helsinki.fi/en/open-positions/bioinformatician-the-organismal-and-evolutionary-biology-research-programme>

Virpi Ahola virpi.ahola@helsinki.fi

“Ahola, Virpi M” <virpi.ahola@helsinki.fi>

UKansas 1yr EvolutionaryGenetics

The Department of Molecular Biosciences, University of Kansas, seeks an assistant researcher with interests and experience in molecular biology and *Drosophila* husbandry. The successful candidate will work with on genomic, genetic and evolutionary aspects of selfish genetic elements using *Drosophila*. Projects include, but are not limited to CRISPR genome editing, fluorescence microscopy and *Drosophila* mating experiments. This position consists of an initial 1-yr appointment beginning in May 2018. The applicant should be extremely organized, work well with others, have a willingness to learn, and be able to participate at many levels in the laboratory.

For a complete announcement and to apply online, go to <https://employment.ku.edu/staff/11467BR>. A complete online application includes the following materials: CV, Cover letter, contact information for three reference letters. Initial review of applications begins April 15, 2018 and will continue as long as required to identify a qualified pool. Contact Rob Unckless (unckless@ku.edu) for more information.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the university’s programs and activities. Retaliation is also prohibited by university policy. The following

persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Executive Director of the Office of Institutional Opportunity & Access, IOA@ku.edu, 1246 West Campus Road, Room 153A, Lawrence, KS 66045, 785-864-6414, 711 TTY (for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses); Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

“Unckless, Robert L” <unckless@ku.edu>

UNAM Mexico EvolutionaryFunctionalGenomics

The Universidad Nacional Aut  noma de M  xico (UNAM) invites applications to fill a tenure-track Assistant Professor position in Comparative Animal Genomics at the Instituto de Ecolog  a.

Located in the main campus of UNAM to the South of Mexico City, the Institute of Ecology (<http://web.ecologia.unam.mx/>) harbours 40 researchers grouped in four Departments: Evolutionary Ecology, Functional Ecology, Ecology of Biodiversity, and the National Laboratory for Sustainability Sciences. It is a leading Ecology Institute in Mexico and has strong links with similar Institutes both within Mexico and abroad.

We are searching for an independent researcher in Evolutionary and Functional Genomics willing to collaborate with the members of the Department of Functional Ecology and of the Institute in general.

The successful candidate will be required to develop an independent research program in Evolutionary and Functional Genomics. It will be expected that she/he develops collaborations, primarily but not exclusively with members of the Departamento de Ecolog  a Funcional. Lecturing regularly at undergraduate and graduate programmes is compulsory.

Candidates should hold a PhD degree, or equivalent, on Biology or Ecology, and be competent or the study of genome function and evolution. To be considered, an applicant must have a strong publication record (> 20 high-impact peer-reviewed papers in the relevant area), a track record of securing competitive funds, and demonstrable experience teaching and supervising students. Ability to teach in Spanish is expected.

Selection will be based 1) on the strength of the candidate's CV, 2) on a written research proposal (only the outline is needed) combining the study of evolutionary and functional genomics, and 3) on the merits of a work program specifying the research (including collaborations with local colleagues), teaching and supervision activities to be conducted in the following three years.

The application should include a letter addressed to the director of the Institute, Dr Constantino MacÍas Garcia stating the candidate's reasons to apply, Curriculum vitae, a brief description of current and future research interests, the proposal and work plan specified above, a copy of the PhD title, birth certificate and the documents supporting the CV (only the first page of published papers, letters/e-mails indicating that papers have been accepted for publication), and evidence of theses supervision.

All documents should be sent electronically as a single PDF file to secacad@iecologia.unam.mx. Applications will be received from the 20th of March till the 20th of April 2018. Shortlisted candidates will be required to send the documents by post to: Instituto de Ecología, UNAM, Ap. Postal 70-275, Ciudad Universitaria, Ciudad de México, CP 04510, México.

Constantino MacÍas Garcia <maciasg@unam.mx>

uOttawa QuantitativeBiology

TENURE-TRACK POSITION IN QUANTITATIVE BIOLOGY Department of Biology, University of Ottawa

Applications deadline: March 15

The Department of Biology at the University of Ottawa is hiring a tenure track Assistant Professor in quantitative biology whose research focuses on the development or application of statistical approaches to addressing complex biological questions. We are particularly interested in candidates who would complement and extend our existing strengths in evolution, ecology, genomics, and statistical genetics. The successful applicant is expected to develop an internationally-recognized research program and to contribute to undergraduate and graduate training. Preference will be given to candidates who can teach biostatistics at the undergraduate and graduate level in French and English.

The successful candidate will join an innovative and collaborative department of over 40 researchers working in all fields of biology including biodiversity, computa-

tional biology, cell and molecular biology, developmental biology, ecotoxicology, evolutionary biology, and physiology. The Department maintains close connections and collaborations with researchers in the Ottawa region including federal government science departments, the Ottawa Hospital Research Institute, the Canadian Museum of Nature, and Carleton University. The Faculty of Science supports several core facilities including a Molecular Biology and Genomics Laboratory to provide access to advanced molecular biology/genomics equipment. Access to high-performance computing and data storage is available through Compute Canada. —

Application deadline: Review of applications will begin March 15, 2018 and will continue until the position is filled.

For additional details see the full job posting here: <https://www.uottawa.ca/vice-president-academic/-faculty-affairs/faculty-recruitment/openings> (click on 'Faculty of Science') To appear in Nature shortly.

hrundle@uottawa.ca

UPennsylvania ResProf PDF HumanGenomics

Human Population Genomics Postdoctoral/Research Assistant Professor Positions at the University of Pennsylvania

The Tishkoff lab at the University of Pennsylvania is seeking candidates at either the postdoctoral or Research Assistant Professor level for population genomics positions. We are integrating genomic, transcriptomic, metagenomic, metabolomic, and epigenomic datasets generated from a large sample of ethnically diverse Africans. We use evolutionary, statistical, and population genetics approaches to understand the genetic architecture of a number of anthropometric, cardiovascular, metabolic, and immune related traits for which we have detailed phenotype data. We are also interested in inferring the demographic history of African populations, determining the genetic basis of adaptation during human evolutionary history, and characterizing the evolution of gene regulation in humans. We are applying functional genomics approaches to determine the impact of candidate causal variants on gene regulation and chromatin interaction. Candidates will have an opportunity to participate in a large NIH collaborative effort involving analysis of whole genome sequence data from over 100,000 participants. Candidates will also

have an opportunity to develop creative, independent projects. There will be opportunities to work together with an outstanding team of collaborators with expertise in statistical and population genetics including Iain Mathieson, Yoseph Barash, Ben Voight, Casey Brown, Yun Song, Hongzhe Li, Scott Williams, Eleazar Eskin, Josh Akey, and Sharon Browning.

The ideal candidates will have skills in computer programming (PERL and/or Python and/or C++) and using statistical environments (R/MATLAB) as well as expertise in population genetics theory and/or quantitative analyses of complex traits. Experience with large genome-scale datasets is a plus. Candidates for the Faculty Research Assistant Professor position must have a proven track record of productivity. They will be expected to show independence, have excellent writing skills, willingness to apply for grant funding (with opportunities to be PI on grant applications) and willingness to help supervise graduate students. The Research Assistant Professor position is conditional upon approval by the Department of Genetics at UPenn. Salaries are commensurate with qualifications and experience.

The Department of Genetics is centrally located at the School of Medicine within the UPenn campus and is within short walking distance to the Children's Hospital of Pennsylvania as well as the Departments of Biology, Computer Science, Bioengineering and Anthropology located on the main campus. Outstanding core facilities are available for high throughput sequencing, genotyping, and gene expression studies and for bioinformatics and computational biology analyses. Philadelphia is a vibrant city with excellent cultural events and plenty of parks and hiking/biking trails. It is also centrally located between New York City and Washington DC, with easy access via a short train or bus ride.

Candidates should send curriculum vitae, a statement of interest, and contact information for three references via e-mail to Dr. Sarah Tishkoff, Departments of Genetics and Biology, University of Pennsylvania, tishkoff@pennmedicine.upenn.edu. The starting dates of positions are flexible.

Dr. Sarah Tishkoff Departments of Genetics and Biology University of Pennsylvania tishkoff@pennmedicine.upenn.edu <http://www.med.upenn.edu/tishkoff/> "Tishkoff, Sarah" <tishkoff@pennmedicine.upenn.edu>

URhodeIsland ResTech Genomics

The shared lab of Carlos Prada (<https://www.carlosprada.org>), Jon Puritz (marineevoeco.com) and Hollie Putnam (putnamlab.com) at the University of Rhode Island is currently looking for a lab technician. This is a full time position available for one year with the possibility of renewal. The ideal candidate will have recently completed a Bachelor's in a biological science, and have experience in both molecular lab techniques as well as marine field work experience.

For more information and to apply, please follow this link: <http://jobs.uri.edu/postings/3211> Please feel free to contact any of the PIs for more information.

X Jon Puritz, PhD

Assistant Professor Department of Biological Sciences
University of Rhode Island 120 Flagg Road, Kingston,
RI 02881

Webpage: MarineEvoEco.com

"The most valuable of all talents is that of never using two words when one will do." -Thomas Jefferson

Jonathan Puritz <jpuritz@uri.edu>

URichmond 1yr EvolutionBiology

The Department of Biology at the University of Richmond seeks to fill two full-time visiting faculty positions (non-tenure track) for the 2018-19 academic year, beginning August 2018 and ending May 2019. Both positions have the possibility of renewal for a second year. We are looking for broadly-trained biologists with expertise in cellular/molecular biology, ecology/evolution, and/or interdisciplinary training spanning both concept areas. Applicants should demonstrate a strong commitment to high quality undergraduate education and an interest in teaching at a primarily undergraduate institution (PUI).

The positions entails teaching four units per term, including introductory level courses with lab (where lecture and lab each count as one unit) and upper level electives in the candidate's area of expertise. Research space and

access to equipment may be made available based on synergy with existing faculty research programs. Applicants must have a Ph.D. in hand by August 20, 2018.

Applicants should click “Apply Now” at the top of the page (bitly.com/2Ft90XU) and upload a cover letter, a statement that addresses their teaching experiences and their vision for being a teacher-scholar at a PUI, a current curriculum vitae, and the names of three references who can address teaching effectiveness and potential. References will be contacted once a short-list of candidates is made. Review of applications will begin immediately and qualified applicants will be considered until the position is filled. Questions concerning the position and application process should be directed to Dr. Omar Quintero (oquinter@richmond.edu).

The University of Richmond is committed to developing a diverse workforce and student body, and to modeling an inclusive campus community which values the expression of difference in ways that promote excellence in teaching, learning, personal development, and institutional success. We strongly encourage applicants address how they envision contributing to these goals in their application materials. We are especially interested in recruiting individuals who have interest or experience in broadening access and inclusivity in STEM disciplines (Integrated Inclusive Science) which aligns with the University’s strategic plan (<https://strategicplan.richmond.edu/>). For more information on the department, see <http://biology.richmond.edu/>. The Department of Biology is housed in the Gottwald center for the Sciences, which also houses the Departments of Chemistry and Physics and had an extensive renovation/expansion of laboratory and teaching facilities completed in 2005. Approximately 50 biology majors graduate each year, many of whom go on to attend top graduate and medical schools. Members of the Department of Biology have access to two University-owned field sites that are approximately 15 and 45 minutes away from campus.

R. Jory Brinkerhoff, Ph.D. Associate Professor Department of Biology, University of Richmond Richmond, VA 23173 804-484-1592 jbrinker@richmond.edu

Honorary Senior Lecturer School of Life Sciences, University of KwaZulu-Natal Pietermaritzburg, South Africa
“Brinkerhoff, Jory” <jbrinker@richmond.edu>

UScranton EvolutionaryBiol

ASSISTANT PROFESSOR Department of Biology The University of Scranton

The Biology Department of The University of Scranton is seeking applications for a tenure-track position at the level of Assistant Professor in ecology/environmental biology/evolution to begin August 2018. The area of specialization within these disciplines is open; however, we are particularly interested in applicants with expertise in evolutionary ecology, behavioral ecology, population ecology, microbial ecology, or molecular ecology. Applicants should be able to contribute to the Biology Department’s core courses as well as to the Environmental Science Program and will be expected to develop upper level courses in their specialties. Excellence in teaching and an active research program that involves mentoring undergraduates is expected. A Ph.D. is required by start date and postdoctoral experience is preferred.

The Biology Department is housed in a new state-of-the-art unified science center, <http://www.scranton.edu/academics/sciencecenter>. Visit <http://www.scranton.edu/academics/cas/biology/> for more information about the Biology Department and <http://admissions.scranton.edu/academic-programs/-majors-minors/programs/environmentalscience.shtml> for more information about the Environmental Science Major.

The University of Scranton is a regional institution of more than 5,000 undergraduate and graduate students located in northeast Pennsylvania near the Pocono Mountains. Recognized nationally for the quality of its education, Scranton is one of the 28 Jesuit colleges and universities in the United States. It is committed to providing liberal arts education and strong professional and preprofessional programs in the context of Ignatian educational principles, especially the care and development of the whole person. Drawing on the strengths that have made it a recognized leader in the Northeast, Scranton is committed to a culture of scholarship and excellence, and is moving into the front ranks of American’s comprehensive universities.

The University of Scranton is, by tradition and choice, a Catholic and Jesuit university. The successful candidate will have an understanding of and commitment to the mission and the goals of Jesuit education. The University’s mission statement and a description of the history

and aims of the Ignatian teaching philosophy may be found at <http://www.scranton.edu/mission>. The University is committed to developing a diverse faculty, staff, and student body and to modeling an inclusive campus community which values the expression of differences in ways that promote excellence in teaching, learning, personal and professional development, and institutional success. In keeping with this commitment, the University encourages applications from candidates with diverse backgrounds.

The University of Scranton is an EOE employer/educator. We encourage women, persons with disabilities, veterans and others from underrepresented groups to apply.

How to Apply Interested applicants must apply online at <https://universityofscrantonjobs.com>. The application must include (1) a cover letter, (2) a current curriculum vitae, (3) a statement of teaching philosophy (4) a statement of research interests, (4) three letters of reference, and (5) selected publications.

For questions regarding this position, please contact Dr. Robert Smith or Dr. Janice Voltzow, Co-Chairs of the Search Committee, via email at robert.smith@scranton.edu and janice.voltzow@scranton.edu. Review of applications will begin March 23, 2018, and will continue until the position is filled.

“Anne M. Royer Ph.D.” <anne.royer@scranton.edu>

UTennesseeKnoxville HerbariumCollectionsManager

Job: UTennesseeKnoxville.HerbariumCollectionsManager

The TENN herbarium in the Department of Ecology and Evolutionary Biology at the University of Tennessee - Knoxville is seeking a highly organized, detail-oriented individual to join our department as the Herbarium Collections Manager. This key team member oversees the day-to-day management, preservation, and accessibility of our plant and fungal biodiversity collection, which includes specimen curation, record keeping, and monitoring specimen inflow/outflow. In addition, the Herbarium Collections Manager leads a team of undergraduate students and volunteer assistants with specimen curation and scientific outreach projects. The Herbarium Collections Manager reports to the TENN Herbarium Director, Dr. Jessica M. Budke, and col-

laborates with the Director and Curators to plan and implement herbarium goals, priorities, and programs.

The TENN herbarium houses over 600,000 plant and fungal specimens and is one of the largest collections in the southeastern United States. The Herbarium Collections Manager supports research in the herbarium focusing on taxonomy, systematics, invasive species, conservation of rare plants/fungi, and field botany/mycology. For more information on our collection, see the TENN herbarium website - <http://tenn.bio.utk.edu/> Duties and Responsibilities -

Will include but are not limited to:

1. Oversee the day-to-day management, preservation, and accessibility of this biodiversity collection, which includes specimen curation, record keeping, and monitoring specimen inflow/outflow.
2. Hire, train, schedule, and supervise members of the public as herbarium volunteers and undergraduate student curation technicians to carry out tasks such as label making and mounting, filing, imaging, databasing, and georeferencing specimens.
3. Respond to inquiries from members of the university community, visiting scientific researchers, governmental and consulting agencies, and members of the public.
4. Perform outreach and science communication through herbarium social media pages/feeds.
5. Conduct tours for visiting scholars, students, and the public.
6. Manage the TENN website to share plant information with internet users worldwide.
7. Upload data to and manage online databases containing information on specimens in the TENN collection.

Qualifications -

1. Master's degree or PhD from an accredited university in Plant Sciences, Botany, Ecology, Biology, Horticulture, or related field is required.
2. Previous herbarium/botanical experience (1-3 years) is required.
3. Knowledge of botanical museum principles, practices, and procedures is required.
4. Strong interpersonal communication skills with the ability to lead a team of volunteer and student assistants to complete collection management projects are required.
5. Sound reasoning, analytical thought, attention to detail, creativity, high levels of organization, and innovation in solving minor problems that occur day to day are required.

6. Proficiency with computer software (e.g., Word, Excel, Photoshop, Dreamweaver) is required.
7. Ability to learn new programs to manage and maintain websites/databases as needed.
8. Previous experience with plant/fungal taxonomy and knowledge of plant/fungal families and genera are preferred.
9. Excellent verbal and written communication, including experience communicating through social media (i.e., Twitter, Facebook), is preferred

This is a full-time (12-month), permanent position with health and retirement benefits. Initial appointment for one year starting July 2018, with extension pending positive performance evaluations. Salary commensurate with education and experience.

Please submit a cover letter, resume/CV, and contact information for three references as a single document when applying. Application review will begin April 19, 2018 and continue until the position is filled. To be considered, all applications must be submitted online. https://ut.taleo.net/careersection/ut_system/jobdetail.ftl?job000000DM&tz=GMT-04%3A00

Job

Academic and Instructional Support

Primary Location

USA-Tennessee-Knoxville

Organization

Ecology and Evolutionary Biology

Schedule

Full-time

Campus/Institute Knoxville

Jessica Budke <jbudke@utk.edu>

Worcester MA VisitingProf 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 appli-

cation 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, 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

“Ober, Karen” <kober@holycross.edu>

Other

BotanyConferences UndergradTravelAwards	64	Software Multitest upgrade	69
FrancePyrenees VolFieldAssist LizardBehaviour Apr-Jun	65	Software NewRelease BALi-Phy3 0	69
JoeFelsenstein Talk FundamentalTheorem	65	SouthAfrica VolResAssist Behaviour	69
MilnerPrizeLecture	66	SyracuseU UGSummerResearch Coevolution	70
Minion availability	66	Trinidad Internship GuppyEvolution	71
Namibia Baboon VolFieldWork	66	ULausanne SIBVirtualSeminar JeromeGoudet February28	71
PlantTaxonomists BotanySoc LeadershipAward . . .	67	US NatlMedalScience CallNominations	71
Pyrenees VolFieldAssist EvolBiol	68		

BotanyConferences UndergradTravelAwards

Subject:— Undergraduate Travel Awards:— Enhancing Diversity at the Botanical Society of America Conferences

PLANTS Grants Preparing Leaders and Nurturing Tomorrow’s Scientists Undergraduate Travel Awards:— Enhancing Diversity at the Botanical Society of America Conferences The PLANTS program (Preparing Leaders and Nurturing Tomorrow’s Scientists: Increasing the diversity of plant scientists) will fund up to 12 talented and diverse undergraduates to attend the BOTANY 2018 meeting on July 21-25, 2018 in Rochester, Minnesota. Topics range across all aspects of botany includ-

ing ecology, conservation, biodiversity, plant genomics, evolution, plant systematics, ethnobotany, and botanical education. There are also a number of social functions, specifically targeted at students for networking and fun. The meetings are a great way for undergraduates to understand the breadth of botanical research and education, to meet undergraduate and graduate students with similar interests, and to network with professionals in their area of interest. Students will receive mentoring from graduate students, postdocs and faculty/professionals, and participate in networking events including the Diversity Luncheon and career-oriented activities.— The program covers the normal costs of travel, registration, food and lodging at the meeting. Participants are required to attend the entire meeting, including several scientific talks per day with a mentor, as well as certain professional development and networking activities.— An overview of the scientific conference is available at: botanyconference.org APPLICATIONS: Applications are due by MARCH 15, 2018 and include completion of the online form (including a statement of interest, letter of recommendation, and unofficial transcripts). Applications are welcome from undergraduates from the US including Puerto Rico (we are unable to accept applications from international students) who have interest in plant sciences; the admissions goal is to increase the diversity of students interested in the plant sciences. The application form is located online at http://botany.org/Awards/F_PLANTS.php. Funding is provided by the National Science Foundation and Botanical Society of America,

CONTACTS: For further inquiries, please contact one of the organizers: Anna Monfils – anna.monfils@cmich.edu Heather Cacanindin — hcacanindin@botany.org

DEADLINE: extended to March 15, 2018

– Heather Cacanindin Interim Executive Director Botanical Society of America | Society for the Study of Evolution | Society for Economic Botany www.botany.org www.amjbot.org <http://www.bioone.org/loi/apps> www.plantingscience.org www.evolutionsociety.org www.econbot.org 314-577-9554

Heather Cacanindin <hcacanindin@botany.org>

FrancePyrenees VolFieldAssist LizardBehaviour Apr-Jun

We at the Ethology Lab of The University of Valencia (Spain) are looking for a voluntary field research assistant to get involved with our research on the functional significance of colour polymorphism in the common wall lizard **Podarcis muralis*.*

We are preparing an experiment to conduct in April-June 2018 at the Metatron experimental platform, associated to the Station d'Ecologie Théoretique et Expérimentale UMR5321 (<http://www.ecoex-moulis.cnrs.fr/>), in the french department of Ariège (Midi-Pyrenees).

Tasks will consist mainly on recording the behaviour of lizards held in semi-natural conditions within experimental enclosures. Accommodation and food are provided. The work will span from April 15th to June 30th.

We will review applications as they arrive. Please contact by email for further information and apply as soon as possible (at latest April 1st).

Dr Guillem Pérez i de Lanuza, Post-doc researcher at CIBIO-InBIO (University of Porto). e-mail: guillem.perez-lanuza@uv.es

Msc Javier Abalos, PhD candidate at University of Valencia, e-mail: jal4@uv.es

Javier Ábalos Álvarez <abalosjavier1347@gmail.com>

JoeFelsenstein Talk FundamentalTheorem

I have just posted Joe Felsenstein's (Bs Fisher Memorial) talk from the 2018 Population Genetics group meeting on

Is there a more fundamental theorem of natural selection? (B)

This can be found at the link here <https://youtu.be/ZF3nIMvBBDw> More about the Fisher Memorial Trust can be found here <http://www.senns.demon.co.uk/FisherWeb.html> and the Population Genetics group here

<http://populationgeneticsgroup.org.uk/> Adam Eyre-Walker

School of Life Sciences University of Sussex Brighton BN1 9QG

a.c.eyre-walker@sussex.ac.uk

386779 email: l.d.hurst@bath.ac.uk website: <http://people.bath.ac.uk/bssldh/LaurenceDHurst/Home.html>
Laurence Hurst <L.D.Hurst@bath.ac.uk>

MilnerPrizeLecture

Nominations are sought for the inaugural Milner Prize Lecture.

Candidates for the prize must be early career researchers in any field of evolutionary biology, who have begun their PhD study after January 1, 2011. In addition, nominees will be considered who are more than 7 years from the start of their PhD if they have had career breaks taken for family, caring or health reasons; the nature of the reason must be given. The nomination of the candidate may be by a colleague or self-nominated. The nominations should be sent as a single PDF file to Laurence Hurst, Director of the Milner Centre for Evolution (l.d.hurst@bath.ac.uk). The nomination should include a brief justification, the candidate's CV and list of publications (indicating three most significant papers), a short description of future research plans, and a letter from the candidate approving the nomination. A letter of reference from another colleague (or two in case of self-nomination) should be sent directly to Prof. Hurst.

Nominations and letters of support should arrive no later than May 15th, 2018. Please take care to limit the size of attachments (total < 10 MB) in any one email.

The nomination committee will evaluate the nominations and inform the winner approximately by the end of May 2018.

The prizewinner is expected to attend the Inaugural Conference of the Milner Centre for Evolution (18th-21st September 2018: <http://www.milnercentre.org>), where he or she will deliver the 2018 Milner Prize Lecture. The Milner Centre will cover registration, accommodation, and travel expenses (economy fare).

Laurence D. Hurst

Professor of Evolutionary Genetics Director of The Milner Centre for Evolution Department of Biology and Biochemistry University of Bath Bath Somerset, UK BA2 7AY

tel: +44 (0)1225 386424 fax: +44 (0)1225

Minion availability

Dear Colleagues,

I am interested in running 1-3 trial samples on an Oxford Nanopore Tech MINION, which has the advantage that one can directly sequence RNA with the need to creating cDNA. Their website says that some 6,000 users exist for this tiny, cheap (\$1,000) sequencer the size of a USB drive on which one can sequence hyperlong reads by threading the DNA or RNA strand thru a pore between two chambers. The different size and shape of the different bases lead to different changes in the voltages differential between chambers, allowing deducing the base sequence, as many will know. An even smaller sequencer, the Smidgeon is on the way. I was wondering if any one has a MINION and would be able to let me run a few trial samples or can recommend a genomics center. Areas of proximity for running things in person are New York and Denmark/ Germany/ France.

The equipment is ideal for many uses (detecting viruses in foods without the need for a priory expectations as to what one may find, same for analyses on viruses inside/partly inside micro/nanoplastics in tissues).

Best regards,

Else Fjordingstad PhD Biology (EEB)

Else Fjordingstad <Else.Fjordingstad@gmx.com>

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 re-

cruiting 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>

Plant Taxonomists Botany Soc Leadership Award

Link: <https://cms.botany.org/home/awards/special-funds-and-awards/botany-advocacy-leadership-grant.html>

“The Public Policy Committee is accepting applications for the Botany Advocacy Leadership Award for 2018. Please review the award details at THIS LINK. The award is only given to either BSA or ASPT members and is open to any level of botanical scientist or activist. Applications are due March 30th to our Awards Officer, Andrew Pais (alpais@ncsu.edu).

The American Society of Plant Taxonomists (ASPT) and the Botanical Society of America (BSA) are pleased to invite applications for the annual Botanical Advocacy Leadership Award. This award organized by the Environmental and Public Policy Committees of ASPT and BSA aims to support local efforts that contribute to

shaping public policy on issues relevant to plant sciences.

Examples of such efforts include: * Founding or expanding a native plant society or enhancing its activities. * Hosting a lecture series on plant conservation issues. * Leading campaigns or holding events that spread awareness of plant-related public policy issues (e.g., conservation of native species, control of invasive species, land use management). * Organizing local plant conservation events, such as removal of invasive species, planting a native garden, or restoration of native communities. * Traveling to meet with local or state representatives to lobby for legislation or other initiatives that benefit plant conservation, plant science research and education, or collections.

The recipient of this award will receive \$1000 to be used in the proposed project. They will be recognized at the annual Botany meeting during the awards ceremony. To apply, please send a one-page letter describing the proposed local efforts and their anticipated impact along with a basic one-page budget to show how the funds will be used. All active members of ASPT and BSA are eligible to apply. Applications are due March 30th, 2018 and should be sent as a single .pdf ("YourName.BALAapp.pdf") to Andrew Pais (alpais@ncsu.edu) with the subject line "2018 BALA application". The selected applicant will be notified by April 15th, 2018.

Awardees will be required to submit a brief summary of their activities with an image to the Plant Science Bulletin (PSB) by January 15th of the following year. This synopsis will appear in the March/April issue of the PSB and is intended to highlight the impact of the recipient's efforts in shaping public policy and awareness of plant-related issues. Inquiries about the award may be directed to the chairs of the EPPC for both societies: ASPT/BSA EPPC Awards Chair - Andrew Pais (alpais@ncsu.edu), BSA-Krissa Skogen (kskogen@chicagobotanic.org) and Kal Tuominen (ktuominen@jcu.edu), or ASPT-Ingrid Jordon-Thaden (ingrid.jordonthaden@wisc.edu)."

Morgan Gostel <gostelm@gmail.com>

Pyrenees VolFieldAssist EvolBiol

Field assistants summer 2018: Volunteer positions in evolutionary biology

Nick Barton's group at the Institute of Science and Technology (IST) Austria requires volunteers to assist with field work on plant speciation in the Pyrenees (Spain) this coming summer (late May - early August).

The project: We are studying the evolutionary dynamics underlying species diversification in the genus *Antirrhinum* (snapdragons). A major focus of this research involves field work on natural hybrid zones between two subspecies with different flower colours. Most of the field work is contributing to a long-term pedigree project aimed at establishing a direct link from genotype to phenotype to fitness. With 20,000 samples collected over eight generations (so far), this provides an exciting and powerful system to examine many outstanding questions in speciation and quantitative genetics in wild populations. We are seeking volunteers to assist with the field work, which involves working in teams mapping the location of individual plants (GPS), tagging and sampling them for leaves and flowers, measuring quantitative traits, phenotyping them for flower pigmentation and processing material for later DNA extraction. There may also be opportunities to be involved in other projects we are doing on plant-pollinator interactions, pollen fertility and community ecology surveys. Most of the work is outdoors, however we do spend some time indoors processing samples. The work is highly team orientated, typically in groups of 2-3 in the field and larger groups processing samples back at the research station. This is a great opportunity for anybody looking to obtain experience in field work relating to evolutionary biology, plant ecology and plant-animal interactions. You will also be part of a large multidisciplinary team including researchers from IST Austria, the University of Vienna, John Innes Centre (Norwich, UK) and the University of Toulouse.

The field site is located near Ripoll in a beautiful part of the Pyrenees of North Eastern Spain (Catalonia). We stay in comfortable apartments overlooking a picturesque valley, with close access to hiking trails and small villages. All food, accommodation and travel (within Europe) are covered. However, we cannot offer any further stipend.

For these positions we are looking for hard working and

enthusiastic biology students with a strong interest in working outdoors with plants. You must be meticulous with recording data and also be comfortable working as part of a team. Experience with field-based projects and plants is preferred but not essential.

We require assistance between late May and late July. Depending on the year and the plants, we may extend our time into August. Length of stay is flexible but a minimum stay of 3 weeks is required.

Please send any questions to Dr. Melinda Pickup via the email address below. How to apply? By the closing date of April 6th 2018, please send a statement of your background, CV, why you are interested and the length of time you would be available via email to: melinda.pickup@ist.ac.at

David Field <david.field@univie.ac.at>

Software Multitest upgrade

Dear all

For MultiTest users and those interested in procedures combining probabilities of independent tests, I have updated the notice for MultiTest with (I think) important clarifications. MultiTest implements the generalized binomial procedure of Teriokhin et al. (2007).

A zip file containing the executable with the new user guide is downloadable at <http://www.t-de-meeus.fr/-Multitest.html>. Any comments or suggestions are of course welcome.

All the best

Thierry

– Thierry de Meeus DR1 IRD, Bureau F 211 B UMR 177 IRD-CIRAD “INTERTRYP” TA A-17/G, Campus International de Baillarguet, 34398 Montpellier Cedex 5, France E-mail:thierry.demeus@ird.fr Web site <http://t-de-meeus.fr/TdeMeeus.html> France Tel: +33 (0)4 67 59 37 44; Fax: +33 (0)4 67 59 38 94 Cell: +33 (0)6 19 83 52 60 Burkina Cell: (+226) 76 86 40 88

Thierry de Meeus <thierry.demeus@ird.fr>

Software NewRelease BAli-Phy3 0

BAli-Phy version 3.0 is now available (<http://www.bali-phy.org>).

BAli-Phy is a Bayesian MCMC program for estimating—alignments and phylogenies simultaneously from unaligned sequence data.— Version 3.0 should be faster than version 2.3 and allows specifying priors.

The main new features in version 2.3 are: (<http://www.bali-phy.org/releases/3/>) - Up to 300% faster and 300% less memory. - Allow specifying priors and values for all model parameters. - Ancestral sequences with indels in sampled alignments. - 2D and 3D tree MDS convergence plots. - 'bali-phy help <topic>' for models, functions, distributions, and commands.

You can download binaries for Linux, Mac, and Windows here: - <http://www.bali-phy.org/download.php> Mac users can also install using homebrew.

You can read the updated manual here: - <http://www.bali-phy.org/README.xhtml>

An example of the output for ITS data: - <http://bali-phy.org/Examples/ITS/ITS1-TN-DP3-2/> If you have any trouble using bali-phy, please post your questions to bali-phy-users@googlegroups.com I should be able to respond fairly quickly.

-BenRI

Ben Redelings <http://www.ben-redelings.org> Benjamin Redelings <benjamin.redelings@duke.edu>

SouthAfrica VolResAssist Behaviour

Volunteer Research Assistant Position

We are looking for volunteer research assistants to carry out exciting experiments with captive Damaraland mole-rats, *Fukomys damarensis* at the Kuruman River Reserve, in the South African Kalahari Desert, and run through the University of Cambridge (UK).

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 for the daily running of experiments and will be involved in data collection and management. Other general tasks related to animal handling and husbandry and data handling will also be expected. Some 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 Vulliouid (philippe.vulliouid@gmail.com).

Shortlisted applicants will be invited for a Skype interview.

Deadline: 23th March 2018 (the positions will remain open until filled)

philippe.vulliouid@gmail.com

SyracuseU UGSummerResearch Coevolution

Summer Research Position: Evolutionary ecology of the yucca-yucca moth interaction

Syracuse University June 11, 2018 through August 3, 2017

We are seeking highly motivated undergraduates broadly interested in plant-insect interactions to assist with ongoing research examining the basis of plant host use by yucca moth species. The research includes recording pollination behavior, mating behavior, feeding by larvae, as well as measurement of insect morphology and plant morphology.

Student Experience: Students will work in a laboratory and outdoor setting. Moths are nocturnal and active from twilight to midnight. Students will learn how to handle moths, conduct behavioral recordings, basic experimental design, and will receive training in species interactions. Depending on student motivation, there is the possibility to design and implement an independent project. The student will join a group of undergraduates, graduate students, and faculty conducting research on the patterns of host use by yucca moth pollinators (althofflab.syr.edu).

Requirements: Ability to stand for long periods of time, and work in changing weather conditions. Good communication skills and ability to work in a team-setting is essential.

Application process: Please submit a CV, detailing any relevant skills, unofficial transcripts, a one to two paragraph rationale for your interest in the position, and the names and contact info for two references to Dr. David Althoff at dmalthof@syr.edu. Application evaluation will begin May 5th and will continue until the position is filled. Please direct questions about the position to Dr. Althoff at the above e-mail.

Funding: Students will be paid \$12/hr for eight to ten weeks depending on the field season.

****Under-represented groups in STEM are strongly encouraged to apply****

David M. Althoff Associate Professor Dept. of Biology
T 315.443.1096 107 College Place, Syracuse, NY 13244
althofflab.syr.edu

David M Althoff <dmalthof@syr.edu>

Trinidad Internship Guppy Evolution

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> 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 refer-

ences to David Reznick (gupy@ucr.edu). At least two of the references should be academics.

Ron Bassar <rdb4@williams.edu>

U Lausanne SIB Virtual Seminar Jerome Goudet February 28

Dear all,

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

Jerôme Goudet, Population Genetics and Genomics, University of Lausanne & SIB Wednesday 28 February 2018 at 16:00 - Genopode Auditorium A - UNIL campus "Of men and owls: insights into past demography using computer simulations"

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>

US Natl Medal Science Call Nominations

NATIONAL SCIENCE FOUNDATION 2415 EISENHOWER AVENUE ALEXANDRIA, VIRGINIA 22314

Dear Colleague:

One of the most important and gratifying aspects of participating in the scientific community is the nomination of colleagues for honorary awards in celebration of their exceptional contributions to one of our fields. I am sending this email today to urge you to recognize

one of your peers by submitting a nomination for the 2018 National Medal of Science.

This premier award for American scientists and engineers – considered by some as the US equivalent of the Nobel Prize – was established by the 86th Congress in 1959. It is the highest recognition our Nation can bestow for outstanding cumulative contributions to knowledge or sustained, impactful work in the fields of engineering, chemistry, physics, biology, mathematics, and behavioral and social sciences. Conferred by the President of the United States during a ceremony at the White House, the Medal has been awarded to approximately 500 pioneering individuals. The National Medal of Science program is administered by the National Science Foundation (NSF) in conjunction with the Executive

Office of the President.

Please nominate colleagues and peers who have extraordinarily advanced the scientific enterprise for this prestigious honor. Nominations and three letters of support must be submitted to NSF by April 16, 2018. If you have any questions, please contact the Program Manager for the National Medal of Science at nms@nsf.gov or by phone at 703-292-8040. For more information, please visit the National Medal of Science website at: <http://www.nsf.gov/od/nms/medal.jsp>. I look forward to celebrating new honorees with you in 2019.

Sincerely, /// signed /// France A. Cordova Director
National Science Foundation 2415 Eisenhower Avenue,
Suite 19100 Alexandria, VA 22314

France Córdova <director@nsf.gov>

PostDocs

AuburnU EvolutionaryEcol	73	Norway ComparativeGenomicsRegulation	86
AustralianNatIU CSIRO PhylogeneticInformatics ..	74	NorwegianU 2 PopulationDynamics	87
Beijing AncientGenomics	74	OldDominionU MarineBiodiversity	88
Bielefeld PDF PhD FurSealGenomics	75	Paris AntEvoDevo	88
BielefeldU TheoreticalEvolution	76	QMUL London BirdSongCulturalEvolution	89
Caltech GenomicsConvergenceAntsBeetles	77	ReedC Oregon EvolutionaryGenomics	90
CSIRO EnvironmentalGenomics	78	RutgersU EvolutionaryGenomics	90
DalhousieU StatisticalModellingMetagenomes	78	SGN Frankfurt MammalianSpeciation	90
FloridaStateU RodentPhylogenomicsMacroevolution	79	Smithsonian SMSC ConservationGenomics	92
FredHutch Seattle HIVAntibodyEvolution	80	UArizona Phylogenetics	92
Harvard DiseaseGenomics	80	UArkansas EvolutionBehavior	93
JohnsHopkinsU HIV Evolution	81	UCalifornia Berkeley GeneDrivePopulationGenetics	94
LinkopingU Sweden GenomicsFeralisation	81	UCalifornia Berkeley PathogenEvolutionaryGenomics	95
MaxPlanckInst Seewiesen 3 EvolutionCognition ...	82	UCalifornia SantaCruz 2 eDNA Biodiversity	95
MichiganStateU InsectParasitoidEvolution	83	UCollege London MeioticDrive	96
MNH Stockholm FungalEvolution	83	UCollege London YeastSpeciationGenes	97
Montpellier Classification eDNA	84	UConnecticut 3 EvolutionaryImmunology	97
NatITaiwanU PopulationGenomicsPlantAdaptation	84	UFlorida HumanEvolutionaryGenetics	98
NCState PlantVirusHostAdaptation	85	UGlasgow ExptEvolMicrobes	99
New Zealand ComparativeGenomics	86		

UGlasgow VirusEvolutionEpidemiology	100	UPennsylvania EvolutionInfectiousMicrobes	108
UGothenburg Sweden BirdsMacroevolution	101	UPittsburgh ExperimentalEvolution	109
UIceland Bioinformatics	102	USaoPaulo UCambridge HostParasite	110
UIdaho GalapagosLandSnails	103	UStockholm PopoulationGeneticsGenomics	110
UKonstanz CichlidSpeciesDelimitation	103	UToronto EvolutionDrugResistanceMalaria	111
ULausanne ComputationalPopulationGenomics ..	104	UUlm WildlifeMetaGenomics	112
ULausanne EvolutionaryGenomicsNeurogenetics ..	105	UWisconsin Milwaukee KelpGenomics	113
ULausanne MelaninEvolution	105	UWisconsin StevensPoint PopulationGenomics ...	114
ULausanne PlantEvolution	106	UWyoming PlantMicrobeEvolution	114
UMichigan EvolutionEcologyHerpetology	107	Vienna IST EvolutionaryGenomics	115
UMontana EvolutionaryGenomics	107	WashingtonStateU TasmanianDevilGenomics	115
UMontana EvolutionaryGenomics	108	WayneStateU Detroit FishPopulationGenomics ...	116
UNorthTexasHealthScience BioinformaticsPopulation-Genetics	108		

AuburnU EvolutionaryEcol

Postdoctoral Position in Evolutionary Ecology at Auburn University

The Wolak Research Group at Auburn University (www.auburn.edu/cosam/faculty/biology/wolak/-index.htm) is hiring a Postdoctoral Research Associate to test and develop theory predicting the evolutionary dynamics of genetic effects and phenotypic distributions in response to selection for sexual dimorphism. The main focus of the initial project will be theory development using mathematical or individual-based models. However, beyond this there are opportunities for the postdoc to expand along many possible avenues - including current laboratory experiments and analyses on the empirical study of sexual dimorphisms. The postdoc will be expected to assist with training graduate students, develop synergistic projects, write grants, and produce first authored papers and contribute to co-authored papers. Persons from groups typically under-represented in science are strongly encouraged to apply.

Required: — - A Ph.D. in an appropriate field (including but not limited to evolution, ecology, genetics) at time of hire — - A demonstrated track record of creative, productive research — - The ability to work in a dynamic, collaborative environment with graduate and undergraduate students — - A strong quantitative background — - Excellent communication, organizational, and leadership skills.

Preferred: — - Expertise in quantitative genetics — - Experience building mathematical or individual-based models — - A demonstrated ability to code in at least one programming language

Availability: The position start date is June 1 2018, but can be flexible. This is a one-year, full-time position with the possibility of renewal for a total of 2 years, pending satisfactory work. The postdoc will also benefit from AU fringe benefits and access to conference travel funds within the Wolak Research Group. Additional group funds for independent projects are available upon submission of a written proposal.

If interested, please email the following materials to Matthew Wolak (matthew.wolak@auburn.edu): — - 1) a current CV with contact information for three references — - 2) a 2 page statement of interest in this opportunity with descriptions of relevant skills and experience — - 3) up to 3 PDFs of relevant publications or manuscripts in preparation

Screening of applications will begin 09 April 2018, and continue until the position is filled. Interested persons should submit their application materials before this date to receive full consideration.

This announcement is informal in nature and the selected candidate must be able to meet eligibility requirements to work at Auburn University and in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment.

Matthew Wolak Assistant Professor Dept. of Biological Sciences Auburn University

Matthew E. Wolak, Ph.D. Assistant Professor Department of Biological Sciences Auburn University 306 Funchess Hall Auburn, AL 36849, USA Email: matthew.wolak@auburn.edu Tel: 334-844-9242

Matthew Wolak <mew0099@auburn.edu>

Australian National University CSIRO Phylogenetic Informatics

The Postdoctoral Fellow will drive the development of a next-generation biodiversity informatics platform for integrated analyses and visualisation of environmental and species data (occurrences, sequences, and phenotypes) in a phylogenetic context. The position is part of the dynamic Centre for Biodiversity Analysis and is jointly funded by ANU-CSIRO Centre for Biodiversity Analysis and CSIRO's Environomics FSP <https://research.csiro.au/environomics/>. The appointee will work closely with scientists in CSIRO and ANU and staff at the Atlas of Living Australia to create a platform for analysis, modelling, and visualisation of data that would enable assessments of genetic, phylogenetic, and functional diversity across time and space, and to assess the evolution of species traits and distributions.

Development of test cases would require the appointee to obtain, evaluate, and collate datasets and use them to develop and demonstrate the capabilities of the platform. Experience in phylogenetics, comparative methods, biogeography, and phylogeography is required, as is evidence of ability to conduct and publish high quality research.

For any enquiries regarding the position, please contact Professor Craig Moritz E: Craig.Moritz@anu.edu.au

Dr Sarah Mathews, CSIRO can also be contacted via E: Sarah.Mathews@csiro.au

For more information and to apply go to

<http://jobs.anu.edu.au/cw/en/job/519524/-postdoctoral-fellow> juanitarodrigueza@gmail.com

Beijing Ancient Genomics

Post-doctoral position available: Ancient Genomics

The Fu Molecular Paleontology Lab has a post-doctoral position available. If you have a background in statistical population genetics and/or data science, this might be for you!

Our ancient DNA laboratory pioneered large-scale studies of human population history requiring analysis of large numbers of samples simultaneously. We use ancient DNA to study gene flow between modern and archaic humans, to determine early modern human migration routes and to explore how agriculture influences the population structure of the Neolithic expansion in Europe and Asia.

We are looking for a highly motivated post-doctoral researcher with appropriate experience and interests to work on analysis of these data. Potential projects will investigate the biological history of humans using ancient and present-day genomic data.

The successful candidate will have analytical and computer skills that allow exploration of large and complex genetic data sets, preferably with previous experience in a world class ancient DNA lab. Research is conducted in English. The position will be supervised by Dr. Qiaomei Fu.

Applicants are requested to send their CV, a short statement of their research interests, and the names and contact information of two references to Dr. Qiaomei Fu at fuqiaomei@ivpp.ac.cn. Strong candidates will be expected to participate in a Skype or on-site interview. The position will be open until filled. The position is for two years with a possibility of renewal, and salary will be internationally competitive. Please also address questions to Dr. Fu.

The Fu Molecular Paleontology Lab, consisting of 14 members (including group leaders, postdoctoral scholars, doctoral and master's students and technicians), is a cutting edge international ancient DNA laboratory. It is based at the Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences, near the center of Beijing, China, with easy access to public transportation. The Fu lab focuses primarily on ancient genomic analysis, but the institute's research environment is diverse, with a vibrant community of researchers studying anthropology, archaeology and paleontology. Beijing is a thriving fast-growing city with a robust international community.

Dr. Fu's work has been published in several prominent journals, such as Nature, Science, PNAS, Current Biology, AJHG, etc. One research project was awarded "one of the top 2014 annual ten scientific events" in Nature. Nature also selected her as one of the "Ten Chinese Science Stars" in 2016. She has also received the 'Distinguished Young Scientist' award from the Chinese Academy of Sciences, and was selected for the Thousand Youth Talents program in China, to be a Howard Hughes Medical Institute (HHMI) International Scientist and to be one of China's Top Ten Innovative Pio-

neers of Science and Technology. For more information, her Research Gate site can be accessed here: <https://www.researchgate.net/profile/Qiaomei-Fu> . Melinda Yang <melyang@ivpp.ac.cn>

Bielefeld PDF PhD FurSealGenomics

Postdoctoral position or PhD studentship: fur seal genomics

With Dr Joe Hoffman (Bielefeld University) and Dr Jaume Forcada (British Antarctic Survey)

An outstanding opportunity is available either for a postdoc (3.5 years) or for a Ph.D. studentship (3 years) to work on the ecological and evolutionary genomics of fur seals. The position is available in Joe Hoffman's research group (www.thehoffmanlab.com) in the Department of Animal Behaviour at Bielefeld University. The project runs from now until the end of 2021 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 project: The successful candidate will exploit and continue to build upon an exceptionally detailed long-term study of Antarctic fur seals (*Arctocephalus gazella*) at Bird Island, South Georgia. High quality genome and transcriptome assemblies have already been generated and microsatellite and high density SNP data will be available for ~7000 marked individuals spanning a time series from the mid 1980's to the current day. The aim of this project (sub-project A01 of the collaborative research centre) is to determine how fitness variation is shaped by interactions between individual genetic quality (inbreeding) and the social environment within breeding colonies. We will collect highly detailed observational and biometric time-series data from mother-offspring pairs in two neighbouring colonies of high and low social density. We will then dissect apart the mechanistic underpinnings of fitness variation using a combination of endocrinological and immunological profiling, gene expression profiling, high-density SNP genotyping and methylation profiling. The result will be an unprecedentedly detailed understanding of the behavioural, physiological and genetic mechanisms underpinning fitness variation in a wild vertebrate, which will have important implications for understanding eco-

logical and evolutionary dynamics as well as adaptation to climate change.

Postdoc applicants: We seek a bright and highly motivated postdoc with a strong PhD in a relevant topic (e.g. population genetics, behavioural genetics, evolutionary or conservation genomics). We are looking for two main attributes in particular: (i) The candidate must have a deep understanding as well as practical experience of working with genomic data (experience of gene expression profiling and / or whole-genome resequencing would be particularly desirable) and be proficient in writing custom scripts and working in Unix and R; (ii) As the project involves two field seasons at South Georgia in the South Atlantic, the candidate would ideally also have experience of fieldwork with vertebrates. Experience of working with long-term individual-based datasets from wild animal populations would be advantageous but is not a requirement. The candidate should be able to work both independently and as part of a multidisciplinary team, and a high standard of spoken and written English is expected.

Ph.D. applicants: Bright and highly motivated Ph.D. candidates should hold a B.Sc. or equivalent in a relevant topic (e.g. population genetics, behavioural genetics, evolutionary or conservation genomics). An M.Sc. would also be advantageous but is not necessary. Strong quantitative skills (including proficiency in R) as well as practical experience of working with next generation sequence data (e.g. gene expression profiling or related approaches) would be desirable, but training can be provided. The candidate should also be able to work both independently and as part of a multidisciplinary team, and a high standard of spoken and written English is expected.

The working environment: The successful candidate will join the Hoffman lab, a young and dynamic group comprising three PhD students and two postdocs. They will be based at the Department of Animal Behaviour at Bielefeld University (www.uni-bielefeld.de/biologie/vhf/index.html). The department is the oldest of its kind in Germany and currently hosts around six principal investigators, ten postdocs and twenty PhD students. It offers a stimulating international environment and an excellent research infrastructure including brand new molecular laboratories. The working language of the Department is English. The successful candidate will also have the opportunity to interact closely with the cooperation partner (Dr Jaume Forcada) during two Antarctic field seasons and via placements at the British Antarctic Survey in Cambridge, UK.

Bielefeld University is particularly committed to the career development of its employees. It offers attractive

internal and external training

— / —

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>

BielefeldU Theoretical Evolution

Postdoc position for 3+ years in Theoretical Evolutionary Ecology at Bielefeld University A Postdoc position in theoretical evolutionary ecology is available at the Faculty of Biology at Bielefeld University in the Department of Evolutionary Biology. The position can start as soon as possible and is funded until the end of the year 2021 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 aim of the Postdoc project is to develop ecological and evolutionary theory to contribute towards a better understanding of intra-specific niche variation. The project is entitled “Modelling adaptive individualised niches in behaviour” (sub-project D04 of the collaborative research centre, with Klaus Reinhold). This theoretical project will explore the conditions that favour the evolution of between-individual variation in behavioural niches. The aim is to focus on mate choice and exploration and examine to which extent phenotypic variation can be maintained based on genetic differences and variation in adaptive phenotypic plasticity.

The collaborative research centre: The postdoc 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. Main responsibilities

Research tasks: Development of eco-evolutionary models (90%)

Mathematical analysis of models

Implementation in a programming language, e.g. in R, C++, Python

Simulation studies

Collaboration with other research groups in the collaborative research centre

Writing scientific publications

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

Applicant’s profile

We seek bright and highly motivated postdoctoral researchers with

a university degree in a relevant discipline, e.g. biology, mathematics, physics or bioinformatics

a completed PhD in a relevant field, ideally related to theoretical ecology, population genetics, behavioral ecology or evolutionary ecology

experience with mathematical modeling of evolutionary processes

programming skills in at least one programming language (e.g. R, C++, Python),

ability to work both independently and as part of a team

excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage:

papers in peer-reviewed international journals,

experience in collaborations between empiricists and theoreticians, and

experience with high-performance computing.

Remuneration Salary will be paid according to Remuneration level 13 of the Wage Agreement for Public Service in the Federal States (TV-L). Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programs. Employees have the opportunity to use a variety of health, counselling, and prevention programs. Bielefeld University places great importance on a work-family balance for all its employees.

Application procedure To apply, please provide: (i) a letter of motivation including a statement of your research interests and skills and experience relevant to the position; (ii) a CV including publication list; (iii) names and contact details of two referees willing to write confi-

dential letters of recommendation. All materials should be emailed as a single PDF file to: Klaus.Reinhold@uni-bielefeld.de. The application deadline is April 15, 2018 and interviews will take place shortly thereafter. After the decision, the position should start soon if possible. For further information on the projects and the involved departments, please contact Klaus Reinhold (klaus.reinhold@uni-bielefeld.de) with any informal inquiries.

Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor pursuits. It offers a high standard of living and is well connected to most major European cities. Bielefeld University has received a number of awards for its achievements in the provision of equal opportunity and has been recognized as a family friendly university. The University welcomes applications from women. This is particularly true with regard

— / —

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>

Caltech GenomicsConvergenceAntsBeetles

Postdoctoral position in genomics of convergence and social symbiosis (Parker Lab)

A postdoctoral position is available to study the genomic basis of evolutionary convergence in the lab of Joe Parker at the California Institute of Technology.

Work in the Parker lab is focused on the evolution of complex phenotypes, principally in the context of symbiosis. We use a unique system to explore this phenomenon: the convergent evolution of symbioses between rove beetles and social insects. Rove beetles (family Staphylinidae) are the largest metazoan family, and include multiple remarkable lineages that have evolved to become “social parasites” stealth impostors that infiltrate ant or termite societies, employing radical behavioral, anatomical and chemical adaptations. We have found that many of the most extreme symbiotic phenotypes have evolved convergently numerous times in distantly related lineages. We are now seeking a postdoctoral candidate to probe the genomic basis of complex phenotypic convergence in

this system. Our goals are twofold: i) Pinpoint shared or unique molecular changes that drive the evolution of social symbiosis in rove beetles; ii) Make basic inferences into the long-standing question of how complex phenotypic changes can arise repeatedly and predictably over deep evolutionary timescales.

Aspects of this work will involve two study systems: 1) A deep-time system encompassing symbiont lineages from across the rove beetle subfamily Aleocharinae that are separated by up to 100 million years. 2) A recently-evolved system in which multiple rove beetle lineages have convergently evolved symbioses with a single ant genus in the South Western US. This latter project involves potential fieldwork at sites in Southern California and Arizona. The successful candidate will spearhead genome sequencing of free-living and symbiotic species from across phylogeny, and use comparative genomic tools to understand patterns of genome evolution. There is potential for collaboration with Caltech labs using machine learning and single cell profiling, and the candidate will also lead genome/transcriptome assembly and annotation of several higher quality reference genomes to facilitate functional genetic studies in laboratory model rove beetle species. Depending on the candidate, the project may involve wet lab work to functionally test loci with possible causal roles in symbiosis, or involve collaboration with others to this end.

The following papers illustrate the rove beetle-ant system:

Parker, J., Eldredge, K.T., Thomas, I.M., Davis, S., Coleman, R.T. (2017) Hox-Logic of Preadaptations for Social Insect Symbiosis in Rove Beetles. bioRxiv, 198945

Maruyama, M., and Parker, J. (2017) Deep-Time Convergence in Rove Beetle Symbionts of Army Ants. *Current Biology*, 27, 920-926 PMID: 28285995

Yamamoto, S., Maruyama, M. and Parker, J. (2016) Evidence for Social Parasitism of Early Insect Societies by Cretaceous Rove Beetles. *Nature Communications*, 7: 13658 PMID: 27929066

Candidates

Applications are encouraged from talented and motivated individuals who have a Ph.D. or are nearing completion of their Ph.D. with experience in genome and transcriptome sequencing, genome assembly, annotation, comparative genomics and genome evolution. Interest or experience in machine learning and/or single cell profiling are desirable. Top candidates will have a strong track record of research productivity, excellent communication skills, enthusiasm for basic research and a collegial approach to science. Candidates should send a cover letter, a detailed curriculum vitae, and names and

contact details for three references to joep@caltech.edu
The California Institute of Technology

Caltech is consistently ranked among the top research universities in the world and hosts a diverse and collaborative scientific community. Caltech is located in Pasadena, California, a vibrant city 10 miles north-east of downtown Los Angeles and minutes from the Parker lab's fieldwork sites in the San Gabriel mountains. More info about the Parker lab: <https://www.bbe.caltech.edu/content/joseph-parker> We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, or national origin, disability status, protected veteran status, or any other characteristic protected by law.

dibasic@gmail.com

CSIRO Environmental Genomics

Future Science Postdoctoral Fellowships in Environmental Genomics

- Are you an up-and-coming scientist with a flair for innovation? - An outstanding opportunity to launch your research career. - Join CSIRO's Environomics Future Science Platform (FSP) and be part of the next scientific revolution.

The Environomics Future Science Platform (Environomics FSP) is pleased to announce the opening of its first round of Future Science Fellowships focused on the development of environmental genomic technologies.

We are seeking to recruit outstanding and inventive early career scientists who will develop the environmental genomics technologies of the future.

Two categories of Future Science Fellowship are offered: 1. Fellowships embedded within existing Environomics Future Science Platform projects (3 fellowships); 2. Open-call fellowships where you can propose a line of research that you would like to pursue and that meets the brief of "re-defining the limits of what genomics can do for environmental science and management" (1-2 fellowships).

Postdoctoral Fellows in Environomics are appointed for three years at various CSIRO locations within Australia. You will be mentored by a CSIRO Research Scientist or Engineer and participate collaboratively within the Envi-

ronomics FSP research program. We strongly encourage collaboration with university, government, and industry partners. The fellowships include research costs.

The following fellowships are available: - Mobile DNA Sequencing: Genome-power in your pocket. - Using insects as molecular biosensors of biodiversity and ecological interactions. - eCells: developing novel ways to non-invasively estimate animal abundance through genomics. - Rapid epigenetic age-estimators for vertebrates. - Building a biodiversity informatics software platform (partnership with Centre for Biodiversity Analysis, ANU). - Open call CSIRO Future Science Postdoctoral Fellowships in Environomics.

Information about these positions is available here: <https://research.csiro.au/environomics/work-with-us/> The Environomics Future Science Platform is developing the next-generation technology to investigate and manage genetic resources hidden within Australia's vast biodiversity. Find out more here: <https://research.csiro.au/environomics/> . Further enquiries can be directed to: EnvironomicsFutureSciencePlatform@csiro.au

The Commonwealth Scientific and Industrial Research Organisation (CSIRO) We imagine. We collaborate. We innovate. At CSIRO, we do the extraordinary every day. We innovate for tomorrow and help improve today for our customers, all Australians and the world. We do this by using science and technology to solve real issues. Diversity is the compass that navigates our innovation. We provide an inclusive workplace that respects, values and actively pursues the benefits of a diverse workforce.

We work flexibly at CSIRO, offering a range of options for how, when and where you work.

Applications close: 11:59pm AEDT, 18 March 2018.

Apply here: <https://jobs.csiro.au/go/Postdoctoral-research-fellows/990000/> "Noni.Lauder@csiro.au" <Noni.Lauder@csiro.au>

DalhousieU Statistical Modelling Metagenomes

Postdoctoral fellowship position in statistical modelling and analysis of microbial communities

A position is immediately available (re-opened) to work on a collaborative project between researchers at Dalhousie University (Dr. Joseph P. Bielawski & Dr. Hong

Gu, Dept. of Mathematics & Statistics) and the University of Montreal (Dr. B. Jesse Shapiro, Dept. of Biological Sciences). The project is part of a large-scale research initiative, ATRAPP, funded by Genome Canada and focused on genomic solutions to the challenge of assessing, predicting and preventing harmful toxic blooms.

The successful candidate will develop novel statistical models for analyzing the structure and metabolic interactions of complex microbial communities based on amplicon data and metagenomic data. Candidates with skills in Bayesian modelling, machine learning and/or time-series analysis would be a better fit for the position.

Qualified applicants must have a Ph.D. in statistics, applied mathematics, computer science, bioinformatics, or a related field in computational biology. A strong background in statistics, and proficiency with scripting and programming languages in one or more of R, python, perl, C/C++, BUGS or Stan is preferred.

This position is based at Dalhousie University (Halifax, NS). The recipient will join the Centre for Genomics and Evolutionary Bioinformatics (CGEB), which is a vibrant interdisciplinary research environment at Dalhousie University (<http://cgeb.dal.ca>). The recipient will also have the opportunity to visit the University of Montreal to interact with a diverse group of biologists and computational biologists.

Start date: Review of applications will begin immediately and continue until the position is filled. The start date is negotiable. Applications will be reviewed as they are received. We thank all applicants, however, only selected candidates will be contacted. Interested parties should forward a cover letter, cv, statement of research interests, and a sample of recent writing (article, report or other publication) as well as contact information for 3 references to:

Joseph P. Bielawski Department of Biology Department of Mathematics and Statistics Dalhousie University P.O. Box 15000 Halifax, NS, Canada B3H 4R2 (or) email to j.bielawski@dal.ca

J.Bielawski@Dal.Ca

FloridaStateU RodentPhylogenomicsMacroevolution

Post-doctoral position

Rodent phylogenomics and diversification

An NSF-funded post-doctoral is available beginning summer or fall 2018 (post-doc) in the lab of Scott Stepan at Florida State University studying the adaptive radiation of sigmodontine rodents (Muroidea) in South America. The position will initially be for two years with possible extension for up to two additional years. Primary responsibility during the first one to two years will involve Next-gen sequencing up to 100 species using phylogenomic methods to resolve the rapid radiation of tribal-level lineages following the colonization of South America, and preparation of manuscripts on the diversification of sigmodontines and their relatives. Subsequent research avenues include overseeing data collection and analysis of post-cranial morphology and/or testing macroevolutionary patterns of diversification. A significant component of the latter could include comparative quantitative genetics and reconstructing historical patterns of selection after accounting for the genetic variation and covariation among traits. Successful applicants will have opportunities to develop independent research questions involving systematics, molecular evolution, biogeography, macroevolutionary trends, and adaptive radiations.

The Ecology and Evolution program is a highly interactive and supportive environment that works closely with the Computational Evolutionary Biology group in the Dept. of Scientific Computing.

Post-doc applicants must have a Ph.D. in biology or related field and be accomplished in Next-generation sequencing, associated bioinformatics assembly, and phylogenetic analysis. Extension years could include 2D and 3D digitization of museum specimens and possibly computational projects. Salary will start at \$47,600 plus family health insurance. Start date is negotiable. Review of applications will begin April 17 but applications will be accepted until the position is filled. Additional information on the Stepan Lab and more details about the project are available from www.bio.fsu.edu/faculty-steppan.php, and on the Ecology and Evolution group at www.bio.fsu.edu/ee/index.html. Applicants should submit a cover letter, CV, statement of research interests and experience relevant to this position, names and

contact information for three references (include in cover letter), and pdfs of two relevant publications.

For more information, contact

Dr. Scott Stepan

Department of Biological Science

Florida State University

Tallahassee, FL 32306-4295

e-mail: stepan@bio.fsu.edu phone: (850) 644-6536

“stepan@bio.fsu.edu” <stepan@bio.fsu.edu>

FredHutch Seattle HIVAntibodyEvolution

Hello evolution community–

Did you know that antibodies evolve within you every day to fight off pathogens? This Darwinian system of mutation and selection is carefully orchestrated by your immune system. We have a postdoc position available to study this beautiful evolutionary system. Here is a summary:

- position of at least two years duration with solid pay and great benefits - the project is to learn about anti-HIV antibody development and coevolution using data coming from a unique HIV superinfection cohort for which the viral history has been carefully characterized
- there will be many opportunities to develop and deploy new methods in a team pushing the boundaries of Bayesian phylogenetic analysis - we will work with collaborators to validate inferences using lab techniques
- the larger research group is highly collaborative, with deep expertise in virology, protein evolution, and structural/functional analysis - we're a Python shop looking for someone who isn't afraid of large-scale data analysis and has high standards for organization and code clarity

For details and how to apply, see <https://b-t.cr/t/506> .

Don't be afraid to drop me a line if you have questions!

Erick – Frederick “Erick” Matsen, Associate Member Fred Hutchinson Cancer Research Center <http://matsen.fredhutch.org/> Erick Matsen <ematsen@gmail.com>

Harvard DiseaseGenomics

Summary

The Department of Biomedical Informatics (DBMI) at Harvard Medical School and the Farhat-Lab is looking for a Postdoctoral Fellow in infectious disease genomics.

Mycobacterium tuberculosis displays a remarkable range of variability in antibiotic resistance phenotype. Elucidating the biological mechanisms for these differences is a fundamental question in the study of infectious diseases in general and in *Mycobacterium tuberculosis* specifically as it allows for the more accurate prediction of phenotype from genotype, and improved clinical and diagnostic interpretation of molecular diagnostics. Specifically here the project will focus on the detection of gene-gene/mutation-mutation interaction effects using whole genome sequencing data from clinical isolates of *M.tb*.

Responsibilities

The Postdoctoral Fellow will be responsible for developing and applying computational methodologies to identify novel infectious disease genomic markers and to assess their diagnostic and surveillance potential.

Basic Requirements

We are an interdisciplinary lab. Candidates may have a PhD degree in Network science, evolutionary biology, bioinformatics, computational biology, biostatistics, or a related field. The candidate interested in this position must be highly motivated and demonstrate initiative in assigned tasks and have experience working with large multivariate data sets, and have thought of or is highly interested in studying variable interactions in such datasets.

Additional Requirements

Experience in programming R, Python, and/or Perl and statistical analysis or at least an interest in learning these skills will be necessary. The candidate and PI can work together to delineate the fellows training needs and develop a program to fulfill this utilizing the department and university's wide range of resources.

Terms

The position is available on 3/15/2018 and can be renewed annually.

How to apply

Email applications including curriculum vitae, summary statement of personal objective and research interests, PDFs of the best two papers, and the names and email addresses of three references to mrfarhat@partners.org

Harvard Medical School is an Equal Opportunity/Affirmative Action Employer.

Women and minorities are especially encouraged to apply.

For additional information:

<http://farhat-lab.hms.harvard.edu/> Maha Farhat, MD, MSc Assistant Professor Department of Biomedical Informatics, Harvard Medical School Assistant Physician

Pulmonary and Critical Care, Massachusetts General Hospital

“Farhat, Maha Reda” <Maha_Farhat@hms.harvard.edu>

JohnsHopkinsU HIV Evolution

Postdoctoral Position: African HIV Evolutionary and Epidemic Dynamics

Our group at Johns Hopkins University in Baltimore, MD is looking for a postdoctoral fellow to work on projects related to HIV phylodynamics aimed at understanding geography of HIV transmission networks and the role of mobility and migration on HIV incidence and epidemic dynamics in Sub-Saharan Africa. The ideal applicant will have expertise in phylogenetics or computational biology, quantitative experience in epidemiology, statistics, and/or ecology and an interest in public health research related to disease prevention and control in global settings. The successful applicant will be working with Dr. Kate Grabowski in the Department of Pathology at Johns Hopkins Hospital. They will also work closely with the Hopkins Infectious Disease Dynamics Group (iddynamics.jhsph.edu), as well as project collaborators at Oxford (Christophe Fraser), University of Edinburgh (Andrew Rambaut), Imperial College (Olli Ratmann), and University College London (Deenan Pillay). Applicants with, or nearing completion of, a doctoral degree in evolutionary biology, computational biology, epidemiology, biostatistics, or a related field will be considered.

The successful applicant will work primarily with Dr. Kate Grabowski and colleagues on PANGAEA-HIV (Phylogenetics And Networks for Generalized Epidemics in Africa) consortium studies, a project funded by the Bill

and Melinda Gates Foundation that aims to improve our understanding of HIV epidemiology in order to design targeted HIV control strategies and to understand impact of HIV interventions. The successful applicant will be expected to lead analyses using these genetic and epidemiologic data to understand the spatiotemporal patterns of HIV transmission and other aspects of HIV epidemic dynamics in sub-Saharan Africa in collaboration with a team of global experts in infectious disease epidemiology and evolutionary biology. Through PANGAEA-HIV, the successful applicant will have access to next generation HIV sequencing and corresponding epidemiological data from over 15,000 persons in sub-Saharan Africa. This work will be highly connected to ongoing HIV control work throughout Sub-Saharan Africa, and the successful applicant will have the chance to share results with policy and operational partners including the Centers of Disease Control and Ministries of Health.

The successful applicant be joining a highly collaborative group who work on projects ranging from empirical data collection to theoretical modeling of disease dynamics. In addition to PANGAEA-HIV, there will be ample opportunities to collaborate on other Johns Hopkins studies and with the Rakai Health Sciences Program (a world renowned HIV research organization in southern Uganda) to work on cross-cutting projects focused on issues in infectious disease transmission and control both related and unrelated to HIV.

The position will be for 1-2 years, depending on applicant interest and career plans. Interested candidates should contact Dr. Kate Grabowski (mgrabow2@jhu.edu) with a CV, statement of interest, and references. Application will be considered on a rolling basis and should be submitted by May 1, 2018.

– M. Kate Grabowski, PhD ScM Assistant Professor, Department of Pathology Johns Hopkins University 443 Carnegie Building Baltimore, MD 21287 Tel: 4432875736 Email: mgrabow2@jhu.edu

Kate Grabowski <mgrabows@jhu.edu>

LinkopingU Sweden GenomicsFeralisation

Postdoctoral position: "The Genomics of Feralisation"

Dept of Biology, AVIAN Behavioural Genomics and Physiology Group, Linköping University, Sweden

The Wright Lab (part of the AVIAN Behavioural Genomics and Physiology Group) at Linköping University, Sweden, is looking for two new recruitments - a motivated technician and post-doc as part of a newly acquired ERC consolidator grant. The project is aimed at studying the genomics of feralisation, using Hawaiian and Bermudan chickens as a model.

In the case of the post doc we are looking for a candidate with a strong background in quantitative genetics and bioinformatics. The project will involve a large amount of Whole Genome Sequence data (including RNA-seq and methylation-seq data). The project will require selective sweep mapping, population genomics analysis of admixture as well as GWAS analysis (based on both expression and standard phenotypes).

The project itself has recently been funded by an ERC consolidator grant and is aiming to use a series of different populations of feralised chickens (domestic birds that have escaped and are now living wild throughout the Hawaiian Island chain) to map the genes and polymorphisms underlying their rapid responses to newly imposed selective forces.

Candidates are requested to apply formally as per the official announcement at the following link: <https://liu.se/en/work-at-liu/vacancies?rmpage=-job&rmjob=8069&rmlang=UK> The application must be received by the 13th April at the latest. Pre-selected candidates will be expected to pass a skype or on-site interview. Successful candidates will be offered standard contract for two years, with the option to extend this to a maximum of five years. A PhD in a relevant subject area (e.g. evolutionary biology, genetics, genomics) is essential as is a proven knowledge of relevant research techniques and methodologies and general expertise in the subject area.

The Wright lab is part of the AVIAN behavioural genomics and physiology group, which comprises of a variety of researchers using the chicken as a model. As such there is on-going research in behaviour, physiology, evolution, genetics and genomics amongst others. Linköping University is a large campus-based University with over 30000 staff and students. Linköping itself is the fifth largest city in Sweden, with an international airport and good rail and bus links throughout the country. For further enquiries about the positions please contact Dominic Wright (domwr@ifm.liu.se or domwright@gmail.com) for additional information.

”domwr@ifm.liu.se“ <domwr@ifm.liu.se>

MaxPlanckInst Seewiesen 3 EvolutionCognition

Animal Minds Project e.V.

The “Animal Minds Project e.V.” advertises 3 post-doc stipends associated to the Comparative Cognition Group at the Max Planck Institute for Ornithology (MPIO) in Seewiesen (located near Starnberg, about 50 km from Munich), an internationally renowned research institution with more than 200 employees working in four departments and nine research groups. The research group of Comparative Cognition runs a research station in collaboration with the Loro Parque Fundación (LPF) on Tenerife, Spain where comparative cognitive studies on parrots and other animals can be carried out. In this regard, “Animal Minds Project e.V.” invites applications for

2 postdoctoral stipends in parrot comparative cognition.

The 2 stipends provide an opportunity to carry out research projects on the evolution and mechanisms of complex cognition in parrots (and corvids) using a comparative approach. The successful candidate will join the Comparative Cognition Group and therefore be affiliated scientifically to the Max-Planck-Institute for Ornithology. (S)he will have access to the greatest parrot collection in the world comprising over 350 (sub)species of parrots and a laboratory with ca. 40 trained parrots (touch screen, exchange paradigm etc.) of 4 species. This allows comparative cognitive studies at a new scale and on a new large-brained model system.

1 postdoctoral stipend on delphinid cognition and vocal learning.

This stipend is intended to allow research on vocal learning ability and cognition of delphinids. The successful candidate obtains access to the necessary research equipment and subjects kept in Zoos and will be affiliated to the Max-Planck-Institute of Ornithology (Comparative Cognition Group).

Application requirements and selection criteria:

Applicants should hold a PhD in animal cognition or experimental/developmental psychology, and have two years of Postdoc research experience in animal cognition and/or developmental psychology of human children and should be qualified by a good publication record. Good statistical skills in relevant subjects are desirable.

High self-motivation and ability to work independently and in a team are an absolute must. Additionally, the position requires team-leading skills, good organization and time management skills and writing proficiency. Basic knowledge of Spanish is helpful. The candidates will be selected according to their scientific qualification and proposed project.

The starting date will be from April 2018 but ideally no later than September 2018. The monthly stipend for a full time engagement on Tenerife will be up to euro 2,325.-. The stipend is available initially for two years but can be extended subject to satisfactory performance. For further information, please contact: info@animalminds.org.

Applications can be made both in English or German Language. Qualified women in particular are encouraged to apply. Please submit a cover letter (describing your research interests, experience and goals), a short description of your proposed research project, your CV, copies of degree certificates and a list of two references as one single PDF via e-mail to: info@animalminds.org

Deadline for applications: 28.03.2018

www.animalminds.org Anastasia Krasheninnikova
<anastacia.k@web.de>

but applicants with a strong evolutionary background who are willing to learn identification and handling of parasitoids will be considered as well. Desirable qualifications include experience conducting research on experimental evolution, working with insect host-parasite systems, expertise in statistical analysis, strong organizational skills, and interest in mentoring undergraduate research. The work will involve field collection of parasitoids and their hosts that may require climbing smaller trees or ladders. Field collections will take place across Michigan and possibly in other states, thus candidates should possess a valid driver's license.

The initial appointment is for one year with potential for renewal for an additional 1.5 years. It is a full-time, benefited position with a salary of \$47,500 and health insurance. Review of applications will begin immediately until a suitable candidate is found. The position begins in June/July 2018. Inquiries about the position can be directed to Marianna Szucs, szucs-mar@msu.edu. Candidates should submit a cover letter describing research interests and carrier goals, curriculum vitae, names and contact information for three references and two representative publications online following the link below: <http://www.careers.msu.edu/cw/-en-us/job/498704/research-associatefixed-term> "Szucs, Marianna" <szucs-mar@msu.edu>

MichiganStateU InsectParasitoidEvolution

The biological control laboratory of Dr. Szucs at Michigan State University at the Department of Entomology invites applications for a postdoctoral position studying contemporary adaptation and evolution of insect parasitoids in response to changing biotic and abiotic conditions. The aim of the research is to improve biological control programs that use parasitoids and to better understand the potential of insects for rapid evolutionary responses in general. The research will involve both field and laboratory components, and if the successful candidate is interested and qualified there may be opportunities to combine laboratory experiments with quantitative genetic and genomics approaches. Collaborators on the project include Drs. Larry Gut and Matt Grieshop from Michigan State University.

Required qualifications include a Ph.D. in evolutionary biology, entomology, ecology or related field and a successful publication record. The ideal candidate will have experience working with hymenopteran parasitoids

MNH Stockholm FungalEvolution

Post-doctoral researcher Botany/Mycology

A two-year postdoctoral position is available in the Department of Botany, Swedish Museum of Natural History, Stockholm. The position is placed within professor Mats Wedin's research group and is a part of the project area "Fungal phylogeny and evolution" funded by the Swedish Research Council (VR). The research group has several additional projects funded by the Swedish Taxonomy Initiative, focussing on taxonomic and phylogenetic biodiversity questions in lichens and associated organisms.

The genetic basis of facultative lichenization - a tool to understand fungal lifestyles

In this project, we will study the genetic basis of the lichen symbiosis utilizing a group of closely related fungi including lichens, saprotrophs, and species with an "optionally lichenized" strategy. The latter form simple lichen thalli when growing on the bark of *Populus tremula* or live as saprobes on *Populus* wood. Data analyses

will include de novo genome assembling and annotation, analysis of differences in genome content, size and structure, gene ontology enrichment analysis for interpreting functions of a set of genes, and analysing the degree of pseudogeneization to investigate the genomic mechanisms for losing lichenization. In a second step, we will use several culturable “optional lichens” to study the genetic basis of the lichenization, combining comparative genomics and transcriptomics data to investigate differences in gene expression of fungal species under different lifestyles, in order to detect regulatory pathways involved in the fungal-algal recognition and their physiological interaction.

Qualifications

Candidates have a recent (max 3 years old) PhD in systematics/evolutionary biology or similar, with experience in lichenology and/or mycology. A demonstrated publication record and excellent English communication and writing skills are expected. Good knowledge in molecular lab work, genomics, transcriptomics, and phylogenetics are required, and experience with axenic culture work, light microscopy, and independent fieldwork is desirable. A valid driving licence is also a strong advantage. The successful candidate will mainly pursue own research, but is expected to participate also in other collaborations subject to discussion.

The preferred starting date is May 1st 2018, but can be discussed. The appointment is for two years.

For more information please contact professor Mats Wedin (mats.wedin@nrm.se). Union representatives are Johannes Lundberg, SACO-S and Anna Sandberg, ST. All can be reached at telephone number + 46 8 519 540 00.

Mark your application, including a cover letter outlining relevant background, experience and motivation, your CV and list of publications, contact information for two references, and copies of educational certificates, with dnr 2.3.1-20-2018, and send it as a single pdf document to rekrytering@nrm.se or to the Swedish Museum of Natural History, Box 50007, SE 104 05 Stockholm, Sweden, no later than March 31st, 2018.

Mats Wedin <Mats.Wedin@nrm.se>

The Methods and Algorithms for Bioinformatics (MAB) team at the computer science department of the University of Montpellier, France (the LIRMM) is looking for talented individuals to fill an 18-months postdoctoral position. The successful candidate will work on a novel approach for the identification of the species behind the DNA found in an environmental sample. The originality of the approach lies in the application within evolutionary analyses of ideas from string algorithmics that avoid the computationally-intensive task of sequence alignment. A detailed description of the research project can be found here: <https://sites.google.com/site/fabiopardi/postdocs>. The applicant should have a background in bioinformatics with an emphasis on algorithmic and software developments for biological sequence analysis and computational genomics. Previous research experience in one of the following topics in bioinformatics will be considered as an advantage: metagenomics, alignment-free sequence analysis, molecular evolution, computational phylogenetics. Regardless of her/his background, the applicant’s past research should show a strong motivation towards solving biologically-relevant problems in a rigorous way, using state-of-the-art techniques and/or developing novel methodologies. Good programming skills, as well as an ability for autonomous work, are essential.

Interested applicants should send a CV, and a brief description of research accomplishments and goals to F. Pardi (pardi@lirmm.fr) and E. Rivals (rivals@lirmm.fr). Applicants should have been awarded a Ph.D. within the last 4 years or should be graduating imminently. Successful candidates are required to start by 1 October 2018 at the latest. The salary for the position is about 2,200 euros net per month plus benefits.

A one-thousand-year-old city, Montpellier is a thriving research community with a multitude of research centers in life sciences. It is the fastest growing city in France where approximately one third of the population are students, and a great location for outdoor activities. The LIRMM is one of the most visible computer science laboratories in France.

Fabio Pardi <pardi@lirmm.fr>

Montpellier Classification eDNA

Postdoc position on alignment-free taxonomic classification of environmental DNA

Natl/TaiwanU Population Genomics-Plant Adaptation

<https://sites.google.com/site/chengrueilee/> Research topic: The genomic and genetic mechanisms of plant

adaptation under natural and artificial selection

Location: National Taiwan University, Taipei, Taiwan

Target species: Wild banana (*Musa itinerans*), mung bean (*Vigna radiata*), and bitter melon (*Momordica charantia*)

Detail: The Lee lab is looking for highly motivated postdoctoral researchers to investigate the genomic architecture under strong natural and artificial selection. Our new projects focus on natural genetic resources in Southeast Asia, and we collaborate with international stock centers such as World Vegetable Center (Taiwan) and the Vavilov Institute (Russia). The study will focus on population genomics investigation of regions under selection, genetic mapping of important agronomic traits and environmental adaptation, and functional validation of candidate genes.

We highly welcome researchers with any of these following experiences: 1. Population genetics, genomics, or genetic mapping studies 2. Molecular biology 3. Linux OS and any programming language

Salary: \$ 64,185 NTD per month + 1.5 month year-end bonuses

Please e-mail any question or these application materials to: chengrueilee@ntu.edu.tw 1. CV 2. Name and e-mail of two referees 3. PDF of relevant publications

<chengrueilee@ntu.edu.tw>

NCState PlantVirusHostAdaptation

Postdoc: Experimental evolution and phylodynamics of plant virus emergence

A postdoctoral research position is available in the phylodynamics research group led by David Rasmussen at NC State University in the Bioinformatics Research Centre and the Department of Entomology and Plant Pathology. The main aim of the project is to understand how vector-borne plant viruses adapt to new host environments and expand their host range. Viral adaptation to new hosts will be studied in the lab, where we can experimentally manipulate transmission between different host species and regularly re-sequence viral populations. To reveal the genetic basis of host adaptation, experimental evolution studies will be combined with newly developed phylodynamic methods for tracking the population dynamics of individual viral lineages and quantifying their fitness.

Questions of interest include:

Do fitness tradeoffs between hosts limit adaptation to multiple hosts?

How do the fitness effects of individual mutations vary across hosts?

Can selection resolve fitness tradeoffs (i.e. antagonistic pleiotropy) and, if so, how?

Is the evolution of generalists constrained more by genetic or by ecological factors like vector dynamics?

Applicants must hold a PhD in plant pathology or related field of biology. Previous lab experience handling plant viruses or other pathogens is highly desired. Additional knowledge of data analysis in Python, R or Matlab is also desired. Candidates with both wet lab and bioinformatics skills will be given the highest consideration, but is not essential. The candidate will also be expected to publish and present their work at conferences, help supervise students and may occasionally be involved in grant writing. Most importantly, the candidate must possess strong problem-solving skills and a record of self-directed, innovative research.

Initial appointment is for one year, but renewable for up to 3 years. Start date would ideally be Summer 2018.

To apply, please send a CV, a 1-2 page cover letter describing previous experience and research interests, and the contact info for two references to drasmus@ncsu.edu. Application deadline: April 20th, 2018.

David Rasmussen

Assistant Professor

Bioinformatics Research Center

Dept. of Entomology and Plant Pathology

North Carolina State University

Ricks Hall 312

1 Lampe Dr,

Raleigh, NC 27607

Web: phyldynamics.wordpress.ncsu.edu

Twitter: @davorasmussen

David Rasmussen <drasmus@ncsu.edu>

New Zealand Comparative Genomics

A two year postdoc is available at Landcare Research in New Zealand to contribute to a project on genome assembly and comparative genomics.

Project summary

We are seeking to fill a postdoctoral position funded by Genomics Aotearoa and located with Associate Professor Thomas Buckley at Landcare Research, Auckland. Genomics Aotearoa is a national network funded to improve capability in, and outcomes from genomics in New Zealand. The successful application will be required to work with a nationally distributed team across universities and Crown Research Institutes.

We are seeking an enthusiastic and driven Postdoctoral Fellow to join a Genomics Aotearoa team working on developing high quality genomes for outcomes in conservation biology (including pest control) and primary production.

New Zealand faces considerable challenges in conservation and primary production that can be improved by the use of genomics technologies. Your research will focus initially on developing tools and technologies to produce the high-quality genomes required to achieve outcomes for species of scientific, primary production, pest and conservation importance. In later years, generation and understanding of genome data from large numbers of individuals from key species will be generated and studied.

This project provides an exciting opportunity, working with an outstanding national team, to generate genomics data and tools for a wide range of applications, and the freedom to generate high impact publications from that data.

Applicants must have a PhD in bioinformatics or genomics. Skills in genome assembly, RNAseq, annotation, bioinformatics analysis of large data sets, genome evolution, coding, and bioinformatics training are desirable and experience working with genome data is essential. Preference will be given to applicants with skills in bioinformatics and genome assembly.

The appointment is for 2 years with the possibility of extension. The successful applicant will be expected to take up the position before July 2018. The successful candidate will ideally:

- * hold a PhD in biology with proven publication track record and conference presentations
- * have experience with the bioinformatic analysis of genomic data sets especially whole genome assembly and annotation
- * have an understanding of comparative genomics, population genomics and associated models and methodology
- * have experience in genomics experimental design
- * have the ability to relate to people in all circumstances and to work well in a team
- * be versatile, demonstrates initiative in solving problems
- * work well under pressure, self motivated
- * be well organised, capable of independently and effectively planning time and resources

The two year, full time position will be based at Landcare Research in Auckland. If you would like to take advantage of this great opportunity please view the position description and apply online clicking the 'Apply Now' button below. Applications must include a cover letter, CV and evidence of the required skills as per the position description.

<https://careers.sciencenewzealand.org/jobdetails/-ajid/Ddtv8/27345-Postdoctoral-Fellow-in-Genomics,27345.html>

For further details about our organisation and the relevance of our science please visit our website: www.landcareresearch.co.nz Applications close on Tuesday 16 April 2018 at 5.00pm.

Thomas Buckley

Research Leader, Invertebrate Systematics Manaaki Whenua-Landcare Research

Associate Professor, University of Auckland

T +64 9 574 4116

E buckleyt@landcareresearch.co.nz

www.landcareresearch.co.nz

Norway Comparative Genomics Regulation

Postdoctoral fellow within comparative analysis of genome regulation

The successful candidate will be funded through the project "REWired", recently funded by the Norwe-

gian Research Council FRIPRO program (2018-2021). The project is addressing fundamental knowledge gaps regarding the role of whole genome duplication in adaptive evolution, using salmonid fish as a model system. Specifically, our aim is to test if functional redundancy in a duplicated genome spark evolution of novel adaptive functions. The candidate will also work in close collaboration with a PhD-student funded through a second FRIPRO funded project “TRANSPROSE”, which aims at understanding the importance of transposable elements in the evolution of gene regulatory innovation.

A key element in this project is collaboration with Rori Rohlf at San Francisco State University and use her computational framework (EVE) to assess the importance of whole genome duplication on adaptive evolution of gene function. The candidate will therefore be expected to spend significant time in the Rohlf-lab during the project.

The main tasks will be to: - Compile a multi-omics (RNA-Seq, ChIP-Seq, ATAC-Seq) comparative dataset from 10 fish species (wet-lab work will be carried out by others). - Identify genes under adaptive evolution using the EVE statistical framework. - Integrate analyses of gene expression evolution with information on transposable element activity and epigenetic marks to understand the mechanistic drivers of gene regulation evolution.

For more detailed information about the project, please contact Simen RÅ©Åd Sandve (srsandve.org, or simen.sandve@nmbu.no).

More information: <https://www.jobbnorge.no/en/-available-jobs/job/149000/postdoctoral-fellow-within-comparative-analysis-of-genome-regulation-refno-18-01262> –

Rori Rohlf Assistant Professor Department of Biology
San Francisco State University

pronouns: she/her/hers

Rori Rohlf <rrohlf@sfsu.edu>

NorwegianU 2 PopulationDynamics

Two postdoc positions are available for 3 years at the Department of Biology, Centre for Biodiversity Dynamics (CBD), the Norwegian University of Science and Technology in Trondheim. The positions are funded by a grant from the Research Council of Norway, and will be part of the project “Spatial differentiation of a bird metapopulation: quantifying eco-evolutionary dynamics in space”, which is led by Professor Bernt-Erik SÅther, and involves other researchers at CBD. Further information about CBD is available at: www.ntnu.edu/cbd The aim of the project is to examine how local population dynamics and dispersal affect the spatial structure of populations using house sparrows as model organism. We will achieve this by an integrated approach linking ecological and evolutionary processes based on a unified stochastic modelling framework. Our aim is to examine the relative contribution of environmental covariation, interchange of individuals and differences in strength of density dependence for the degree of spatial synchrony of the population dynamics and ongoing phenotypic divergence in space. We expect the results will show that including spatial processes are essential for understanding how natural populations will respond to changes in the environment.

The successful candidates should hold a PhD in biology but candidates with a PhD in mathematical sciences may also be considered if the competence is relevant. We are searching for candidates that can document experience with theoretical or empirical analyses in population dynamics and/or quantitative genetics. Experience with the software R must be documented, and is mandatory. Both candidates will be involved in a network of collaborators both at CBD and internationally and must therefore possess good communication and social skills. The candidates will also be involved in some field work. We seek candidates who are able to work efficiently and goal-oriented, and who are highly motivated for the research.

The successful candidates should start in May 1 2018, but the starting date is negotiable.

The application deadline is March 24th 2018, and applications need to be submitted through the “Jobbnorge” web page: <https://www.jobbnorge.no/en/available-jobs/job/148272/post-doc-positions-in-population-dynamics-quantitative-genetics> Further

information about the positions can also be obtained from professor Bernt-Erik S  ther, Centre for Biodiversity Dynamics, NTNU, Tel. +47 90578544, E-mail: Bernt-Erik.S  ther@ntnu.no

Dr. Henrik Jensen Associate Professor Centre for Biodiversity Dynamics Department of Biology NTNU NO-7491 Trondheim NORWAY

E-mail: Henrik.Jensen@ntnu.no Office: +47 73596949 Mobile: +47 91897064

Work web: <https://www.ntnu.edu/biology/jensen-lab> Private web: www.inlicio.com Henrik Jensen <henrik.jensen@ntnu.no>

OldDominionU MarineBiodiversity

Postdoctoral Research Associate - Marine Molecular Ecology

The Department of Biological Sciences at Old Dominion University, a ‘‘Doctoral Research-Extensive’’ state university, has a Post-Doctoral Research Associate position available in marine molecular ecology. This position is supported by an NSF-funded PIRE (Partnerships for International Research and Education) Project utilizing fish collections from the 1907-1910 Philippine Albatross Expedition housed at the Smithsonian Institution in DC to examine genetic and species-level changes in marine biodiversity over the past century of intense fisheries exploitation and habitat degradation in the Philippines. Applicants must have a PhD in molecular ecology, population genomics, marine phylogeography, or a closely related field at the time of employment. A strong background in molecular biology and experience with processing large datasets from next-generation sequencing methods is strongly preferred, including working in UNIX or LINUX environments and familiarity with bash, python, or perl scripting. The successful candidate will be expected to live in the Philippines for up to three months during summer to conduct field and laboratory work and to mentor undergraduate REUs and graduate students from collaborating institutions. Competitive applicants will comfortable coordinating and conducting research in the field and have some teaching experience; AAUS Scientific Diver certification is desired. The appointment begins Spring 2018 with the potential for a one-year renewal. Position is limited to U.S. citizens. Salary is dependent on qualifications. Application deadline is April 6th, 2018.

Job Responsibilities Field and laboratory work in marine molecular ecology: 1. Coordinate and conduct field and laboratory research in the Philippines and U.S. 2. Collect and sample marine fishes via market and dive surveys 3. Collect, analyze and interpret large-scale genomic data 4. Lead a comparative research project utilizing Albatross and contemporary collections with the expectation of publishing a peer-reviewed manuscript

Support international partnerships and capacity building: 1. Facilitate an annual two-week Bioinformatics Training Workshop at Silliman University 2. Support and assist graduate and undergraduate students during a 9-week REU program over the summer

Additional tasks: 1. Spend three months each summer in the Philippines 2. Participate in collaborative, multi-institutional and international research project both independently and as a team player 3. Assist Principal Investigator, co-PIs, and project collaborators and personnel as needed 4. Classroom teaching in the U.S. and Philippines as needed 5. All other duties, as assigned

Highly motivated and interested candidates are encouraged to apply by sending a CV, a statement of your interest in the position, including prior research and future career goals (2-page maximum), and the names and contact information for at least three references to aacki002@odu.edu. Review of applications will begin following the April 6th deadline. Questions can be directed to Dr. Amanda Ackiss.

aacki002@odu.edu aacki002@odu.edu

Paris AntEvoDevo

POST-DOC POSITION ANT EVO-DEVO, PARIS, FRANCE The position is a full time, 2-year contract. Expected starting date: September 2018

ANR-funded project SOCIODEV: Understanding social evolution through the study of embryogenesis in ants.

Over 15000 ant species are known so far and present highly diverse morphologies, behaviour, colony structure and chemical recognition. Yes, we know very little about their mechanisms of embryogenesis, although this knowledge can shed light on the evolution of sociality. The SocioDev project aims at unravelling the mechanisms of embryo development across a representative selection of ant species and test how these mechanisms can inform us about their social lifestyle.

The project is coordinated by Dr. Abderrahman Khila,

Institute of Functional Genomics, CNRS, ENS Lyon.

The post-doc will work on one task on this large project, focussing in particular on testing the possible link between the mode of embryogenesis and chemical recognition of larvae by nestmate workers. This task involves behavioural assays, chemical analyses and manipulations, and RNAseq experiments to analyse hydrocarbon biosynthesis pathways in the embryos.

The successful applicants will have a PhD in behavioural biology or evolutionary biology and a solid track record. Experience with insects and chemical analysis is welcome. Candidates should be fluent in English.

The post-doc will be based at the Laboratory of Experimental and Comparative Ethology, University of Paris 13 (<http://leec.univ-paris13.fr>), working with Prof. Patrizia d'Ettorre but will spend extended periods of time at Institute of Functional Genomics, Lyon, working with Dr. Abderahman Khila (<http://igfl.ens-lyon.fr/equipes/a.-khila-developmental-genomics-and-evolution>).

Candidates should send, in one single PDF file: a) letter of interest, b) Curriculum Vitae with publication list; c) contact information (e-mail, phone) for two referees who can provide letters of recommendation.

DEADLINE for receiving applications: 15 April 2018

Contact: Patrizia d'Ettorre, dettorre@leec.univ-paris13.fr

“dettorre@leec.univ-paris13.fr” <dettorre@leec.univ-paris13.fr>

QMUL London BirdSongCulturalEvolution

A Postdoctoral Research Assistant position is available at Queen Mary University of London (QMUL) as part of a project funded by the BBSRC. The project 'Machine learning for bird song learning' seeks to develop and apply new methods for assessing the similarity between complex bird song syllables, guided by the perception of birds themselves, and to apply this to examine the evolution of song learning behaviour.

This particular research position will play two key roles in the project. First, you will lead the effort to use operant conditioning techniques to examine how birds judge the similarity of song syllables. This will involve using existing operant conditioning techniques to ex-

amine how zebra finches assess song syllable similarity. It will also involve the development of new methods (in collaboration with Dr Robert Lachlan) to carry out operant conditioning with free-living wild birds. Second, you will collate data-sets of song variation from free living populations, and (again in collaboration with Dr Lachlan) carry out comparative analyses using cultural evolutionary simulations fitted to data, and based on song comparisons using our new methods in order to compare processes of song learning between species. The project will therefore allow you to develop skills in two cutting edge areas of behavioural biology.

The project will require that you travel to collaborate with project partners in the Netherlands (Wageningen) and the UK (Cornwall).

The ideal candidate for this position should have a PhD in animal behaviour and communication. Experience in working with both captive and wild birds, in operant conditioning methods, and with evolutionary theory would be desirable. A track record of peer-reviewed publications is essential.

This is a full-time, fixed term post available for a period of 3 years. The start date is 1st June 2018. The salary is in the range of 32,956 - 38,709 per annum and is inclusive of London allowance. The salary will be dependent on qualifications, skills and experience.

Candidates must be able to demonstrate their eligibility to work in the UK in accordance with the Immigration, Asylum and Nationality Act 2006. Where required this may include entry clearance or continued leave to remain under the Points Based Immigration Scheme.

Informal enquiries for further information are welcomed and may be made to Dr Robert Lachlan, email: r.f.lachlan@qmul.ac.uk or Tel +44 (0)20 7882 5058

For further information about the School, please see <http://www.sbcs.qmul.ac.uk>. To apply please click the link below

Application enquiries should be directed to recruitment@qmul.ac.uk

The closing date for applications is 6 April 2018. Interviews will be held shortly thereafter.

<https://webapps2.is.qmul.ac.uk/jobs/-job.action?jobID=3154> <http://www.findapostdoc.com/-search/job-details.aspx?jobcode=7789> <http://www.jobs.ac.uk/job/BIF688/postdoctoral-research-assistant/> Dr R.F. Lachlan Lecturer in Psychology, Department of Biological and Experimental Psychology School of Biological and Chemical Sciences Queen Mary University of London Mile End Road, London, E1 4NS United Kingdom

Office: 3.18 G. E. Fogg Phone: +44 (0)20 7882 5058
 E-mail: r.f.lachlan@qmul.ac.uk
 r.f.lachlan@qmul.ac.uk

ReedC Oregon EvolutionaryGenomics

Post-doc Position in Evolutionary Genomics/Computational Biology in the Schaack Lab

A post-doc position is available in the lab of Sarah Schaack at Reed College in Portland, OR. The successful candidate will be involved in the analyses of genomic datasets for several ongoing projects involving the analysis of whole genome sequence and transcriptome datasets from long-term mutation-accumulation experiments using cladocerans. In addition, there are opportunities to initiate new projects based on the previous experience of the successful applicant, the resources in our lab (<https://sites.google.com/site/schaackwork/>), and other publicly-available data.

Requirements: Experience with analyzing NGS sequence data, programming, and a working knowledge of computational tools and statistics related to genome-wide datasets. In addition to a background in sequence analysis and computational biology, oral and written communication skills are essential .

Notably, the successful applicant can, but need not necessarily, re-locate to Portland, as the position does not require lab work. For those that would be interested in moving to/staying in Portland, Reed is a highly rigorous undergraduate institution with a strong research emphasis, offering a unique training environment for post-docs. Features include close collaboration with the PIs, the opportunity to work with talented undergraduates, and the chance to network with other post-docs in the department and with biologists throughout Portland and the region. The scientific and intellectual environment at Reed is stimulating and provides a number of opportunities for interactions (including an excellent weekly seminar series, journal clubs, and discussion groups).

Salary will be based on the NIH post-doc pay scale and will be commensurate with experience. To apply, submit a cover letter detailing your research interests, a CV, and contact information for 3 references to schaack@reed.edu with your /YOURLASTNAME/_POSTDOC in all caps in the subject line. To receive full consideration, send

materials on or before March 25, 2018, however applicants will be considered until the position is filled and the start date is as soon as possible. Informal inquiries are welcome.

Reed College is an Equal Opportunity Employer. Candidates from underrepresented groups are strongly encouraged to apply.

Sarah Schaack, PhD Associate Professor Reed College schaackmobile@gmail.com <https://sites.google.com/site/schaackwork/> Sarah Schaack <schaackmobile@gmail.com>

RutgersU EvolutionaryGenomics

A postdoctoral position in evolutionary genomics is available in the Ellison Laboratory in the Department of Genetics at Rutgers University. The position involves using comparative genomic approaches to study the evolution of 3D genome organization in *Drosophila*. Candidates should have a PhD in a biology-related field, experience with genomic analysis in Unix/Linux environments, and proficiency in Python and/or Perl. The position is primarily computational although there are opportunities for wet lab work. Previous experience working with *Drosophila* is beneficial but not necessary. The start date is flexible and salary will be determined based on the NIH pay scale.

Rutgers-New Brunswick is a leading national research university and the preeminent public institution of higher education in the state of New Jersey. The campus offers a vibrant and diverse research community and is close to New York City and Philadelphia.

Interested applicants should send a CV and a brief statement of research interests to ellison.laboratory@gmail.com

Ellison Laboratory <ellison.laboratory@gmail.com>

SGN Frankfurt MammalianSpeciation

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

Postdoc (m/f) - Mammalian genomics: speciation and gene flow (full time)

Your tasks

- Sequencing, assembly, and annotation of mammalian genomes
- Evolution, gene flow, and population genomic analyses of large multispecies data sets
- Involve classic taxonomy, biogeography and related fields with comparative genomics
- Managing massive-RAM server and genomics software
- Acquiring third-party funding

Your profile

- PhD in Biology, Genetics, Bioinformatics or related subjects
- Experience with de novo genome assembly and mapping of vertebrate genomes
- Exceptional interest in mammalian evolution
- Experience and solid understanding of comparative genomics or evolutionary biology research
- Teamwork oriented and excellent communication skills with proficiency in written and oral English

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
- 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
- Flexible working hours - annual special payment - company pension scheme - Senckenberg ID card for free entry in museums in Frankfurt - a holiday of 30 days/year

Place of employment: Frankfurt am Main Working hours: Full time (40 hours/week) Type of contract: initially limited for 2 years Salary: according to the German collective agreement TV-H (pay grade E 13)

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 lim-

ited for two years. The Senckenberg Gesellschaft fuer Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fuer Naturforschung.

How to apply

Please send your application, mentioning the reference of this job offer (ref. #12-18004) until April 15th, 2018 by e-mail (attachment in a single pdf document) and include a cover letter detailing your research interests and experience, a detailed CV, a list of publications and copies of your certificates, transcripts and grades to:

Senckenberg Gesellschaft fuer Naturforschung Senckenberganlage 25 60325 Frankfurt a.M.

E-Mail: recruiting@senckenberg.de

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

– Mit freundlichen Grüßen / Best regards

Isabel Gajcevic, M.A. Personalsachbearbeiterin

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

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

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

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Gruppe Personal & Soziales - 1319 Elsen, Carina

Mitarbeiter/in Personalbeschaffung (Recruiting) - 1313 di Biase, Maria - 1313 Helm, Jessica - 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1467 Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Uwe Fritz, Prof. Dr. Ingrid Kröncke Präsidentin: Dr. h. c. Beate Her-aeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Senckenberg forscht für Ihr Leben gern!
www.200jahresenckenberg.de recruiting
recruiting@senckenberg.de recruiting
recruiting@senckenberg.de

Smithsonian SMSC Conservation Genomics

Postdoctoral Research Fellow - Conservation Genomics of Critically Endangered African Antelopes

The Smithsonian-Mason School of Conservation (SMSC) is accepting applications for a Postdoctoral Research Fellow. The position is a 12-month appointment renewable up to 3 years and will be based at the Smithsonian Conservation Biology Institute (SCBI) in Front Royal, VA.

The successful candidate will contribute to ongoing, cutting-edge research on the conservation genomics of the critically endangered African antelopes. The research will include assembly and annotation of the genomes, generation of whole genome sequences from additional individuals, and analyses related to patterns of genome-wide diversity, inference of historical demography, and comparative analyses of closely related species. The position involves focused research on developing novel approaches to establishing self-sustaining populations of endangered ungulates *ex situ*, developing genomic tools for managing small populations, and creating and facilitating networks of people across sectors taking action for conservation. The incumbent will have office space, access to SI's Hydra computing cluster, and a competitive post-doctoral level salary supplemented by excellent state employee benefits.

For more information about the position and to apply, please visit <https://jobs.gmu.edu/postings/42521> . – Klaus-Peter Koepfli, Ph.D.

Smithsonian Conservation Biology Institute National Zoological Park 3001 Connecticut Avenue NW Washington, DC 20008 USA Mobile (USA): +1 310 903 0197 E-mail: KoepfliK@si.edu OR klauspeter.koepfli527@gmail.com

Dobzhansky Center for Genome Bioinformatics Saint Petersburg State University 41A Sredniy Prospekt Saint Petersburg 199034 RUSSIA Mobile (Russia): +7 911 829 5068 Skype ID: klauspeter.koepfli

<klauspeter.koepfli527@gmail.com>

Klaus-Peter Koepfli <klauspeter.koepfli527@gmail.com>

UArizona Phylogenetics

Postdoc position at the University of Arizona

The Kacar (<https://kacarlab.org/>) and Sanderson labs (<http://ceiba.biosci.arizona.edu/index.htm>) in the Departments of Molecular and Cell Biology and Ecology and Evolutionary Biology at the University of Arizona are seeking a postdoctoral researcher for a NASA Exobiology Program funded project focusing on the phylogenetic history and evolution of bacterial translation machinery.

The primary role of the postdoc will be creating and developing new phylogenetic algorithms, and integrating these new algorithms with existing phylogenetic data on ancestral ribosomal proteins. The postdoc will also be involved in testing general questions about phylogenomic methodology. The position is for approximately two years, starting in the summer or fall of 2018. The postdoc will primarily be located in the Kacar Lab, will be supervised by Kacar and Sanderson and is expected to attend both Kacar and Sanderson lab group meetings.

The University of Arizona is one of very few universities that offers an astrobiology program with a molecular and cell biology focus while also hosting one of the top ecology and evolution departments in the world, with considerable faculty expertise in phylogenetic theory, molecular evolution, genetics and evolutionary biology in general. Tucson is a vibrant, affordable, diverse, and livable city (and is now a UNESCO World City of Gastronomy!). It is surrounded by spectacular scenery (including numerous national parks, monuments, and wilderness areas) and the amazing biodiversity of the Sonoran Desert.

Minimum qualification include a Ph.D. in biology or related subjects and a promising publication record. Preferred qualifications include demonstrable experience with molecular evolution, and ancestral sequence reconstruction. Salary is competitive.

To apply please visit <https://uacareers.com/postings/-27228> For specific questions contact Betul Kacar at betul@arizona.edu. Submit your application by April 15, 2018 for full consideration, but applications will be considered until the position is filled.

Michael J. Sanderson, Professor Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721

Office: BSW 412 Phone:520-626-6848
 email:sanderm@email.arizona.edu

lab web site: <http://ceiba.biosci.arizona.edu> Ceiba phylogenetic tree visualization: <http://sourceforge.net/projects/ceiba> PhyLoTA Browser: <http://phylota.net> r8s software: <https://sourceforge.net/projects/r8s> sanderm00@gmail.com

UArkansas EvolutionBehavior

Westerman Lab Postdoctoral Fellow in Behavioral Genomics at The University of Arkansas

The Westerman Lab at the University of Arkansas is seeking a creative and motivated Postdoctoral Fellow to investigate the genetics and neurobiology of mate preference plasticity in butterflies, to begin as soon as late Spring/Early Summer 2018. The Westerman Lab studies mechanisms underlying behavioral diversity and plasticity, with a focus on sensory system development and visual learning in butterflies. Current research topics include the role of genetics and social environment in mate preference development, behavioral and developmental plasticity, and sensory biases. The lab is an integrative animal behavior group, and integrates a wide range of techniques, including, but not limited to, genomics, transcriptomics, controlled laboratory experiments, histology, and field ecology. Research incorporates both tropical butterflies and those native to Northwestern Arkansas, and takes advantage of multiple species-rich field sites within a 30-minute drive of campus. For more information, please visit the lab website at

<http://www.ericawesterman.org> . The successful candidate will be expected to work in close collaboration with Dr. Westerman on a comparative behavioral genomics project, as well as to develop independent research projects within the scope of the lab. In addition, the successful candidate will be expected to collaborate with fellow lab members, and will have the opportunity to mentor undergraduate and graduate students. Dr. Westerman is building collaborations within the Biology Department, as well as with faculty in both the Entomology and Psychological Sciences Departments at UARK. Postdocs in the lab will have the opportunity to work across discipline, and will be encouraged to initiate and develop innovative collaborative projects.

This technically integrative lab embraces creative approaches to studying animal behavior. Candidates with a strong background in genomics, neurobiology, and

development are particularly encouraged to apply.

Funding is currently available to support this position for two years, with the possibility for extension depending on funding and project progress.

Minimum Qualifications:

- Ph.D. in biological sciences or a related field by start of appointment
- Demonstrated expertise in genomics, bioinformatics, neurobiology, or developmental biology techniques
- Experience with either multivariate statistics or statistical analysis of genomic data
- Demonstrated evidence of excellent writing skills

Preferred Qualifications:

- Experience using CRISPR/Cas9
- Experience in animal behavior experimental design
- Experience in live animal husbandry
- Experience in chemical ecology
- Experience in microscopy

For a complete position announcement and information regarding how to apply, visit <http://jobs.uark.edu/postings/25954> . Applicants must submit a cover letter/letter of application, curriculum vitae, and a two-page description of research accomplishments and future plans uploaded to the 'Other Document' link. A list of three professional references (name, title, email address, and contact number) willing to provide letters of reference will be requested during the application process.

For more information, please contact:

Dr. Erica Westerman

Assistant Professor

Department of Biological Sciences

University of Arkansas

ewesterm@uark.edu

The University of Arkansas is an equal opportunity, affirmative action institution. The university welcomes applications without regard to age, race/color, gender (including pregnancy), national origin, disability, religion, marital or parental status, protected veteran status, military service, genetic information, sexual orientation or gender identity. Persons must have proof of legal authority to work in the United States on the first day of employment. All applicant information is subject to public disclosure under the Arkansas Freedom of Information Act.

Erica L. Westerman Assistant Professor Department of Biological Sciences University of Arkansas Science & Engineering, Room 416 Fayetteville, AR 72701 ewesterm@uark.edu <http://www.ericawesterman.org> Erica Lynn Westerman <ewesterm@uark.edu>

UCalifornia Berkeley GeneDrivePopulationGenetics

POSTDOC POSITION IN POPULATION GENETICS OF GENE DRIVE SYSTEMS

The Marshall Lab (www.MarshallLab.com) at the UC Berkeley School of Public Health (<http://sph.berkeley.edu/>) is seeking to hire a postdoctoral scholar to work on mathematical and computational aspects of gene drive systems in mosquito vectors of malaria, dengue fever and Zika virus. The position is initially for one year, with the possibility of extension, and is available immediately. Salary is commensurate with experience, and full benefits are included.

The project will involve: * Ascertaining design criteria for gene drive systems to spread desirable genes (e.g. those conferring disease refractoriness or a fitness load) into a mosquito population and to remediate them from the environment if needed, * Quantifying rates of mosquito movement within and between human communities based on identity by descent and other methods, * Understanding the long-term evolution of gene drive systems based on data from experimental gene drive studies in yeast.

This is part of an exciting collaborative project with numerous molecular and computational biologists and ecologists mostly throughout the University of California system. We collaborate with molecular biologists (Professors Omar Akbari and Ethan Bier at UCSD, Professor Anthony James at UCI and Professor Craig Montell at UCSB), ecologists (Professor Greg Lanzaro at UC Davis), mathematical modelers (Professor David Smith at the University of Washington), evolutionary biologists (Professors Justin Meyer and Sergey Kryazhimskiy at UCSD), and population geneticists (Professor Montgomery Slatkin at UC Berkeley). There is also a great opportunity to expand upon our collaborations with the Center for Theoretical Evolutionary Genomics at UC Berkeley (<http://cteg.berkeley.edu/>). The successful candidate will have access to this extraordinary network of scientists.

An ideal candidate will have: * A strong background in applied mathematics, statistics and/or computer science, * Experience with population genetics and/or genomic analysis, * An interest in mosquitoes and/or mosquito-borne diseases.

If you are interested in the position, please send: (1) your CV, including a list of publications and the names and email addresses of three potential referees; (2) PDFs of your two most significant publications or manuscripts to date; and (3) a short cover letter describing your research interests and motivations for joining our lab to John Marshall (john.marshall@berkeley.edu). For best consideration, please apply by April 16th, 2018. Inquiries are also welcome. Additional information about the research in the Marshall Lab can be found at www.MarshallLab.com < <http://www.marshalllab.com/> >.

UC Berkeley has a large and vibrant genomics and computational biology community spanning the School of Public Health, the Center for Computational Biology, the Department of Integrative Biology, the Center for Theoretical Evolutionary Genomics, the Departments of Mathematics and Statistics, the Institute for Data Science, and more. UC Berkeley offers competitive salaries, excellent benefits and is an equal opportunity employer. The City of Berkeley and the surrounding San Francisco Bay Area is known for its progressive values, vibrant social and cultural scene, and beautiful surrounding environment.

'Marshall, John M.' <john.marshall@berkeley.edu>

UCalifornia Berkeley PathogenEvolutionaryGenomics

A postdoctoral researcher position for a highly motivated young scientist is available in the group of Rodrigo Almeida in the Department of Environmental Science, Policy and Management, at the University of California, Berkeley, to study the dynamics of plant pathogen epidemics, host adaptation, and specialization. The position is funded by a Horizon 2020 collaborative project dedicated to the emerging plant pathogen *Xylella fastidiosa*. Topics of interest include, but are not limited to: identification of genes underpinning pathogen host adaptation and specialization, exploration of pathogen genetic diversity and selection forces leading to disease emergence. Within the broad scope of the project, developing novel research questions will be encouraged.

Requirements

Applicants must have a Ph.D. in an area related to microbial genomics, evolution, or population genetics; computational, programming, and quantitative skills are required. The successful candidate will be independent and have good writing skills, yet be able to work in an interdisciplinary environment where collaboration and synergistic interactions are expected.

Responsibilities

Researcher will be responsible for experimental design, data analyses, preparation of research manuscripts and project reports. Post-doctoral researchers in our group are also expected to help mentor and work with students and peers when necessary.

Appointment

One year renewable to two years based on satisfactory performance. Salary commensurate to experience; starting annual salary for UC Berkeley postdoctoral researchers immediately after obtaining a PhD is US\$48,216 'V salary scale follows NIH/NRSA stipend. Start date is negotiable, but strong preference will be given to candidates that can start by early Summer 2018.

Application

Prepare a single PDF with i) a 2-page CV that lists publications and computational skills, ii) a research statement (up to 2 pages), and iii) three references who could be contacted. Position will remain open until

filled; applications will be reviewed immediately upon receipt. We hope to close the position by March 31st, 2018. Send PDF directly to Rodrigo Almeida: email-*rodrigoalmeida@berkeley.edu*

Rodrigo Almeida <rodrigoalmeida@berkeley.edu>

UCalifornia SantaCruz 2 eDNA Biodiversity

We are hiring two post-docs as follows:

1. UCSC-based HHMI Post-Doctoral Scholar in Environmental DNA Research, Education, and Outreach

HHMI Post-Doctoral Scholar in Environmental DNA Research, Education, and Outreach

University of California 'V Santa Cruz

Summary:

UC Santa Cruz department of Ecology and Evolutionary Biology (EEB) is recruiting one full-time postdoctoral scholar to perform environmental DNA (eDNA) research and science education outreach. The position is ideal for a candidate with a background in molecular biology. In collaboration with project partners in the department of Ecology and Evolutionary Biology (EEB) at UC Los Angeles, the postdoctoral scholar will help establish a new education program called eSIE: environmental DNA for Science Investigation and Education, supported by a grant from the Howard Hughes Medical Institute (HHMI) jointly awarded to UCSC and UCLA. The scholar will work with a team of researchers and science education experts on eDNA research that connects to the eSIE program.

Why eDNA?

eDNA is a highly sensitive molecular approach to catalog biodiversity in any ecosystem. The results can reveal a near complete diversity profile of the ecosystem from microbes to plants and animals, and can enable tracking biodiversity changes over time. UCLA and UCSC have pioneered cutting-edge methods to obtain eDNA data, from citizen science to packaged computational pipelines. Our goal with the eSIE program is to use the excitement and wide application of eDNA as a new gateway for students to enter research avenues in the environmental sciences.

The postdoctoral role in the eSIE program:

The postdoctoral scholar will help co-develop and man-

age eSIE program while receiving training focused on the advancement of science education. eSIE reaches a broad undergraduate constituency by involving hundreds of students annually in CALeDNA bioblitzes on UC Natural Reserves (www.ucedna.com). The postdoc will help select field sampling, ideally around research questions of their interest, and travel to do field collections at natural reserves around the entire state. eSIE will also launch a multidisciplinary flipped course to introduce undergraduates formally to STEM subjects through DNA and eDNA activities. The postdoc would co-design the course with the eSIE team, and receive training through the Center for Education Innovation and Learning in the Sciences (<https://ceils.ucla.edu>) at UCLA (remote learning possible). The eSIE program also supports students who enter research labs. The postdoc would be expected to occasionally work with student research interns.

Research scope:

The postdoc will be encouraged to pursue environmental science research that uses the eSIE-generated eDNA data and sample collections. They will join the lab group of Beth Shapiro < https://www.eeb.ucsc.edu/faculty-singleton.php?&singleton=true&cruz_id=bashapir > (UCSC), who's lab focuses on evolution, paleogenomics, and conservation genomics. They will also join the UC Conservation Genomics Consortium community that conducts many eDNA projects.

Preparation:

Candidates should have a PhD in biology or a related science field and molecular biology laboratory experience evidenced by a strong record of scholarship. The ideal candidate would have demonstrated interest or some experience working in science communication and education research, as well as undergraduate teaching or public outreach. Candidates should demonstrate strong written and verbal communication skills, interest in pedagogical innovation, educational assessment, and scholarship, excellent organization and management abilities, experience working with diverse groups. Candidates also should possess skills in mentorship. They must be willing to travel within California, including multiple trips per year between Santa Cruz and Los Angeles, and lead fieldwork excursions to collect eDNA on UC Natural Reserves. Candidates must have a valid driver's license.

The postdoctoral position is a minimum two-year appointment starting Spring 2018, with salary commensurate with experience and following the UC salary scales. To apply submit a cover letter, CV, and contact information for three references here, or send all documents directly to Beth Shapiro (bashapir@ucsc.edu).

For inquiries about the position, please contact Robert Wayne (rwayne@ucla.edu) or Beth Shapiro (bashapir@ucsc.edu).

Review of applications will begin immediately and continue until the position is filled.

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, national origin, disability, age or protected veteran status. For the

— / —

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>

UCollege London MeioticDrive

Postdoctoral position: 'Sexual Selection, Condition Dependence and Meiotic Drive'

Department of Genetics, Evolution and Environment, University College London

The Stalk-Eyed Fly Research Group led by Andrew Pomiankowski and Kevin Fowler is seeking an experienced and motivated evolutionary biologist Postdoc to assist in delivery of a NERC-funded grant 'Sexual Selection, Condition Dependence and Meiotic Drive'.

They will undertake large-scale experimental evolution experiments, analysis of sperm competition and genotype-by-environment interactions in laboratory populations, make behavioural observations, carry out experiments at field sites in Malaysia and analyse genomic sequences for evidence of selection. Good insect husbandry, laboratory and field skills, experience using genetic markers and high competence in statistical analyses are strongly preferred. Experience of working with and supervising students and technical staff are highly desirable. The post holder should be highly motivated, with good organisational skills and be able to work independently without the requirement of day-to-day supervision. The project has a major genomics component which will be carried out in collaboration with Prof Terry Burke, University of Sheffield.

The post is available to start within 3 months of 1 April 2018. 34,635-36,549 per annum, inclusive of London

Allowance. The appointment is for 3 years in the first instance.

A PhD in a relevant subject area (for example, evolutionary biology, genetics, genomics) is essential as is proven knowledge of relevant research techniques and methodologies and demonstrable general expertise in the subject area.

The Department of Genetics, Evolution and Environment is a world leading research centre with a highly diverse group of researchers www.ucl.ac.uk/biosciences/departments/gee If you would like to discuss the post, please contact Professor Andrew Pomiankowski ucbh-pom@ucl.ac.uk

Formal applications (cover letter, CV, three referees) by 27th March via www.jobs.ac.uk/job/-BHZ265/research-associate/ "Pomiankowski, Andrew" <a.pomiankowski@ucl.ac.uk>

UCollege London YeastSpeciationGenes

Postdoctoral position: 'Identification and analysis of speciation genes in yeast'

The Department of Genetics, Evolution and Environment is seeking to appoint a postdoctoral Research Associate to join Dr Duncan Greig's research group in UCL's new Centre for Life's Origins and Evolution (CLOE).

The Research Associate will be an active member of a research project using budding yeast (*Saccharomyces cerevisiae*, *Saccharomyces paradoxus*, and hybrids between them) to map, isolate, and analyse the genetic differences between species that contribute to their reproductive isolation. The project will focus on two traits, fertility and adaptation to temperature. The project will require classical yeast genetics methods including crossing, tetrad dissection, growth assays, library screening and genetic manipulations, as well as high throughput sequencing and computational analysis. The Research Associate will also be required to assist in the development of research proposals and the planning and delivery of the results, so that the research objectives of the project are met. They will be expected to produce independent, original contributions to the subject area.

This post is available immediately and is funded for 35 months in the first instance. Salary is Grade 7:

GBP 34,635 per annum inclusive of London Allowance. (Please note that appointment at Grade 7 is dependent upon having been awarded a PhD; if this is not the case, initial appointment will be at research assistant Grade 6B with payment at Grade 7 being backdated to the date of final submission of the PhD thesis)

The successful candidate must hold (or be close to obtaining) a PhD in a relevant subject area and demonstrable comprehensive knowledge in the subject area of evolutionary biology, especially genetics of speciation, AND/OR yeast biology and genetics. Proven knowledge of research techniques and methodologies is also essential. The post holder must demonstrate excellent written & verbal communication skills and the ability to present complex information effectively to a range of audiences. Experience in statistical analysis in biology (e.g. GLMs) AND/OR bioinformatic analysis of high-throughput sequence data is essential.

For informal enquiries about the job, please contact Dr Duncan Greig (d.greig@ucl.ac.uk). To apply for the position or to read a full job description and person specification, please follow this link:

https://atsv7.wcn.co.uk/search_engine/-jobs.cgi?SID=amNvZGU9MTcxMzYxNSZ2-dF90ZW1wbGF0ZT05NjUmb3duZXI9NTA0MTE3OCZvd25lcnR5cGUwJmpvY19yZWZfY29kZT0xNzEzNjE1JnBvc3RpbmdfY29kZT0yMjQ
"Greig, Duncan" <d.greig@ucl.ac.uk>

UConnecticut 3 EvolutionaryImmunology

University of Connecticut: Postdoctoral researcher in Evolution and Immune Genetics.

A postdoctoral researcher position is available in Dr. Daniel Bolnick's research group (<https://bolnicklab.wordpress.com>), in the Department of Ecology and Evolution at the University of Connecticut.

Tasks: Recent work by the Bolnick lab identified naturally evolved variation in stickleback fishes' resistance to a severe cestode parasite (Weber et al 2017 American Naturalist; Weber et al 2017 Proceedings of the National Academy of Sciences). The postdoc will spearhead an NIH-funded study of the genetic and immunological basis of rapidly-evolving host resistance to cestode infection, and cestode immune suppression. Activities include experimental infections, immune challenges transgenic manipulations of the host and possibly cestode,

immune phenotype measurements, and genetic mapping. Some field research will also be likely. The postdoc will be responsible for conducting lab and field work, co-supervising laboratory technicians and students, data analysis and publication.

Duration: The position is available for up to four years, subject to annual review of performance. The position could extend longer, contingent on availability of additional grant funds. The postdoc should be able to start in summer or fall 2018, exact dates to be negotiated with the PI.

Compensation: Starting salary will be between \$45-\$50,000 depending on experience, plus health benefits.

Qualifications: Applicants must have a PhD in genetics, immunology, evolutionary biology, or a closely related field. Prior experience with molecular genetics or immunology is essential (preferably both). Expertise in CRISPR/cas9 gene editing is a strong plus. Previous research experience and publications should demonstrate a commitment to basic research, good work ethic, lab skills, organizational ability, and publication productivity.

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

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

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

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

The application file should be emailed to Dr. Daniel Bolnick (daniel.bolnick@uconn.edu). Include the subject line "Immune Genetics Postdoc: <YOUR NAME>". Applications must be received by April 2, 2018 for full consideration, though the position is open until filled.

For questions about this position, please email Dr. Bolnick (daniel.bolnick@uconn.edu). For information about the Bolnick Lab (presently at the University of Texas, moving to Connecticut this summer), visit the lab website (<https://bolnicklab.wordpress.com>), lab photostream (<https://www.flickr.com/photos/98765823@N08/albums>), and Dr. Bolnick's Google Scholar page (<https://scholar.google.com/citations?user=cfwxm0AAAAAJ&hl=en>).

The University of Connecticut is an Equal Opportunity

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

The Bolnick Lab is simultaneously searching for three postdoctoral researchers, and two laboratory technicians. With multiple positions open, this advertisement may be of interest to dual career couples.

University of Connecticut: Postdoctoral researcher in Ecological and Evolutionary Immunology.

A postdoctoral researcher position is available in Dr. Daniel Bolnick's research group (<https://bolnicklab.wordpress.com>), in the Department of Ecology and Evolution at the University of Connecticut.

Tasks: Recent work by the Bolnick lab identified naturally evolved variation in stickleback fishes' resistance to a severe cestode parasite (Weber et al 2017 American Naturalist; Weber et al 2017 Proceedings of the National Academy of Sciences), including the evolution of a protective but damaging immune response. This postdoctoral position is intended to pursue creative basic research related to the evolution and ecology of host defense and parasite immune evasion. Open questions include the ecological and historical context that favors versus inhibits the

— / —

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>

UFlorida HumanEvolutionaryGenetics

Post-doctoral position in Human Evolutionary Genetics and Epigenetics, Laboratory of Connie Mulligan, Department of Anthropology, Genetics Institute, University of Florida, Gainesville, FL, USA

Post-doctoral position to work on two ongoing NSF and internally funded projects: 1) 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, specifically behavior and 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>. 2) Investigation of genetic, epigenetic, and biological signatures of war trauma exposures and impact of a program intervention in Syrian refugees. This is a collaboration with Catherine Panter-Brick (Anthropology, 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 intergeneration 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 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/>.

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 one of the top 10 public universities in the country with a university-wide commitment to genetics research. The Department of Anthropology (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 In-

stitute (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 $\sim 1\text{A}\frac{1}{2}$ 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.

— 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>

UGlasgow ExptEvolMicrobes

Post-Doctoral Position at University of Glasgow in Experimental Evolution & Ecology of Salmonid-associated microbiota.

Appointee will make a leading contribution to a project aimed at understanding the significance of salmonid gut microbiota, part of which involves the development of a model salmon gut microbiome simulator (SalmoSim). In addition to developing a model system to understand microbiome ecology and evolution, the project will explore the contribution of commensal microbiota to salmonid physiology, health and nutrition. The post will integrate you into an international team of researchers between the UK, Ireland and Norway and you will play a role in advising several established PhD students in the lab. See <http://fisheye.ucc.ie/> for consortium details.

Specifically, the post holder will conduct, manage and publish research in the area of environmental microbiology, host-microbe interactions and nutrition as well as assist in managing and directing this complex and challenging project. The post represents an exciting opportunity for an advanced post-doctoral researcher enthusiastic to make a footprint in a rapidly growing field. There will be significant opportunity for interacting with commercial and industrial partners as well as to lead on excellent and pioneering research.

Salary will be on the Research & Teaching Grade, level

7, pounds 34,520 - pounds 38,833 per annum. This post is offered on a full time (35 hours) and open-ended basis with funding to April 2020 and the possibility of a 6-12 month extension. DEADLINE 16th April 2018

If interested, please email Martin Llewellyn (Martin.llewellyn@glasgow.ac.uk) for further details and apply through this link: <http://www.jobs.ac.uk/-job/BIG357/research-associate/> Martin Llewellyn <Martin.Llewellyn@glasgow.ac.uk>

UGlasgow VirusEvolutionEpidemiology

Postdoctoral position in virus evolution and epidemiology

A 2.5-year postdoc position is available in the research group of Roman Biek in the Institute of Biodiversity, Animal Health and Comparative Medicine at the University of Glasgow.

We are looking for a computational biologist interested in pathogen evolution and epidemiology to work on a project aimed at uncovering the role of evolutionary and environmental factors in virus emergence, spread and persistence, using bluetongue virus (BTV) as the study system. BTV is an RNA virus responsible for a globally important vector-borne disease in domestic and wild ungulates that has made repeated incursions into Europe in recent decades. Previous work in our group has highlighted the importance of genomic reassortment (Nomikou et al., 2015) and of large-scale environmental variability in the spread of European BTV strains (Jacquot et al. 2017). The aim of the current project is to study dynamics of BTV emergence and transmission, and the underlying mechanisms, at the scale of individual outbreaks through the integrated analysis of genomic, spatial and temporal data. The post is funded as part of a large European research consortium entitled "Understanding pathogen, livestock, and environment interactions involving bluetongue virus" (PALE-Blu, <http://www.palebludata.com>).

The applicant should have a PhD in a relevant field of biology or bioinformatics. Previous experience in computational analysis of genetic sequence data and strong quantitative skills will be essential, ideally including familiarity with high-throughput sequencing and large genomic data sets. The genetic data will be generated through project collaborators, so the work is exclusively

focussed on data analysis and no lab skills are required. Knowledge of epidemiological models, phylodynamic approaches, and pathogen evolution would be desirable but not essential. The candidate should be self-motivated and be able to work independently and have excellent communication skills. In addition to drafting scientific papers, the candidate would be expected to present at scientific conferences and manage collaborations with project partners.

Salary will be on the Research & Teaching Grade, level 6/7 - 28,098 - 31,604/34,520 - 38,833 per annum.

This post is available immediately (though exact starting time is negotiable) and is offered on a full time and open-ended basis with funding to October 2020.

Potential applicants are encouraged to make informal inquiries to roman.biek@glasgow.ac.uk. Formal applications need to be submitted under <http://www.jobs.ac.uk/job/BIH789/research-assistant-research-associate/>. The application deadline is 19 April 2018.

The University of Glasgow's Institute of Biodiversity, Animal Health and Comparative Medicine (IBAHCM) is internationally recognised for its research expertise in quantitative ecological and evolutionary approaches for studying the dynamics of infectious disease and providing solutions for their control. In the 2014 REF, Glasgow was ranked 3rd in the UK in Agriculture, Veterinary and Food Science, with 82% of impact and 91% of outputs considered 'internationally excellent' or 'world leading'. Biek is a member of the Boyd Orr Centre for Population and Ecosystem Health at Glasgow, representing an interdisciplinary group of ecologists, veterinary scientists, evolutionary biologists, mathematicians and engineers, which was awarded the Queen's Anniversary Prize in 2013. <http://www.gla.ac.uk/boydorr/> In Oct 2016 the Institute of Biodiversity, Animal Health & Comparative Medicine was awarded an Athena SWAN Silver departmental award. The award demonstrates our commitment to best practice in recruiting and supporting the career development and progression of female scientists, addressing gender inequalities in higher education. <http://www.gla.ac.uk/researchinstitutes/-bahcm/institute/athenaswan/> References

Nomikou, K., Hughes, J., Wash, R., Kellam, P., Breard, E., Zientara, S., Palmarini, M., Biek, R*. and Mertens, P*. , 2015. Widespread reassortment shapes the evolution and epidemiology of bluetongue virus following European invasion. *PLoS Pathogens*, 11(8), p.e1005056. doi:10.1371/journal.ppat.1005056 *joint senior authors
Jacquot, M., Nomikou, K., Palmarini, M., Mertens, P. and Biek, R., 2017. Bluetongue virus spread in

Europe is a consequence of climatic, landscape and vertebrate host factors as revealed by phylogeographic inference. *Proc. R. Soc. B*, 284(1864), p.20170919. doi:10.1098/rspb.2017.0919

Dr. Roman Biek Institute of Biodiversity, Animal Health and Comparative Medicine University of Glasgow Rm 401, Graham Kerr Building, Glasgow G12 8QQ

Email: roman.biek@glasgow.ac.uk

— / —

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>

U**Gothenburg Sweden** Birds**Macroevolution**

https://www.gu.se/english/about_the_university/job-opportunities/vacancies-details/?id=2001 Researcher in Anthropogenic biases in macroecological and macroevolutionary patterns in birds

Project description Birds are one of the most charismatic and well-studied group of animals, yet we know very little about how humans have affected their global patterns of diversity and evolutionary history. This project is part of a larger initiative funded by the Swedish Research Council titled “Is biodiversity understandable from contemporary distributions?” with Søren Faurby (goo.gl/9S6nuP) as a PI and Tim Blackburn (goo.gl/9LWXfk; a bird macro-ecologist at University College London) and Manuel Steinbauer (goo.gl/UEiG7T; an island biologist at Friedrich-Alexander University Erlangen-Nürnberg) as co-applicants. The work will involve close collaboration with this team as well as additional researchers at Gothenburg University, especially members of the Antonelli Lab (<http://antonelli-lab.net/>). Earlier work by the PI has discovered substantial biases in macro-scale analyses of mammals, when conclusions are drawn based only on present-day distributions (e.g. <http://onlinelibrary.wiley.com/doi/10.1111/ddi.12369/full>; <http://www.pnas.org/content/113/4/868.short>; <http://onlinelibrary.wiley.com/doi/10.1111/ecog.02287/abstract>). The goal of this project is to investigate whether those biases are restricted to mammals (which could be particularly sensitive to anthropogenic impacts), or are more general and affect other

organisms.

Job assignments - Retrieving and analyzing information on the taxonomy of extinct birds - Estimating and analysing potential present-natural distribution of all bird species and the differences between these and contemporary patterns

Employment The employment is a full-time position for 18 months. The physical placement will be at the University of Gothenburg, Department of Biological and Environmental Science but may include shorter stays at University College London or Friedrich-Alexander University Erlangen-Nürnberg.

Eligibility The applicant must hold a PhD in an area relevant for the tasks at hand (macroecology, ornithology, spatial analysis, macroevolution, palaeontology, or related fields). Note that the thesis must be awarded prior to the Closing date of this position.

Necessary qualifications - Documented capacity to work in groups and independently - Advanced skills in R or potentially another analytical platform - Excellent communication skills, written and spoken, in English are necessary since we work in an international environment.

Desirable qualifications - A strong publication record (relative to the applicants’ scientific age) - Experience with handling and ideally generating large databases - Experience with spatial and macro-evolutionary analyses - Knowledge of the study group (birds) - Experience in palaeontology and or taxonomy

The application should be written in English and must include: - A cover letter with the applicant’s justification for the application which describes how the applicant meets the selection criteria and potentially her/his plans for this project (max. two A4 pages) - A list of qualifications (full CV) - Certificate of PhD exam and other relevant education - Complete list of publications, including submitted and accepted manuscripts highlighting the up to five most important papers related to the application - Contact information for at least two referees that are familiar with the applicant’s work - A single pdf including all the documents above for easier evaluation

How to apply In order to apply for a position at the University of Gothenburg, you have to register an account in our online recruitment system. It is the responsibility of the applicant to ensure that the application is complete in accordance with the instructions in the job advertisement, and that it is submitted before the deadline. The selection of candidates is made on the basis of the qualifications registered in the application.

***Closing date:** 2018-04-15*

For further information please contact Assist. Prof. Søren Faurby Email: soren.faurby@bioenv.gu.se

-

Søren Faurby <http://antonelli-lab.net> Sören Faurby
<soren.faurby@bioenv.gu.se>

Uceland 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 Pálsson (apalsson@hi.is).

Deadline

The application deadline is through the 3rd April, 2018

<https://ugla.hi.is/radningar/index.php?sid=-2448&starf=295> - Arnar Pálsson - 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/
Arnar Pálsson <apalsson@hi.is>

Biological Sciences University of Idaho Phone: 208-885-4016

E-mail: ceparent@uidaho.edu Lab website: <http://parentlab.weebly.com/> “Parent, Christine (cepARENT@uidaho.edu)” <cepARENT@uidaho.edu>

UIdaho GalapagosLandSnails

Hi, The Parent Lab at the University of Idaho seeks a dynamic and highly motivated postdoc researcher to conduct independent research on the evolutionary ecology of adaptive radiation using a suite of evolutionary, ecological, and biogeographical approaches. Galapagos land snails of the genus *Naesiotus* is the most speciose adaptive radiation on these islands and present an opportunity to quantify phenotypic diversification across islands varying in community complexity. The postdoc will have substantial flexibility in pursuing ongoing projects in this system, potentially focusing on analyses of genomic data, quantitative genetics, and multivariate phenotypic variation. Alternative research directions will also be considered. Our lab is affiliated with IBEST < <http://www.ibest.uidaho.edu/> > (Institute for Bioinformatics and Evolutionary Studies) and CMCI < <http://www.cmciuidaho.org/> > (Center for Modeling Complex Interactions), and we have a very interactive department supporting a vibrant community of evolutionary biologists. We are located in a beautiful part of the country, in the nice small friendly town of Moscow in the Pacific Northwest in relatively close proximity to many national parks, Seattle, and Portland. The position will run for a minimum of one year, with opportunity for extension. Start date is as soon as possible but flexible for the right candidate. To apply, please submit as a single PDF file a cover letter detailing interest in the position, a research statement, CV, up to three recent and relevant publications, and contact information for three references to Christine Parent (cepARENT@uidaho.edu). Review of applications starts on April 9th, 2018 and continue until the position is filled.

Basic qualifications: Ph.D. or equivalent degree in biology, evolution, genetics, bioinformatics, or related field. Publications resulting from dissertation and broad interest in the evolution and ecology of adaptive radiation.

Preferred qualifications: Evidence of expertise in any area of genomic basis of adaptation, or quantification of natural selection in the field. There will be opportunities for fieldwork if desired, but this is not required for the position.

Christine Parent, PhD Assistant Professor

UKonstanz CichlidSpeciesDelimitation

Postdoctoral Position: Species delimitations in East African Cichlid Fish adaptive radiations A three year postdoctoral position working with Axel Meyer in the Evolutionary Biology Group at the University of Konstanz in Germany is available immediately. Funding is available through a grant of the German Science Foundation.

The project focuses on empirical and conceptual issues regarding species delimitation and hybridization in East African Rift Lake cichlid fishes. The research will center around the use of whole genome level data to resolve species boundaries in rapidly diversifying cichlid lineages in Lakes Victoria, Malawi, and Tanganyika. The work will make use of previously sequenced high-quality genomes as well as de novo sequencing of cichlid genomes to generate marker sets and guidelines within modern analytical frameworks for genomically diagnosing species. The funding period would be for three years and salary will be determined based on the German salary scheme TV-L E13 (annual before-tax salary is about 68,000 Euros, or about 83,000 USD).

The Evolutionary Biology group in Konstanz is composed of ~20 postdoc and graduate students. The collaborative research environment in the lab is highly integrative, very international, and operates fully in English. Therefore, the ability to speak German would be a plus, but is not essential. Further information on researchers and research in evolutionary biology in the Meyer lab can be obtained here: <http://www.evolutionsbiologie.uni-konstanz.com/> . Konstanz is a very beautiful and pleasant place to live as it borders the third largest lake in Central Europe and lies at the foothills of the Alps. The University of Konstanz is an equal opportunity employer and is rated as one of the best universities in Germany.

Requirements: PhD in biology and/or bioinformatics. Skills we would like you to have: understanding of phylogenetic methodology, knowledge of wet-bench molecular

techniques would be a plus, proven familiarity with high-throughput sequencing analyses, facility with one or more programming languages (such as Python, Perl, or R), and at least three peer-reviewed publications. Applications should be sent to Axel Meyer (axel.meyer@uni-konstanz.de) and include (1) a cover letter explaining your background and motivation, (2) a CV, and (3) email addresses of two references.

The deadline for applications is the 1st of May.

Review of applications will begin immediately and the position filled asap. The starting date is flexible.

darrin.hulsey@uni-konstanz.de

ULausanne ComputationalPopulationGenomics

Post-doctoral position available in Computational Population Genomics

A postdoctoral position in computational population genomics is available in the research group of Anna-Sapfo Malaspinas in the Department of Computational Biology at the University of Lausanne.

In our group, we generally aim at characterizing evolutionary processes while relying on genomics data from both modern and ancient samples. We develop analytical and computational methods to analyze and interpret population genomic data and we apply those methods to novel DNA datasets via collaborative projects.

We are looking for a computational biologist to analyze novel ancient human genomic datasets to further characterize how humans peopled regions such as the Pacific or the Americas. The main project for this position includes the coordination of data generation (potentially including field trips), data analysis with existing computational methods as well as extensive simulations for validations of results. Depending on interests and skill sets, the candidate could also decide to develop novel computational methods to characterize evolutionary processes relying on time serial data. Finally it is possible to set some time aside for i) a personal side project, ii) gaining experience in training master and PhD students and iii) applying for grants for the next academic steps.

Requirements - PhD in computational biology, population genetics or related fields. - Programming experience (e.g. python, R or C/C++, \hat{a} euro \hat{A}). - Good knowl-

edge of probability and statistics, including Markovian processes. - Experience of UNIX environment.

Department of Computational Biology, University of Lausanne Lausanne is a medium-sized city on the shores of Lake Geneva, surrounded by a wine growing region recognized as a UNESCO World Heritage Site, and within one hour of the Alps. It offers a great variety of cultural, recreational and outdoor opportunities.

The University of Lausanne (UNIL) is a higher teaching and research institution where approximately 14,000 students and nearly 4,000 collaborators, professors, and researchers work and study. Ideally situated along the lake of Geneva, near Lausanne's city center, its campus brings together over 120 nationalities.

The department of Computational Biology is a friendly new department within the University of Lausanne with expertises among the groups ranging from disease mapping, quantitative genetics, cancer genomics, phylogenetics, medical genetics and gene expression.

Our group recently moved to UNIL while also joining the SIB Swiss Institute of Bioinformatics. We are a multidisciplinary and international group.

Timeline and contract Starting dates are flexible but the candidate should start in 2018 (ideally before July). It is meant to be a full time position but a lower rate is negotiable e.g. for family reasons. Annual salaries are competitive (about CHF 80,000 ~ USD 80,000 ~ Euro 68,000/year) and there is available funding for three years while contracts are renewed annually.

How to apply Interested applicants should send a CV, contact information for three references, as well as a cover letter stating general research interests as well as motivation to join the group. If the candidate would like to work on their own side project, a short description should be sent along as well.

Please follow the instructions here: popgen.ch/jobs to submit your application.

The review of applications will start on March 1 2018 and will continue until a suitable candidate is found.

– Anna-Sapfo Malaspinas | Population Genomics Group | Department of Computational Biology | Genopode office 4008 | University of Lausanne | CH-1015 | Lausanne, Switzerland | tel: +41 21 692 4149 | website: popgen.ch | email: annasapfo.malaspinas@unil.ch

“annasapfo.malaspinas@unil.ch”
<annasapfo.malaspinas@unil.ch>

ULausanne Evolutionary Genomics Neurogenetics

A postdoc position is available within the lab of Roman Arguello at University of Lausanne's (UNIL) Department of Ecology and Evolution.

We are a newly formed lab interested in understanding the genetic and neural bases of sensory evolution. We take a very interdisciplinary approach that bridges computational/comparative genomics with neurogenetics. Our model organisms are diverse *Drosophila* species from around the globe, and we are particularly interested in the evolution of neural circuits and in the evolutionary processes related to the rapid changes underlying olfaction and temperature preference.

The specific focus for this position will be on olfactory evolution. The projects will relate repeated gains/losses in olfactory receptors to the evolution of their protein sequences, to their neural circuits, and to behavior. This work will test hypotheses about how the olfactory system evolves, and to what extent these changes are repeatable. Due to the cross-disciplinary nature of the research, there is a range of opportunities for contributing to the projects depending on particular interests and strengths (i.e. comparative/population genomics, neurobiology, generation of transgenic tools for new species).

Qualification include a PhD in genetics, evolutionary biology, neurobiology, or a related field, the ability to be self-motivated and to work independently as well as within a small group, good communication skills, comfortable with public presentations, and the ability to clearly document work. Additionally, expertise with several of the following tasks is required, and an interest/willingness to learn some of the others:

- molecular evolution and/or population genomic analyses - statistics and next-generation sequence analyses (programming/scripting in one or more languages such as Python, Perl, R, etc.)
- molecular biology (CRISPR/Cas9 vector designs)
- electrophysiology - histochemistry/microscopy (dissecting, tissue preparations, antibody staining, fluorescent in situ hybridization, confocal imaging)
- fly genetics and maintenance - fly embryo injections for generating transgenic lines and screening

This is a 100% position for an initial duration of one year,

renewable up to 2 or 3 years depending on the start date and funding available. The position is dedicated primarily to research, however some contribution to teaching is expected, including the possibility of assisting with the supervision of master students.

The Department of Ecology and Evolution is a lively, fun, productive, and highly diverse group. While UNIL is a French-speaking university, the working language of the Department and the Lab is English. For more information about the Department of Ecology and Evolution please see its page here: <https://www.unil.ch/dee/en/-home.html> Lausanne is a scenic medium-sized city situated on the edge of Lake Geneva. Life here is good. Its central location within Europe makes traveling by train and plane convenient. And for outdoor enthusiasts, Lausanne sits at the base of Alps and Jura which offer year-round escape and fun.

For more information about the Lab, or for further questions, please visit: arguellolab.org or email Roman at: jacob.arguello@unil.ch

Formal applications need to be done through HR, and must include a cover letter detailing your research interests and background, a CV, and the contact info for references (2-3). Applications should both be uploaded through the University of Lausanne platform (link given below), and sent as a single pdf to jacob.arguello@unil.ch.

Application Link: <https://bit.ly/2Ge0DA5> University equality policy: The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

"jacob.arguello@unil.ch" <jacob.arguello@unil.ch>

ULausanne Melanin Evolution

Evolution and coevolution of melanogenic genes

Melanin is the most widespread pigment in organisms. Synthesis of melanin occurs all across the tree of life, including in Eubacteria, Eukaryota, fungi, plants and animals and, perhaps, Archaea. The widespread capacity of life to synthesize melanin indicates the biological importance of this pigment, possibly from the very early stages of life. Melanins and pigmentations based on them are targets of intense research, particularly in animals and disparate fields such as oncology, biotechnology, evolutionary biology and ecology. From

an evolutionary perspective, there is increasing evidence that the expression of melanin-based coloration is often linked to other aspects of an individual's phenotype. Approximately 120 genes are known to be involved in the production of melanin. However, the rate at which these genes evolved and coevolved throughout the tree of life is unknown. In the present project, we propose to investigate the molecular evolution of melanogenic genes. Specifically, the goal is to determine the events of positive and purifying selection as well as how the different genes coevolved.

Please see Dib L, San-Jose Garcia L, Ducrest A-L, Salamin N, Roulin A. 2017. Selection on the major color gene melanocortin-1-receptor shaped the evolution of the melanocortin system genes. *International Journal of Molecular Sciences* 18, 2618.

The candidate should have a strong background in molecular evolution, phylogenetics and bioinformatics. A good knowledge of evolutionary ecology would be a plus.

Duration: 1 year

Please contact:

Prof. Alexandre Roulin University of Lausanne Department of Ecology and Evolution 1015 Lausanne Alexandre.Roulin@unil.ch

Or

Prof. Nicolas Salamin University of Lausanne Department of Computational Biology 1015 Lausanne Nicolas.Salamin@unil.ch

Alexandre Roulin <alexandre.roulin@unil.ch>

ULausanne PlantEvolution

Postdoc position, Department of Ecology and Evolution, University of Lausanne, Switzerland

A postdoctoral position in plant evolutionary biology is available in the research group of John Pannell in the Department of Ecology and Evolution, University of Lausanne. The postdoc will join a team of other postdocs and PhD students working on aspects of plant evolution, with a current emphasis on the evolution of plant sexual systems, sexual dimorphism, and the resolution of sexual antagonism in dioecious and hermaphroditic plants. For details, see <https://www.unil.ch/dee/pannell-group>. Research scope and skills sought The postdoc's research direction and projects can be tailored to her or his interests and expertise. However, apart from having a strong

interest (and PhD) in evolutionary biology and/or population genetics, we are ideally seeking someone with a skill set that includes at least one of the following: generation and analysis of genomic and transcriptomic NGS data; evolutionary, population genetic or demographic modelling; experimental design and statistics. Experience and an interest in working with plants could be an advantage, e.g., including managing glasshouse, 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 Department of Ecology and Evolution hosts a broad range of research groups, and its members enjoy a lively intellectual and social life. Although the University of Lausanne is francophone, the department is highly international, and all its research activity and seminars are conducted in English. The University has seven faculties and approximately 14,300 students and 3,900 researchers from over 120 countries. It is situated on a beautiful campus on the shores of Lake Geneva, and is close to the Swiss and French Alps.

Contract details The position is envisaged at 100% 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 John Pannell (john.pannell@unil.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 both be uploaded through the University of Lausanne platform (link given below), and sent as a single pdf to john.pannell@unil.ch. Applications received by April 06 will receive full consideration.

Application link: <http://bit.ly/2FTtgX0>

University equality policy The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

John Pannell <john.pannell@unil.ch>

UMichigan EvolutionEcologyHerpetology

Postdoctoral position: Evolutionary ecology of reptiles and amphibians

A postdoctoral position in the evolutionary ecology of reptiles and amphibians is available in Alison Davis Rabosky's lab at the University of Michigan, Ann Arbor. The postdoctoral researcher will both collaborate on and develop projects in one or more of the following areas: evolutionary genomics of snake coloration and venom, the evolution of integrated anti-predator phenotypes (e.g., behavior and coloration) in snake mimicry systems, morphological evolution and diversification across squamates, and/or the evolutionary origin and stability of novel phenotypes more generally. While our lab has ongoing projects in all of these areas, we welcome integration of independent research in related areas as part of this collaboration. This position is expected to have some combination of laboratory and field work, especially targeting reptile and amphibian communities in the Neotropics.

We are especially seeking applicants with a strong background in both evolution and herpetology, as well as generation and analysis of high throughput genomic data or 3-dimensional CT-based morphological data. Programming experience in R and/or Python is highly desirable, as is a love of scientific writing.

The position offers exciting opportunities for independent research, mentoring, and career development, as we have an outstanding group of researchers in evolutionary biology and biodiversity science in the Department of Ecology and Evolutionary Biology. We also welcome applicants with particular interest in contributing to and/or utilizing our world-class herpetological collections in the UM Museum of Zoology (<https://lsa.umich.edu/ummz/herps.html>).

Applications should be sent to ardr at umich.edu. Please include a cover letter describing your research interests and background, a CV, one reprint of your favorite first-author publication or other writing sample, and contact information for three references. Review of applications will begin on March 31, 2018 and will continue until the position is filled (start date is flexible). Any questions about the position can be directed to Alison Davis Rabosky (<https://lsa.umich.edu/eeb/people/faculty/>

[ardr.html](#)).

More information about the Davis Rabosky lab can be found at: <http://www-personal.umich.edu/~ardr/index.html> "ardr@umich.edu" <ardr@umich.edu>

UMontana EvolutionaryGenomics

Postdoctoral Research Associate - Evolutionary Genomics, University of Montana

The Miller Lab in the Division of Biological Sciences at the University of Montana, Missoula (<http://hs.umt.edu/dbs/labs/miller>) is hiring a postdoctoral research associate in the area of evolutionary genomics. The nature of the project is flexible but should investigate the mechanisms responsible for the origins and maintenance of bacterial diversity. Recent projects have focused on the mechanisms of gene duplicate retention in bacteria with exceptionally high duplication rates, the population genomics of local adaptation along an environmental gradient and the maintenance of variation by ancient balancing selection (<http://www.nature.com/articles/s41559-017-0435-9>). A Ph.D. in biology or a related field is required, and the successful candidate will demonstrate a strong background in molecular evolution and genomics as well as proficiency with Python and/or Perl.

The Division of Biological Sciences at the University of Montana (hs.umt.edu/dbs) is home to a diverse and highly interactive faculty, and the Miller lab is housed in newly constructed space dedicated to genomics research. Missoula is a great college town located in the heart of the Rocky Mountains with an exceptional quality of life. For more information on this position and our research, please contact Scott Miller at scott.miller@umontana.edu.

To apply, please visit <http://umjobs.silkroad.com> and click the job title for this position (Tracking Code 1811-254) under All Openings. Candidates must apply online and will be asked to upload the following application materials: a cover letter describing research interests and qualifications, a CV, and the names and contact information for three references. The appointment is a 12-month Letter of Appointment with flexible start date, renewable for up to two years with a possible extension to a third year.

University of Montana is an ADA/EOE/AA/Veteran's Preference Employer

“Scott.Miller@mso.umt.edu”
<Scott.Miller@mso.umt.edu>

UMontana Evolutionary Genomics

Postdoctoral Research Associate Evolutionary Genomics, University of Montana

A postdoctoral position on the evolution of gene regulatory pathways and the developmental basis of speciation is available in the laboratory of Jeffrey Good at the University of Montana, Missoula. The position is part of an NIH-funded research program on the evolution of gene expression during embryonic development and the contribution of hybrid regulatory breakdown to mammalian speciation. The research utilizes a systems genomics approach combining experimental quantitative genetics in rodent models with high-throughput genomic methods (transcriptomics and epigenomics) to link mechanisms of gene regulatory evolution to complex phenotypes in developing placenta and embryos. We seek a candidate with a strong background in molecular biology, quantitative genetics, evolution, and/or genomics. A Ph.D. in biology or a related field is required. Candidates with previous experience collecting and analyzing large-scale genomic data are strongly encouraged to apply.

The University of Montana offers a vibrant research community. The Good lab shares newly constructed molecular and computational space with five other outstanding groups, as part of an entire floor dedicated to evolutionary genomics research. Missoula is a great college town located in the heart of the Rocky Mountains of western Montana. For further information on this position and our research please visit the Good Lab website (thegoodlab.org) and email Dr. Good directly at jeffrey.good@umontana.edu. All applicants are encouraged to contact Dr. Good prior to applying.

To apply, please visit <http://umjobs.silkroad.com> and click the job title for this position under Current Openings. Candidates must apply online, and will be asked to upload the following application materials: a cover letter describing your research interests and qualifications, a CV, and the names and contact information for three references. Applications will be reviewed upon receipt and the position will remain open until filled. The position is available immediately with a flexible start date contingent on the needs of the preferred candidate.

ADA/EOE/AA/Veteran's Preference Employer

Jeffrey M. Good, Ph.D.

Associate Professor Division of Biological Sciences
The University of Montana 32 Campus Drive, HS104
Missoula MT 59812 Phone: 406-243-5771 Fax: 406-243-4184 Website: <http://www.thegoodlab.org/> jeffrey.m.good@gmail.com

UNorthTexasHealthScience Bioinformatics Population Genetics

The Budowle lab (<https://www.unthsc.edu/graduate-school-of-biomedical-sciences/molecular-and-medical-genetics/laboratory-faculty-and-staff/>) at the University of North Texas Health Science Center is seeking a postdoctoral research associate in the fields of bioinformatics and population genomics. Candidates must be proficient in at least one coding language, be able to work both independently and in a group setting, and be motivated to apply their talents to the field of forensic genetics. The ideal candidate would have a solid grounding in computation, population genetics and statistics. Well-qualified candidates would have proficiencies in 2 of the 3 areas. The current projects in the lab pertain to mixture interpretation and the analysis of massively parallel sequencing data, especially as it applies to short tandem repeats and mitochondrial markers. The position is available for at least 1 year with the possibility of renewal after that.

Interested candidates should send their CVs and a brief statement of their research interests and goals to August at August.Woerner@unthsc.edu for more information.

“August.Woerner@unthsc.edu”
<August.Woerner@unthsc.edu>

UPennsylvania Evolution Infectious Microbes

Postdoctoral Researcher University of Pennsylvania, Department of Biology

The Evolution and Ecology of Disease Systems laboratory (<https://web.sas.upenn.edu/brisson-lab/>) at the University of Pennsylvania is searching for a postdoctoral researcher to investigate evolutionary or ecological

processes in vector-borne microbial pathogen systems. Vector-borne diseases are one of the most prevalent types of emerging infectious diseases worldwide and are a major threat to public health. Our current research aims are to identify the factors that govern the emergence of these pathogens by identifying patterns of, and processes affecting, their population dynamics. The main duties of the postdoctoral researcher could include applying advanced molecular tools, processing and analyzing next generation sequence data including quality control and bioinformatics, or applying advanced statistical analyses to existing datasets. The ideal candidate must have enthusiasm for evolutionary- or ecologically-based questions and could have experience designing and troubleshooting advanced molecular protocols, analyzing population genetic or genomic data, or building and applying machine-learning algorithms.

The Department of Biology has a long-standing tradition of maintaining an integrated research and educational program across all basic biological sciences including Ecology and Evolution, Plant Sciences, Molecular and Cellular Biology, Genomics, and Neuroscience. The Department values interdisciplinary research, collaboration, and collegiality, emphasizing Life in its Natural Context. The University of Pennsylvania has a strong group of evolutionary biologists that frequently interact with each other and with an accomplished group of microbiologists in the Medical and Veterinary schools. Unlike many universities, the proximity of the medical, veterinary, and arts and science schools are centrally located on the Philadelphia campus, which promotes a cross-talk and collaboration. The University of Pennsylvania is an equal opportunity employer. Minorities, women, individuals with disabilities, and protected veterans are encouraged to apply.

The position is available as early as Fall 2018. Salary is commensurate with experience based on the NIH guidelines.

To apply, please send (1) a cover letter outlining your previous experiences that make you suited for this position as well as your research, training, and career goals, (2) CV, and (3) Contact information for 3 references via email to dbrisson@sas.upenn.edu.

Please send enquiries to dbrisson@sas.upenn.edu

Dustin Brisson, Associate Professor Director, Evolution and Ecology of Disease Systems Laboratory Department of Biology University of Pennsylvania Philadelphia PA 19104-6018 <http://www.bio.upenn.edu/faculty/-brisson/> <https://web.sas.upenn.edu/brisson-lab/> "Brisson, Dustin" <dbrisson@sas.upenn.edu>

UPittsburgh Experimental Evolution

Postdoc:Pittsburgh_Experimental.Evolutionary.Ecology

The Turcotte Lab (www.martinturcotte.net) at the University of Pittsburgh is hiring a postdoc to experimentally test the dynamic interplay between rapid evolution and community ecology in the field. Field experiments could be combined with lab experiments, modeling, comparative approaches, or theoretical development. Although I have some projects in mind, this position is independent of current grants and thus allows you to develop your own research questions. Start date is flexible but I would prefer the candidate to begin as soon as possible.

The Department of Biological Sciences at Pitt is a dynamic and growing team of enthusiastic researchers and educators (6 new Assistant Prof. hires in E&E in the last 1.5 years). The department also runs the Pymatuning Lab of Ecology, which is equipped with lab space and housing to facilitate field-based research. The City of Pittsburgh is a vibrant and beautiful place to live. It is often voted the 'Most Livable City in the U.S.'.

Requirements: Candidates must have a PhD in Ecology, Evolution, Genetics, or related topics. The position is for 1 year with the option to extend for up to 2 more years. A valid drivers license is required.

To apply for the position please send an email to me (turcotte@pitt.edu) including a cover letter stating why you are interested in the lab and your past research experience. Please also include your C.V., the contact information for three references, and up to 3 PDFs of relevant publications or manuscripts in prep. Applicants should submit their materials by March 30, 2018 to ensure full consideration.

Martin Turcotte, Ph.D. Assistant Professor, Department of Biological Sciences University of Pittsburgh

"Turcotte, Martin" <TURCOTTE@pitt.edu>

USaoPaulo UCambridge HostParasite

Host-parasite ecology, evolution and genomics

Universidade de Sao Paulo and University of Cambridge

We are seeking candidates interested in applying for a FAPESP postdoctoral fellowship (<http://www.fapesp.br/en/5427>) to work on a project on host-parasite ecology, evolution and genomics. The project is a collaboration between Rodrigo Cogni's lab at Universidade de Sao Paulo in Brazil and Frank Jiggins's lab at Cambridge University in the UK. The project has ongoing support from a Young Investigator Award from FAPESP and a Newton Advanced Fellowship from the Royal Society. We will investigate how the bacterial endosymbiont *Wolbachia* and polymorphisms in the *Drosophila* genome affect the virome of *Drosophila* species in the wild. The project (1) uses modern next-generation sequencing technologies to discover new viruses in insects, (2) it is the first study to comprehensively investigate virus resistance in wild *Drosophila* populations, and (3) it uses natural population of extremely biodiverse communities of South-American *Drosophila*. Fellows will have the opportunity of guide the directions of the research depending on their interests.

The initial fellowship would be for two years in Sao Paulo and one year in Cambridge, with the possibility of renewing for another year. FAPESP pays 7,174 reais/month (tax free), relocation costs and 12,914 reais/year for training, conferences and research expenses for the time in Sao Paulo, and 2,200 pounds/month (tax free), relocation costs and 3,900 pounds/year for training, conferences and research expenses in the UK. All work can be performed using English, no Portuguese proficiency required. Applications for the fellowship will be prepared with the Brazilian supervisor, and can be sent at any time of the year.

We are seeking highly motivated candidates who have a deep interest in this area of research. Applicants must have, or will shortly obtain, a PhD. Ideally the candidate's past work will be in ecology, genetics or evolutionary biology. To be competitive for the fellowship, candidates must have a strong publication record (please email your CV to Rodrigo rodrigocogni@gmail.com to discuss this requirement). If you are interested please contact Rodrigo before April 30th.

The Labs: <http://ecologia.ib.usp.br/ecoevo/> and <http://www.jiggins.gen.cam.ac.uk/> Enquiries: rodrigocogni@gmail.com

Rodrigo Cogni

Assistant Professor, Department of Ecology, Universidade de São Paulo Royal Society-Newton Advanced Fellow

Rua do Matão 321, Trav. 14 (sala 353) Cid. Universitária, São Paulo-SP CEP: 05508-090 E-mails: rodrigocogni@gmail.com and rcogni@usp.br <http://ecologia.ib.usp.br/ecoevo/> Rodrigo Cogni <rodrigocogni@gmail.com>

UStockholm PopulationGeneticsGenomics

<https://www.su.se/english/about/working-at-su/-jobs?rmpage=job&rmjob=4992&rmlang=UK> Postdoctoral Fellow in Population Genetics/Genomics of Brown trout and Arctic char with a focus on Biodiversity Conservation

The position will be held in the Department of Zoology, a vibrant international community consisting of five interactive and collaborative divisions: Ecology, Ethology, Population Genetics, Functional Morphology, and Systematics and Evolution. The advertised position will be part of the Division of Population Genetics.

Project description

The focal area of the research is population and conservation genetics/genomics and will be carried out within funded projects in Linda Laikre's group aimed at developing goals and guidelines for maintaining genetic biodiversity of metapopulations (Swedish Research Council Formas) and strategies for including genetic diversity in environmental monitoring efforts (collaboration with the University of Gothenburg and the Swedish Agency for Marine and Water Management).

We use new mathematical tools developed in cooperation with mathematicians at Stockholm University to explore the dynamics of the genetically effective population size (N_e) of metapopulations. To empirically estimate rates of microevolution we use brown trout (*Salmo trutta*) and Arctic char (*Salvelinus alpinus*) inhabiting Swedish mountain lake systems as models, and the present position is primarily connected with this part of the projects. We take advantage of our frozen tissue bank collection

spanning extensive material from several decades back in combination with new collections; fieldwork will be carried out in remote mountain areas of the County of Jämtland, Sweden during the summer of 2018 for revisiting locations from which old material is available. We use SNP markers in combination with individual DNA sequencing and pool sequencing and apply new approaches for genomic data analyses to explore rates of genetic change at different regions of the genome in collaboration with Dr. Christopher Wheat in our division using new approaches developed by his group.

There are good opportunities to contribute own research ideas in addition to the work planned by the lab. Also, there are good opportunities for interacting with other research groups and divisions of the department, and with collaborating labs at other scientific institutions as well as with Swedish management authorities.

Main responsibilities

The position is 100 percent research and will include analyses of SNPs and of individual as well as pool sequencing data.

Qualification requirements

Postdoctoral positions are appointed primarily for purposes of research. Applicants are expected to hold a Swedish doctoral degree or an equivalent degree from another country. The applicant must have a PhD in population genetics, evolutionary genetics, bioinformatics or a similar field from an accredited college/university.

Assessment criteria

The degree should have been completed no more than three years before the deadline for applications. An older degree may be acceptable under special circumstances, which may involve sick leave, parental leave, clinical attachment, elected positions in trade unions, or similar.

In the appointment process, special attention will be given to candidates with a strong interest in population and conservation genetics/genomics, statistical analysis, and with good experience from analyses of nuclear genes/loci and DNA sequencing data. Bioinformatics skills are appreciated. Applicants should have a strong record of writing and publishing high quality scientific papers. Also, the applicant needs to work well both independently and in teams.

Terms of employment

The position involves full-time employment for a maximum of two years, with the possibility of extension under special circumstances. Starting date as soon as possible, according to agreement.

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 Professor Linda Laikre (PI and host for the position), telephone: +46 8 16 42 83, linda.laikre@popgen.su.se.

Union representatives

Ingrid Lander (Saco-S), telephone: +46 708 16 26 64, sacco@saco.su.se, Lisbeth Häggberg (Fackförbundet ST and Lärarförbundet), telephone: +46 8 16 20 00 (operator), and seko@seko.su.se (SEKO).

Application

Apply for the position at Stockholm University's recruitment system by clicking the "Apply" button. It is the responsibility of the applicant to ensure that the application is complete in accordance with the instructions in the job advertisement, and that it is submitted before the deadline.

Please include the following information with your application

Your contact details and personal data

— / —

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>

UToronto
EvolutionDrugResistanceMalaria

A postdoc position is available in the lab of Nicole Mideo, in the Department of Ecology & Evolutionary Biology at the University of Toronto. The position is part of an NIH-funded study of drug resistance in malaria parasites. The aim of the project is to use longitudinal amplicon sequencing data to look for phenotypic signatures of resistance in malaria infections, i.e., variants with increasing relative abundance over the course of treatment.

The successful candidate will be involved in developing approaches for analysing (and ultimately analysing) relative abundance time series data. The ideal candidate will have experience analysing such data in any context.

A PhD in ecology, evolution, biology or a related field is required.

Collaborators on this grant have been collecting data from malaria clinics in sub-Saharan Africa, so that we can contribute to identifying drug resistant parasites and tracking their spread globally. One key challenge in these areas is that most infections harbour multiple parasite genotypes, and when resistance is rare (and its underlying genetics unknown) its effects are hard to detect. More background for this project can be found in some of our previously published papers, including an opinion piece outlining the challenge of within-host diversity as well as potential approaches for overcoming it (<https://www.sciencedirect.com/science/article/pii/S1471492213000767>) and an analysis of previously collected data (<https://academic.oup.com/emph/article/2016/1/21/2802531>).

The position is available for 2 years, subject to annual review. The expected start date is July 1, 2018, but there is flexibility on that.

To apply, please send (1) a cover letter outlining your previous experiences that make you suited for this position as well as your research and career goals (2) a CV, and (3) contact information for three people who can provide a reference via email to nicole.mideo@utoronto.ca.

The University of Toronto is a leading academic institution with over 60 faculty members specialising in ecology and evolution. Strong links exist between the Department of Ecology and Evolutionary Biology and the Royal Ontario Museum, the Centre for Global Change Science, the Dalla Lana School of Public Health, the School of the Environment, the University network of leading academic research hospitals (www.uhn.ca, sunnybrook.ca) and research groups with provincial and federal government agencies. The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas. Toronto is also a vibrant and cosmopolitan city; one of the most desirable in the world in which to work and live.

Nicole Mideo Assistant Professor Department of Ecology & Evolutionary Biology University of Toronto 25 Willcocks St. Toronto, ON M5S 3B2

<https://mideo.eeb.utoronto.ca> Tel: 416 978 1316

Nicole Mideo <nicole.mideo@utoronto.ca>

UUm WildlifeMetaGenomics

The Institute of Evolutionary Ecology and Conservation Genomics / University of Ulm invites applications for a Postdoc position in Wildlife Metagenomics

Applications are invited for a 2-year postdoc position investigating the effects of environmental changes on the dysbiosis of wildlife gut microbial communities and associated fitness/health consequences. Our research focus on the relationships between land-use changes, wildlife genome-wide and immune genetic diversity, host's microbiome, and viral and helminthic co-infections. We offer a very stimulating, multi-national research community with excellent infrastructure.

We are looking for a skilled, creative and highly-motivated postdoc who is able to work independently and in a team. The position requires social, teaching, organizational and time-management skills. A high standard of spoken English and manuscript writing proficiency is required. The candidate should be willing to support teaching and supervising undergraduate and PhD students' projects as well as developing and performing own research. Candidates should hold a completed doctoral degree and have a strong background in evolutionary ecology and genomics, microbiome and metagenomics research, and should be qualified by a very good publication record. Preference will be given to a candidate with own practical experience with next generation sequencing and analysis of large bacterial and metagenomic data sets generated by the candidate, including bioinformatic data processing (Qiime2), multivariate modelling and statistics, and R and Python programming languages.

Please send your application as a single (!) pdf file to Prof. Dr. Simone Sommer (simone.sommer@uni-ulm.de). The pdf must include a letter describing your past research experience and particular skills and motivation for this position (max. 2 pages), an outline of planned own future projects (max. 2 pages), a CV, a summary of the PhD thesis, 2-3 letters of recommendation or contact details of referees and your publication list. The candidates will be selected according to their scientific qualification and proposed project plan. The anticipated starting date is July 2018.

The position is open until filled, and applications will be reviewed continuously, but for full consideration please

apply by May 1st, 2018. Remuneration is in accordance with TV-L 13 (100%). The applicants assessed as the best qualified will be called to an interview, which might be carried out online.

Physically disabled applicants receive favorable consideration when equally qualified. Job sharing is always possible for full time positions. The University of Ulm is committed to increase the share of women and teaching positions and therefore explicitly encourages female candidates to apply. The appointment is made by the Central University Administration. Please indicate the index number 48.

Simone Sommer <Simone.Sommer@uni-ulm.de>

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/department-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](mailto:albertof@uwm.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 researchers 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 Tel: 414-229-6343

Filipe AOs Alberto <albertof@uwm.edu>

UWisconsin StevensPoint PopulationGenomics

Postdoc: Population genomics of Great Lakes fishes at UW-Stevens Point

The Larson Lab at the USGS Wisconsin Cooperative Fishery Research Unit (UW-Stevens Point) is looking for a postdoctoral researcher to conduct genomics research on cisco populations throughout the Great Lakes region. The successful applicant will focus on analyzing RAD data from over 60 populations of cisco to investigate population structure at neutral and adaptive markers. Opportunities to work on additional projects such as population genomics in walleye and eDNA metabarcoding will also be available. Competitive applicants should have a strong background in bioinformatics and proficiency in one or more scripting languages such as Perl or Python. The full listing can be found at https://larsonlab.files.wordpress.com/2018/02/larson_wicfru_genomics_postdoc.pdf and information on how to apply can be found at https://larsonlab.files.wordpress.com/2018/02/uwsp_how-to-apply-instructions.pdf. The application deadline is April 9 and we are looking for someone to start in early summer but starting dates are flexible. Please direct any additional questions to Wes Larson (wes.larson@uwsp.edu).

“Larson, Wes” <Wes.Larson@uwsp.edu>

UWyoming PlantMicrobeEvolution

Three postdoctoral positions in the evolution of plant-microbe interactions and microbial ecology

Position descriptions available below and on the UW job site (positions 9465, 9480, 9466) at <https://tinyurl.com/yd3qoag3> Post Doctoral Research Associate in Plant-Microbe Interactions (position 9480): The Weinig lab at the University of Wyoming (<http://www.uwyo.edu/botany/people/faculty/cynthia-weinig.html>) is seeking a postdoctoral researcher to collaborate on research studying 1) the effects of host plant genetic pathways in selecting microbial taxa and communities and 2) the

consequences of microbes to host plant performance. Minimum requirements include a Ph.D. in a relevant discipline as well as demonstrated ability to work as an independent and innovative researcher, experience conducting plant or soil microbial ecology experiments, expertise in bioinformatics of biomarker gene sequencing, and history of peer-reviewed publication. More specific preferred qualifications include proficiency in environmental DNA extraction, amplicon preparation, and field experience.

Post Doctoral Research Associate in Microbiology and Microbial Ecology (position 9465): The Ward research group at the University of Wyoming (<http://www.naomiwardlab.com/>) is seeking a postdoctoral researcher in microbiology and microbial ecology. Minimum requirements include a Ph.D. in a relevant discipline, and experience in successful cultivation of diverse bacterial taxa from environmental samples. Additional preferred qualifications include expertise in genomic, proteomic, or metabolomic approaches to microbial ecology, as well as fieldwork experience.

Postdoctoral research associate in Microbial Ecology (position 9466): The van Diepen Soil Microbial Ecology lab (<https://sites.google.com/site/lindavdiepen/home>) at the University of Wyoming is seeking a postdoctoral researcher with expertise in microbial ecology and physiology, biogeochemistry, and microbial genomics. Minimum requirements include a PhD in a relevant discipline, proficiency in bioinformatics, and R programming or other statistical software. Additional preferred qualifications include experience with microbial culturing techniques, environmental metagenomics and transcriptomics analysis, field work, and method development.

This search is part of a cluster hire of postdoctoral research associates, supported by a new 5-year, \$20 million NSF EPSCoR RII Track-1 grant to the University. In this project we will study microbial life and its ecological consequences; additional details can be found at <http://www.uwyo.edu/epscor/microbial-ecology>. To apply, please complete the online application through <https://tinyurl.com/yd3qoag3> with the correct position number (positions 9465, 9480, 9466). Please upload a single PDF file containing a cover letter, CV, contact information for three references, and two papers describing recent research. Review of applications will continue until a suitable applicant is identified.

The University of Wyoming is an Equal Employment Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability or protected veteran status or any other characteristic protected by law and University policy.

Please see www.uwyo.edu/diversity/fairness . Cynthia Weinig <cweinig@uwyo.edu>

Vienna IST EvolutionaryGenomics

The Evolutionary Genomics laboratory (Kondrashov Group - <http://ist.ac.at/research/research-groups/-kondrashov-group/>) is looking for motivated postdocs or technicians with extensive experience in the laboratory to spearhead empirical assays of complex fitness landscapes. We are looking for candidates with extensive experience in molecular and synthetic biology techniques, such as genome modification and complex DNA design. Experience with competition or growth assays of yeast or bacteria and programming experience is welcome, but not strictly necessary. Our laboratory strives to create an open and interdisciplinary intellectual environment, encouraging all members to contribute to project design and eventually pursue independent research interests. For the purposes of this call we are looking for someone to contribute to a series of specific projects, however, parallel design and implementation of independent work will be encouraged.

Candidates are requested to send their CV and a short (1/2 page) statement of purpose, including a statement if the application is for postdoc or technician, to Alex Mally (alexandra.mally@ist.ac.at). The positions will be open until filled and pre-selected candidates will be expected to pass a Skype or on-site interview. Successful candidates will be offered a standard contract in the IST salary scale for a minimum of 2 years and extendable to maximum of 5. Candidates are also encouraged to apply to the independent IST Plus fellowship by March 15 (<http://ist.ac.at/research/postdoctoral-research/-istplus/>).

The Kondrashov Group is based in the Institute of Science and Technology, Austria, a commutable distance from Vienna. It boasts an incredibly interdisciplinary environment, with physics, mathematics and biology on the same tightly knit campus. Vienna is consistently classified as providing one of the highest standards of living in the world, with IST providing additional support, such as an on-campus daycare.

Fyodor Kondrashov <fkondrashov@gmail.com>

WashingtonStateU TasmanianDevilGenomics

POSTDOCTORAL RESEARCHER

Washington State University School of Biological Sciences

We are seeking 1-2 postdoctoral researcher(s) to work on evolutionary genomics and transcriptomics of Tasmanian devils and Tasmanian devil facial tumor disease, a transmissible cancer. This NIH/NSF-funded international collaboration builds on over 20 years of research tracking the spread of the unique infectious cancer across Tasmania and consequent endangerment of the iconic Tasmanian devil. Reference genomes and transcriptomes are available for both tumor and devil, and the successful applicant will have an unprecedented opportunity to analyze thousands of devil genotypes and hundreds of tumor samples taken both before and after epizootics to test for selection throughout both genomes, coevolution, patterns of resistance, and phenotypic evolution of Tasmanian devils aided by pedigree reconstruction. The position is centered in the lab of Dr. Andrew Storfer (www.wsu.edu/~storfer) at Washington State University, in collaboration with Dr. Paul Hohenlohe at the nearby University of Idaho (8 miles away). Both universities have genomics core facilities, including the Institute of Bioinformatics and Evolutionary Studies (IBEST; <http://www.uidaho.edu/research/ibest>), the WSU Genomics Core Facility (<https://labs.wsu.edu/genomicscore/>) and the WSU Kamiak High Performance Computing cluster (<https://hpc.wsu.edu/>) with state-of-of-the art equipment, computational facilities and staff support.

Review of applications will begin on April 15, 2018 and continue until the position is filled. A Ph.D. in Biology or a related discipline, combined with genomics and bioinformatics experience is required. Desired qualities also include a background in pedigree reconstruction, population genomics, phylodynamics, infectious disease evolution, and/or cancer genomics. Start date is negotiable, but is anticipated to be between May and August, 2018. Salary and benefits are competitive. Position is for 1 year, with continuation for additional year(s) pending satisfactory progress. To apply, please send in pdf format a CV, and names, addresses and email addresses of 3 references, a research statement, and up to 3 representative reprints via email to: Andrew Storfer (astorfer@wsu.edu).

WSU is an Equal Opportunity/Affirmative Action/ADA educator and employer.

Andrew Storfer, PhD Professor School of Biological Sciences Washington State University Pullman, WA 99164 USA Phone: (509) 335-7922 Fax: (509) 335-3184 astorfer@wsu.edu www.wsu.edu/~storfer Andrew Storfer <andrew.storfer@gmail.com>

WayneStateU Detroit FishPopulationGenomics

The Dowling lab in the Department of Biological Sciences at Wayne State University invites applications for a Postdoctoral Fellow. The individual will assist with multiple aspects of research focused on evolution and conservation of fish biodiversity, with focus on species from the southwestern United States. Examples of projects include identification and application of SNP markers for population genomic and demographic studies of endangered species and identification of sex determining loci in an allopolyploid species.

Applicants are expected to have a Ph.D. degree in biology or a related field, with bioinformatic and laboratory experience required. The principal duties will be the collection and analysis of genomic data and writing reports and manuscripts. Applicants should be proficient with basic molecular procedures (DNA/RNA extraction, PCR, electrophoresis, sequencing) and have experience with command line data analysis (e.g., R or Python). Preferred qualifications include experience with shell scripting (Unix/Linux systems), and preparation of RAD-seq or other NextGen sequencing libraries.

Wayne State University is a large urban university in downtown Detroit, Michigan, in an area that is going

through a renaissance. In 2014, USA Today named it one of its “10 Up-and-Coming Neighborhoods around the USA,” and Detroit has also drawn recognition as a travel destination (<https://tinyurl.com/y7agk4ex>). The area has many excellent museums, theatres, libraries, concert halls, and professional sports venues. Among the cultural institutions within easy walking distance of the main campus are the main branch of the Detroit Public Library, the Detroit Institute of Arts, the Charles H. Wright Museum of African American History, the Michigan Science Center, the Fisher Theatre, Detroit Children’s Museum, and the Detroit Historical Museum. The state of Michigan has a wealth of historical and outdoor opportunities (<https://tinyurl.com/yaoscmof>) and is within easy driving distance of large metropolitan centers like Chicago, IL and Toronto, ON.

Those who work and study at Wayne State know Detroit is on the rise. Over the past year, the national media has taken notice, too. This year, a variety of publications touted the city as a must-visit destination. Salary will be commensurate with training and experience. Additional information on the position and instructions for application are provided at the following web address:

https://jobs.wayne.edu/applicants/jsp/shared/-Welcome_css.jsp Posting is job number 043026 under Research Assistants/Associates.

If you have any questions please email Tom Dowling (thomas.dowling@wayne.edu).

Thomas Dowling
Department of Biological Sciences
5047 Gullen Mall
Wayne State University
Detroit MI 48202
313-577-3020
Thomas Dowling <thomas.dowling@wayne.edu>

Workshops Courses

Arnold Arboretum Plant Morphology Jun11-22 Deadline 117	128
AuburnU Alabama Bioinformatics Jun4-8 118	NorthCarolingMichigan Avida-ED Summer 129
Australia StructuralModelling Jun18-22 118	OberaegeriSwitzerland TamingTheBEAST June17-22 129
Barcelona Morphometrics Jun19-22 119	ObergeriSwitzerland BEAST Jun17-22 130
Barcelona PhylogeneticAnalysisUsingR Sep3-7 . . . 119	Portugal 2 EvolBiol Apr 131
Berlin MolecularPhylogenies Apr9-13 deadline . . . 120	Reminder MexicoCity PCMs Jun26-29 132
Berlin Paleogenomics May7-11 121	Seattle StatGenetics Jul9-27 132
Berlin PopulationGenomics May14-18 121	Sweden Bioinformatics with R Jun11-21 132
Berlin SignaturesSelection-GWAS Oct22-26 123	Turin EvolGameTheory Jul16-19 132
Berlin TransposableElements Apr23-27 124	UK PhylogeneticComparativeMethods Oct22-25 . . 133
Edinburgh EvolvingPopulations Jul2018 124	UK QuantModellingGenomes Apr30-May4 134
Faro Portugal Phylogenetics Sep24-29 125	UPorto ModellingSpeciesEnvAdaptation Apr23-27 135
Hinxton UK GeneticAnalysis Jul18-24 126	Virginia ConservationBioinformatics Oct10-19 . . . 135
IndianaU TranscriptomeAssembly Apr30-May1 . . . 126	Virginia ConservationGenetics Aug19-30 Deadline 136
Kaunas Lithuania ForestTreeGenomics Jun4-7 . . . 127	WellcomeUK DrosophilaGenomics Jul30-Aug3 . . . 137
Lima Peru TeachersOfEvolution Jul30-Aug5 127	WellcomeUK EvolutionCancer Apr24 138
LundU EvolutionaryBiologyUsingR May-Jun 128	
Montpellier DrosEU AdaptationGenomics Aug23-24	

Arnold Arboretum Plant Morphology Jun11-22 Deadline

Deadline approaching!!

This two-week short course (June 11 'V 22, 2018) will be taught by experts from around the world as an intense lecture, laboratory, and living collections learning experience. The course will be based at the Weld Hill Research Building at the Arnold Arboretum in Boston (Massachusetts), which offers a state-of-the-art microscopy laboratory for teaching and sits amid the 15,000+ living specimens of more than 2,200 species at the Arnold Arboretum.

This course will provide a working knowledge of concepts that are central to understanding the developmental basis for the remarkable structural and functional diversity of plants. Topics include developmental dynamics, evolutionary diversification, and ecological and physiological function. Ultimately, this course aims to provide the skills necessary to interpret the vast array of morphologies that exist among plants. Each day will consist of lecture and laboratory sessions, with ample opportunity to explore the Arnold Arboretum.

There are no course fees, room and board are provided, and funds are available to help defray costs of participant

travel.

Course Instructors: Pamela Diggle (University of Connecticut), Peter Endress (University of Zurich), William (Ned) Friedman (Harvard University), Cynthia Jones (University of Connecticut).

Application Deadline: Applications must be submitted by 11:30 pm March 15th, 2018. Application instructions are available on the course website: <https://www.arboretum.harvard.edu/education/aa-summer-course/> Eligibility: microMORPH summer short courses are open to postdoctoral researchers, graduate students, and undergraduates in their final year of study (who have been admitted to a graduate or professional program for the fall of 2018). Non-US-citizens are welcome to apply (but are responsible for obtaining the appropriate visa to be able to attend the course).

How to Apply: For full application instructions (including list of required documents) and to submit applications, please visit the microMORPH website (<https://www.arboretum.harvard.edu/education/aa-summer-course/> . Questions or Comments? Contact Pamela Diggle at pamela.diggle@uconn.edu

Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788 <tel:860-486-4788>

Pamela Diggle <diggle@colorado.edu>

AuburnU Alabama Bioinformatics Jun4-8

5th Annual Bioinformatics Bootcamp at Auburn University June 4-8, 2018

Additional information can be found at auburn.edu/bioinformatics.

The College of Sciences and Mathematics (COSAM) will sponsor the 5th Annual Bioinformatics Bootcamp at Auburn University June 4-8, 2018. Instructed by Les Goertzen, Scott Santos, Ken Halanych, Laurie Steverson, Rita Graze, Jamie Oaks from the Department of Biological Sciences < <http://www.auburn.edu/cosam/departments/biology/index.htm> > at Auburn University < <http://www.auburn.edu/> >.

The Bootcamp is a week-long workshop emphasizing hands-on training in numerous aspects of next generation DNA sequencing data analyses such as sequence assessment and quality control, genomic and transcriptomic assembly, annotation, differential expression, phylogenomics and more. Additionally, the workshop provides instruction in the Linux operating system command-line environment, basic scripting and many widely used open-source software packages. Registration for the workshop is \$500.

To apply:

Please provide a brief (half page) statement of interest describing how the AU Bioinformatics Bootcamp will benefit your research and a 2-page CV.

Application materials should be submitted by March 25th, 2018 as a single PDF via email to bioinformatics@auburn.edu. Notifications will be sent to applicants starting April 1st, 2018.

Kenneth M. Halanych Schneller Chair, Alumni Professor Curator of Marine Invertebrates Biological Sciences Department Life Sciences Bld. 101 Auburn University Auburn, AL 36849

<http://metazoan.auburn.edu/halanych/lab/index.html>
Phone: (334)-844-3222 e-mail: ken@auburn.edu

Editor-In-Chief The Biological Bulletin <http://www.journals.uchicago.edu/toc/bbl/current> Kenneth Halanych <ken@auburn.edu>

Australia StructuralModelling Jun18-22

“Structural Equation Modelling for Ecologists and Evolutionary Biologists (SEMR02)”

This course will be delivered by Jon Lefcheck (who wrote the SEM package piecewise) and will take place from 18th - 22nd June 2018 at Myuna Bay sport and recreation, Australia.

Full details can be found using the link below.

http://bit.ly/2Ga0yk4SEM_OZ Course Overview: The course is a primer on structural equation modelling (SEM) and confirmatory path analysis, with an emphasis on practical skills and applications to real-world data. Structural equation modelling is a rapidly growing technique in ecology and evolution that unites multiple hypotheses in a single causal network. It provides an intuitive graphical representation of relationships among variables, underpinned by well-described mathematical estimation procedures. Several advances in SEM over the past few years have expanded its utility for typical ecological datasets, which include count data, missing observations, and nested or hierarchical designs.

We will cover the basic philosophy behind SEM, provide approachable mathematical explanations of the techniques, and cover recent extensions to mixed effects models and non-normal distributions. Along the way, we will work through many examples from the primary literature using the open-source statistical software R (www.r-project.org). We will draw on two popular R packages for conducting SEM, including lavaan and piecewiseSEM. Participants are encouraged to bring their own data, as there will be opportunities throughout the course to plan, analyze, and receive feedback on structural equation models.

Monday 18th - Classes from 09:00 to 17:00 Introduction to SEM Module 1: What is Structural Equation Modeling? Why would I use it? Module 2: Creating multivariate causal models Module 3: Fitting piecewise models Readings: Grace 2010 (overview), Whalen et al. 2013 (example)

Tuesday 19th - Classes from 09:00 to 17:00 SEM Using Likelihood Module 4: Fitting Observed Variable models with covariance structures Module 5: What does it mean to evaluate a multivariate hypothesis? Module 6: Latent Variable models Module 7: ANCOVA revis-

ited & Nonlinearities Readings: Grace & Bollen 2005, Shipley 2004 Optional Reading: Pearl 2012, Pearl 2009 (causality)

Wednesday 20th - Classes from 09:00 to 17:00 Piecewise SEM Module 8: Introduction to piecewise approach Module 9: Incorporation of random effects models Model 10: Autocorrelation Reading: Shipley 2009; Lefcheck 2016

Thursday 21st - Classes from 09:00 to 17:00 Advanced Topics with Likelihood and Piecewise SEM Module 11: Multigroup models and non-linearities Module 12: Composite Variables Module 13: Phylogenetically-correlated data Module 14: Prediction using SEM Module 15: How To Reject A Paper That Uses SEM Readings: Grace & Julia 1999, von Hardenberg & Gonzalez 2013

Friday 22nd - Classes from 09:00 to 16:00 Open Lab and Final Presentations

Email oliverhooker@prstatistics.com

Check out our sister sites, www.PRstatistics.com (Ecology and Life Sciences) www.PRinformatics.com (Bioinformatics and data science) www.PSstatistics.com (Behaviour and cognition)

1. March 19th - 23rd 2018 BEHAVIOURAL DATA ANALYSIS USING MAXIMUM LIKELIHOOD IN R (BDML01) Glasgow, Scotland, Dr William Hoppitt <http://www.psstatistics.com/course/behavioural-data-analysis-using-maximum-likelihood-bdml01/> 2. April 9th - 13th 2018 NETWORK ANALYSIS FOR ECOLOGISTS USING R (NTWA02) Glasgow, Scotland, Dr. Marco Scotti www.prstatistics.com/course/network-analysis-ecologists-ntwa02/ 3. April 16th - 20th 2018 INTRODUCTION TO STATISTICAL MODELLING FOR PSYCHOLOGISTS USING R (IPSY01) Glasgow, Scotland, Dr. Dale Barr, Dr Luc Bussierre <http://www.psstatistics.com/course/introduction-to-statistics-using-r-for-psychologists-ipsy01/> 4. April 23rd - 27th 2018 MULTIVARIATE ANALYSIS OF ECOLOGICAL COMMUNITIES USING THE VEGAN PACKAGE (VGNR01) Glasgow, Scotland, Dr. Peter Solymos, Dr. Guillaume Blanchet www.prstatistics.com/course/multivariate-analysis-of-ecological-communities-in-r-with-the-vegan-package-vgnr01/ 5. April 30th - 4th May 2018 QUANTITATIVE GEOGRAPHIC ECOLOGY: MODELING GENOMES, NICHES, AND COMMUNITIES (QGER01) Glasgow, Scotland, Dr. Dan Warren, Dr. Matt Fitzpatrick

— / —

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

Barcelona Morphometrics Jun19-22

Dear Colleagues,

Transmitting Science is offering the 5th edition of the course 'INTEGRATION AND MODULARITY WITH GEOMETRIC MORPHOMETRICS'.

Instructor: Chris Klingenberg (University of Manchester, UK).

Dates: June 19th-22nd, 2018.

Place: Sabadell, Barcelona (Spain)

Course overview

The aim of this course is to provide participants with an overview of morphometric approaches to studying morphological integration and modularity. The concepts of integration and modularity will be introduced and discussed in different contexts (e.g. development, individual variation, evolutionary change). The theoretical basis and application of different methods for analysing integration and modularity in geometric morphometric data will be presented. Lectures will be combined with hands-on demonstrations of the analyses. Participants are encouraged to bring their own morphometric data for analysis and discussion in the course.

The course will be taught using the software MorphoJ.

More information and registration: <https://www.transmittingscience.org/courses/geometric-morphometrics/integration-modularity-geometric-morphometrics/> With best regards

Sole

Soledad De Esteban-Trivigno, PhD. Scientific Director Transmitting Science
<http://www.transmittingscience.org/>
soledad.esteban@transmittingscience.org

Barcelona PhylogeneticAnalysisUsingR Sep3-7

Dear Colleagues,

Registration is open for the fifth edition of the course PHYLOGENETIC ANALYSIS USING R, September 3rd-7th, 2018. — INSTRUCTORS: Dr. Emmanuel Paradis (Institut de Recherche pour le Développement, France) and Dr. Klaus Schliep (University of Massachusetts, USA).

More information: <https://www.transmittingscience.org/courses/evolution/-phylogenetic-analysis-using-r/> This course is for biologists dealing with the analysis of multiple molecular sequences at several levels: Populations, species, clades, communities. These biologists address questions relative to the evolutionary relationships among these sequences, as well as the evolutionary forces structuring biodiversity at different scales. The objectives are: (i) to learn the theoretical bases phylogenetic analysis, (ii) to know how to choose a strategy of molecular data analysis at the inter- or intraspecific levels, (iii) to be able to initiate a phylogenetic analysis starting from the files of molecular sequences until the interpretation of the results and the graphics. The software used for this course will be centred on the R language for statistics. This will include the use of specialized packages particularly ape, phangorn, and adegenet.

Requirements: Knowledge of multivariate statistics,— phylogenetics— and— molecular evolution.— User level of R.

PLACE: —Capellades, Barcelona (Spain).

Organized by: Transmitting Science and the Institut Català de Paleontologia M. Crusafont.

With best regards

Sole

Soledad De Esteban-Trivigno, PhD. Scientific—
Director Transmitting Science (<http://www.transmittingscience.org/>)

soledad.esteban@transmittingscience.org

Berlin MolecularPhylogenies Apr9-13 deadline

Course: Molecular phylogenies in biodiversity

Dates: 9-13 April 2018

Where: Botanisches Museum, Königin-Luise-Straße 6-8, Berlin

Instructor: Dr. Diego Fontaneto
<https://scholar.google.de/citations?user=-WO97K4QAAAAJ&hl=en> Application deadline is: March 10th, 2018.

Overview:

This course will introduce ecologists interested in biodiversity to the use of molecular phylogenies to address questions that cannot be addressed by using only ecological data in their studies. After a short introduction on how to obtain reliable molecular phylogenies, the focus of the questions that could be addressed will be on taxonomy, community ecology, and comparative methods.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at early-career researchers in ecology interested in widening their analytical toolbox. The course is structured in a way that even an inexperienced and naïve attendee could take advantage of the possibilities offered by the inclusion of molecular phylogenies in its analyses. There will be a mix of lectures and hands-on practical exercises using freely available software and online resources.

Most of the steps will be performed in R, but no previous knowledge on this statistical platform is required. All scripts will be carefully explained to allow all attendees understanding the rationale and usage of the statistical approaches.

LEARNING OUTCOMES

- Understand how to read, interpret and obtain molecular phylogenies, with a focus on the concepts and rationale behind phylogenetic methods
- Learn tools from DNA taxonomy
- Learn how to include phylogenies in the analyses of community ecology and in comparative analyses
- Hand-on experience on all the steps

- Being comfortable with using R when including molecular phylogenies in ecological analyses

Please visit our website for more information about the course: <https://www.physalia-courses.org/courses-workshops/course28/> Here is the full list of our courses and Workshops: <https://www.physalia-courses.org/-courses-workshops/> Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org

<http://www.physalia-courses.org/> =0A=0ATwitter: @physacourses

mobile: +49 15771084054

<https://groups.google.com/forum/#!forum/physalia-courses> info@physalia-courses.org

Berlin Paleogenomics May7-11

Course: Paleogenomics

Berlin , 7th -11th of May 2018

Where: Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin, Königin-Luise-Straße 6-8, Berlin (Germany)

Instructors:

Dr. Claudio Ottoni (University of Oslo (Norway))

Dr. Amine Namouchi (University of Oslo (Norway))

Overview This course will introduce biologists to the main bioinformatic tools for the analysis of Next Generation Sequencing (NGS) data from ancient samples. Through a series of theoretical and practical hands-on sessions, the main goal of this course is to provide a clear understanding of the most common bioinformatic methods adopted in a wide range of paleogenomics projects (from metagenomic screening of ancient samples, to NGS reads mapping and phylogenetic tree reconstruction). Particular attention will be given to quality control, DNA damage assessment and variants calling. A basic introduction to NGS platforms and the main file formats used in most common bioinformatics pipelines will be provided. Each day will consist of a mix of introductory lectures on the theoretical background of the programs that will be used, followed by hands-on exercises using command line tools performed by the participants under guided supervision.

Target Audience & ASSUMED BACKGROUND The

course is aimed primarily at researchers (MSc and PhD students, postdoctoral fellows, engineers) interested in learning the different steps from NGS raw data analysis to phylogenetic tree reconstruction in archaeological samples. The hands-on sessions are targeted to beginners and more advanced users alike. The practical sessions will cover the most common pipelines adopted in paleogenomics, and can be applied to a wide range of projects, from metagenomics to genome resequencing. Attendees should have a background in biology and some familiarity with genomic data.

STRUCTURE The course material will be delivered over 5 days, in 10 half-day sessions. These lessons will build off of one another, and feature a mix of lecture and in-class exercises.

For more information about the course program, please visit our website: (<https://www.physalia-courses.org/-courses-workshops/course27/>)

Here is the full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops/>)

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org

<http://www.physalia-courses.org/> Twitter: @physacourses

mobile: +49 15771084054

info@physalia-courses.org

Berlin PopulationGenomics May14-18

Dear all, we have the last 6 spots left for the course “ Introductory Population Genomics: From Data to Inference” (<https://www.physalia-courses.org/courses-workshops/course9/>)

May 14-18 2018, Berlin (Germany)

Registration deadline: 14th April 2018.

Instructors:

Dr Martin I. Taylor (University of East Anglia, UK): <https://scholar.google.com/citations?user=8ZycEewAAAAJ&hl=en> Dr Lewis Spurgin (University of East Anglia, UK): (<https://scholar.google.co.uk/citations?user=3D9Grw5YgAAAAJ&hl=en>)

Overview

Next generation sequencing has revolutionized evolutionary biology allowing unprecedented resolution and insight into evolutionary questions that appeared intractable only a few years ago. The course will cover the basics of population genomic analysis from SNP data onwards and will cover the key analyses that may be required to successfully analyze a population genetic data set. The course will NOT cover steps prior to generation of a .vcf file or SNP data set such as NGS data demultiplexing, clustering and SNP calling (This is covered in detail in the Introduction to RADseq course). This course will introduce Linux and the command line environment, basic perl and python usage, file conversions and manipulation, population structure and differentiation in R, outlier analysis, landscape / seascape genomics and introgression. Having completed the course, students should have a good understanding of the software and methods available for population genomic analysis and be competent in population genomic analysis.

Targeted Audience & Assumed Background

This workshop is aimed at postgraduate students and early career researchers who are interested in using population genomic tools in their research. No previous experience of bioinformatics is required, but an underpinning in evolutionary biology and basic population genetics concepts such as Hardy Weinberg Equilibrium and FST are desirable. The course will use a range of software including the Linux operating system and R.

TEACHING FORMAT

The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of a combination of lectures and practical exercises, with breaks at the organisers' discretion. There will also be time for students to discuss their own problems and data.

Session content

Monday 14th - Classes from 9:30 to 17:30

Session 1- Introduction to Linux and the command line (Dr. Martin Taylor)

- Installation of required software
- Introduction to linux operating system
- Working on the command line. Basic bash shell commands and navigation.
- Introduction to Perl and Python

Session 2 - Understanding genomic data formats (Dr. Martin Taylor)

- Understanding and working with VCF files using VCF tools

- Data conversion and manipulation using Plink
- Text editors

Tuesday 15th - Classes from 9:30 to 17:30

Session 3- Introduction to genetic analysis in R (Dr. Lewis Spurgin)

- Introduction to R
- Reading data into R
- Data manipulation in R
- Introduction to Adegenet and other genetics packages

Session 4- Genomic diversity estimation (Dr. Lewis Spurgin)

- Estimating heterozygosity and nucleotide diversity
- Hardy Weinberg
- Linkage disequilibrium
- Introduction to ggplot2

Wednesday 16th - Classes from 9:30 to 17:30

Session 5- Population structure and differentiation (Dr. Martin Taylor & Dr. Lewis Spurgin)

- Estimating and understanding FST
- Visualising genetic structure using MDS and PCA
- STRUCTURE and related software
- Estimating migration

Session 6- Identifying selection within populations (Dr. Lewis Spurgin)

- Marker-based genetic diversity
- Introduction to sliding windows
- Tajima's D and related statistics
- Introduction to GO analyses

Thursday 17th - Classes from 9:30 to 17:30

Session 7-Identifying selection among populations (Dr. Lewis Spurgin)

- FST outlier analysis
- EigenGWAS

Session 8-Incorporating landscape and seascape into population genomics (Dr. Martin Taylor)

- Seascape / landscape genetics
- Environmental / genomic correlation

Friday 18th - Classes from 9:30 to 17:30

Session 9-Hybridisation and introgression (Dr. Martin Taylor)

- Identifying hybrids and introgression using genotype data

Session 10-Summary data troubleshooting session (Dr Martin Taylor & Dr Lewis Spurgin)

- Time to answer questions on any areas covered during week.

- Talk to us about your own data

For more information about the course, please visit our website: (

— / —

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

Berlin SignaturesSelection-GWAS Oct22-26

GENOME-WIDE SIGNATURES OF SELECTION AND ASSOCIATION STUDIES Berlin, 22nd-26th October 2018

General Topic: Genome-wide analysis of selection signatures and genotype-phenotype associations

INSTRUCTORS:

Dr. Pablo Orozco-terWengel (Cardiff University, Wales (UK)) (<https://scholar.google.co.uk/citations?user=urqxLJgAAAAJ&hl=en>)

Dr. Filippo Biscarini (CNR, ITA) (https://www.researchgate.net/profile/Filippo_Biscarini)

Overview

This course will introduce students, researchers and professionals into the field of using genomics data to identify meaningful genomic regions. The course comprises two approaches: one based only on genomic information, which will use populations genetics techniques to detect signatures of selection (both natural and artificial); the other approach will combine genomic and phenotypic data to identify genetic associations for specific phenotypes (i.e. GWAS, genome-wide association studies).

Format

The course is structured in modules over 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.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at advanced students, researchers and professionals interested in learning how to make use of genomic information to study how selection has shaped the genome and how the genome influences measurable phenotypes. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of population genetics, which will take up most of the first half of the course; the second half of the course will be centered mainly on GWAS and related aspects.

Attendees should have a background in biology, specifically genetics. There will be a mix of lectures and hands-on practical exercises using R and the Linux command line, and bespoke software. Some basic understanding of R programming and the Linux environment will be advantageous. Attendees should have also some familiarity with genomic data such as those arising from NGS experiments, including genotyping-by-sequencing (GBS), and commercial genotyping platforms.

Please visit our website to have more information about the course content: (<https://www.physalia-courses.org/courses-workshops/course36/curriculum-36/>)

Here is the full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops/>)

Best regards,

Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org

<http://www.physalia-courses.org/>

@physacourses

mobile: +49 15771084054

<https://groups.google.com/forum/#!forum/physalia-courses> info@physalia-courses.org

Twitter:

Berlin Transposable Elements Apr23-27

“Transposable elements” course.

Where: Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin, Königin-Luise-Strasse 6-8, 14195 Berlin

When: 23-27 April 2018

Spots available: 4

Instructor: Dr. Alexander Suh (Uppsala University (Sweden)) (<https://scholar.google.de/citations?user=-J4CG5QAAAAJ&hl=>)

Overview

Transposable elements (TEs) are selfish genetic elements which exist in virtually all eukaryotic genomes. Because TEs contain regulatory or coding sequence for their own ‘survival’ and often occur in large numbers within a genome, they can have strong effects on the transcription or methylation of nearby genes and significantly promote structural variation or genome size expansion. Accurate annotation of TEs is thus important for many studies in genomics and evolutionary biology. However, TEs are rapidly evolving due to arms races with their host genomes and thus often remain undetected in newly sequenced genomes. One may argue that in-depth annotation of TEs is currently one of the biggest bottlenecks in genomics research of non-model organisms. This is because computational TE analyses require knowledge of TE biology as well as some degree of manual curation to overcome incomplete or erroneous annotations. The present course aims to address this bottleneck by teaching TE biology, computational analyses of TEs in genome assemblies (RepeatModeler, RepeatMasker) and raw read data (dnaPipeTE), and manual analyses of TEs (consensus curation, classification).

Format

At the end of this course, attendants should be able to conduct computational analyses of TEs, interpret the results in the light of TE biology, and improve TE annotations through manual curation. To achieve this, the first three days of the course will provide lectures and practicals on all these topics. The last two days of the course consist entirely of supervised individual practicals to further refine the attendants’ skills in computational and manual analyses of TEs, either in their own data

or in a course-specific collaborative project. Participation in the collaborative project will be acknowledged through co-authorship on a planned TE manuscript.

Please visit our website for more information about the course: (<https://www.physalia-courses.org/courses-workshops/course24/>)

Here is the full list of our courses and Workshops: (<https://www.physalia-courses.org/courses-workshops/>)

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org

<http://www.physalia-courses.org/>
@physacourses

Twitter:

mobile: +49 15771084054

<https://groups.google.com/forum/#!forum/physalia-courses> “info@physalia-courses.org” <info@physalia-courses.org>

Edinburgh Evolving Populations Jul2018

We are excited to announce a workshop on “Stochastic models of evolving populations: from bacteria to cancer”, to be held in Edinburgh, UK, 16-20 July 2018. This workshop hosted by the International Centre for Mathematical Science, aims to bring together scientists working on stochastic and computational models of cancer, bacterial and viral evolution. The meeting will explore the similarities between mathematical models used to study seemingly different phenomena such as the growth of cancerous tumors, viral and bacterial infections, and the evolution of drug resistance. Keynote talks will be given by Martin Nowak (Harvard University) and Rick Durrett (Duke University).

Registration is now open! To register and for more information see our website:

<http://www.icms.org.uk/stochasticmodels.php>
“krug@thp.Uni-Koeln.DE” <krug@thp.Uni-Koeln.DE>

Faro Portugal Phylogenetics Sep24-29

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 proce-

dure 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 EMBC countries, and to maintain a reasonable gender balance.

Abstract guidelines

Abstract for a 10 minute PowerPoint presentation that each student will present (200 words)

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: cymaratt@ualg.pt

CCMARATT <cymaratt@ualg.pt>

Hinxton UK GeneticAnalysis Jul18-24

GENETIC ANALYSIS OF MENDELIAN AND COMPLEX DISORDERS

18-24 July 2018

Wellcome Genome Campus, Hinxton, Cambridge, UK

Application and Bursary Deadline: 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 Genòmica (CNAG), Barcelona, Spain)

Guest Instructors:

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> “Sinsheimer, Janet”

<JanetS@mednet.ucla.edu>

IndianaU TranscriptomeAssembly Apr30-May1

De novo assembly of transcriptomes using HPC resources workshop

Hosted by The National Center for Genome Analysis Support at Indiana University

The National Center for Genome Analysis Support, or NCGAS, at Indiana University is offering a National Science Foundation-sponsored, two-day workshop on high performance computing usage and de novo transcriptome assembly. It will take place April 30-May 1 on the IU Bloomington campus.

The workshop will include discussions, lectures, and hands-on tutorials to cover topics important to getting started constructing and analyzing transcriptomes “without the use of a genome. Material will cover both the availability and use of high performance computing (HPC) resources, alongside the task of assembling a new transcriptome, in order to provide a more comprehensive preparation for this and future bioinformatic tasks.

Transcriptome assembly will consist of using four separate assemblers (Trinity, SOAP de novo, Velvet Oases, and TransABySS), with multiple kmers, to be combined and curated with Evigenes. This combined assembly with multiple parameters is considered much more robust than simply using one assembler, and the NCGAS pipeline streamlines the process and allows for customization if desired.

While material will make heavy use of XSEDE and IU machines, the material is transferable to any cluster.

More information here: <https://itnews.iu.edu/articles/-2018/s4es-de-novo-assembly-of-transcriptomes-using-hpc-resources-workshop.php> To apply for the workshop and travel assistance, please fill out this form: <https://redcap.uits.iu.edu/surveys/?s=93PLRF47MM> Sheri Sanders Bioinformatic Analyst National Center for Genome Analysis and Support (NCGAS)

NCGAS is part of the Research Technologies division of UITS; Research Technologies is a PTI Cyberinfrastructure & Service Center.

ss93@iu.edu

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: <http://www.gentree-h2020.eu/-events/event/from-genotypes-to-phenotypes-assessing-forest-tree-diversity-in-the-wild-training-course/> Bruno FADY, PhD, Directeur de recherches Directeur adjoint INRA, FR ECCOREV, UR629 Ecologie des Forêts Méditerranéennes (URFM) Domaine St Paul, Site Agroparc, CS 40509, 84914 Avignon cedex 9 (43,914033 N ; 4,879505 E) tel : +33(0)4 32 72 29 08 - portable : +33(0)6 15 94 33 92 - courriel : bruno.fady@inra.fr www.paca.inra.fr/ecologie_des_forets_mediterraneennes <http://prodinra.inra.fr/au/bfady> Coordinateur : <http://www.gentree-h2020.eu/> Bruno Fady <bruno.fady@inra.fr>

Lima Peru TeachersOfEvolution Jul30-Aug5

This may be a good opportunity for senior PhD students or young professors in the Evoldir network,

<https://www.clubesdecienciaperu.org/instructores>

Clubes de Ciencia (Science Clubs) is organizing a series of workshops on Jul 30th - Aug 5th to boost the interest of STEM fields in young students (freshmen, senior high school).

In my opinion, a club about Evidences of evolution would be a nice idea, and I would be happy to help in the application process. The complete information is on the link, I just copy here the eligibility and what it is covered

Eligibility - Be a current graduate student, postdoctoral researcher, or experienced professional in a STEM field, or in entrepreneurship and innovation in STEM. - International instructors must be based in any country of the Americas or Europe; instructor applications from everywhere else in the world will be considered as well, but with the final selection being subject to budgetary restrictions. - Spanish fluency is not a requirement.

What CdC provides? - CdeCPeru will cover a round

trip flight ticket up to \$900 USD. We will pay up to \$1200 USD in exceptional cases. We will try to accommodate other trip dates, but we will try to keep costs on the lower side due to restrictions on our budget. - CdeCPeru will cover transportation costs from the hotel to the host university, and to any other events related to Clubes. - CdeC Peru will cover breakfast, lunch, and dinner from July 30th to August 5th. - CdeC Peru will cover lodging from July 30th to August 5th. - CdeC Peru will cover up to \$400 USD for materials needed in your Club. - CdeC Peru will make the arrangements to reserve a classroom/lab in one of our host universities (office materials will be provided)

The application deadline is March 15th

Pedro E. Romero Doctor of Natural Sciences Dr. rer. nat.

Pedro Romero <pedro.romero@unmsm.edu.pe>

LundU EvolutionaryBiologyUsingR May-Jun

Dear all,

We are pleased to announce the following upcoming courses organized by GENECO and ClimBEco: “Introduction to R” (2-4 May) and “High-Dimensional Data Analysis in Ecology and Evolutionary Biology Using R” (28 May - 1 June). The course “Introduction to R” is organized particularly for students registered for the second course but is open for anyone interested.

The courses will be given at the Department of Biology at Lund University. Participants can choose to take Part 1, 2 or both.

The courses are free of charge to all GENECO and ClimBEco PhD students, and students enrolled at Lund University, but are open to PhD students from any university to a course fee.

In case of a large number of participants, priority will be given to GENECO and ClimBEco PhD students.

Deadline for registration: April 20, 2018

Read more about the courses and registration on the webpage: <https://www.biology.lu.se/education/phd-studies/geneco-graduate-research-school-in-genomic-ecology/courses-workshops/high-dimensional-data-analysis-in-ecology-and-evolutionary-biology-using-r>
The Geneco & ClimBEco Team

Christina Rengefors Project assistant 'V GENECO Department of Biology, Lund University 223 62 LUND 'V Sweden Phone: +46 46 222 96 14 Mobile: + 46 (0) 725 370 170 E-Mail: Christina.Rengefors@biol.lu.se www.biology.lu.se/geneco Dr. Johan Hollander (Docent) Associate Professor, Marine Biology Aquatic Ecology, Department of Biology Lund University Ecology Building 223 62 Lund, Sweden

Office phone: +46 (0) 46 22 234 73 Cell phone: +46 (0) 70 17 49 660 Fax: +46 (0) 46 222 45 36

Home page: www.lu.se/aquaticecology GENECO: www.biology.lu.se/geneco Johan Hollander <johan.hollander@biol.lu.se>

Montpellier DrosEU AdaptationGenomics Aug23-24

Dear colleagues,

We are happy to announce the *DrosEU /ESEB STN Summer School on Adaptation Genomics*, (<http://droseu.net/>) a two-day event to take place on *23-24 August 2018 at the CNRS campus in Montpellier*, right after the Evolution 2018 meeting (<http://evolutionmontpellier2018.org/>).

The summer school aims at fostering the study of adaptation genomics and evolutionary genetics in a variety of systems and using diverse approaches (e.g., population genomics, life-history analyses, statistical inference based on population and quantitative genetic theory, landscape genomics, GWAS, and Evolve & Resequencing experiments). The school is organized by the European *Drosophila* Population Genomics Consortium (DrosEU) and sponsored by the European Society for Evolutionary Biology (ESEB) and the Mediterranean Center for the Environment and for Biodiversity (CE-MEB). Although DrosEU focuses on *Drosophila*, the research questions, methodological approaches and the conceptual issues addressed by the consortium apply to many species beyond the *Drosophila* model. Our two-day mini-summer school will gather approximately 60 people, especially students and postdocs from within and outside the DrosEU community, as well as invited speakers who are leaders in the field. We will have sessions with 6 invited speakers (each with a 1-hr talk, followed by 30 min of discussion) and 6 contributed PhD/postdoc presentations (20 min plus 10 min of discussion). By bringing together empiricists and theo-

reticians working on different model systems and using different approaches, this meeting will promote fruitful discussions and allow identifying new avenues for the study of the adaptation in natural populations.

Registration is open to everyone on a first come first served basis, but priority will be given to PhD students and postdocs.

Registration deadline: May, 1st.

Link to the registration website: <http://droseu.net/-droseu-eseb-stn-summer-school-on-adaptation-genomics/> *The meeting and the lunches provided during the workshop will be free of charge.*

We look forward to seeing you in Montpellier!

The organizing committee: Nicolas Rode [Montpellier], Sara Guirao & Josefa González [Barcelona], Martin Kapun & Thomas Flatt [Fribourg], on behalf of DrosEU.

Contact: nicolas.rode@inra.fr

Invited speakers:

§*Andrea Betancourt* (University of Liverpool, website < <https://www.flyevolution.net/> >): Transposable element evolution in *Drosophila**

§*Joachim Hermisson* (University of Vienna, website < <http://www.mabs.at/hermisson/index.html> >):* title to be announced shortly*

§*Juliette de Meaux* (University of Cologne, website < <http://www.ag-demeaux.botanik.uni-koeln.de/> >):* Can cis-regulatory variation point to the molecular targets of polygenic selection? Insights from the Arabidopsis genus. *

§*Dmitri Petrov* (Stanford University, website < <http://petrov.stanford.edu/> >): *Evolution on ecological timescales in *Drosophila**

§*Cristina Vieira* (University of Lyon, website < <https://lbbe.univ-lyon1.fr/-Vieira-Heddi-Cristina.html?lang=en> >):* (Epi)genomic environmental stress response in *Drosophila**

§*Renaud Vitalis* (INRA, website < <https://www6.montpellier.inra.fr/cbcp/Personnel/Personnel-permanent/Vitalis> >): *Inferring demographic and adaptive histories from genome-wide polymorphism data*

Nicolas Rode <nicolas.o.rode@gmail.com>

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

Mike Wisner Postdoc in Evolution Education
mwiser@msu.edu

"mwiser@msu.edu" <mwiser@msu.edu>

OberaegeriSwitzerland TamingTheBEAST June17-22

Dear colleagues,

This is a reminder that the March 25 registration deadline for the Taming the BEAST summer school is quickly approaching. If you, your research colleagues or students are intending to apply for this workshop, please ensure this happens before the deadline. We have already had very strong interest in the workshop, and places are strictly limited.

Taming the BEAST is a summer school focusing on the BEAST2 software and consisting of a mix of invited talks, lectures and hands-on tutorials by experts in the field (including several of the core developers of

BEAST2). The aim of this summer school is to equip participants with the skills necessary to confidently perform their own phylogenetic and phylodynamic inferences in Bayesian settings, while providing them with a firm grasp of the theory behind those inferences. Participants are also highly encouraged to bring their own datasets along and to engage with the organizers and speakers to address any problems specific to their own datasets/analyses.

We welcome applications from graduate students and early-career scientists in the life sciences. Preference will be given to applicants who are not from a computational background and applicants who have already collected/assembled a dataset that they need to analyze. However, anyone interested is more than welcome to apply.

Invited speakers: Alexei Drummond (University of Auckland) Vladimir Minin (University of California, Irvine) Alexandra Gavryushkina (University of Otago) Tanja Stadler (ETH Zurich) Sebastián Duchêne (University of Melbourne)

Dates: June 17th to June 22nd (Deadline for registration is March 25th).

Place: Oberaegeri, Switzerland

Registration Fee: 900 CHF (Registration fee includes accommodation and meals).

For more information please visit the summer school website: <https://www.bsse.ethz.ch/cevo/taming-the-beast/overview-2018.html> For information on previous workshop programs, tutorials etc. please visit <https://taming-the-beast.github.io/> We hope to see you there, the Taming the BEAST organizing team

“timothy.vaughan@bsse.ethz.ch”
<timothy.vaughan@bsse.ethz.ch>

ObergeriSwitzerland BEAST Jun17-22

Dear colleagues,

We are happy to announce that registration is now open for our summer school “Taming the BEAST”.

Phylogenetics and phylodynamics are central topics in modern biology. Phylogenetic inferences reconstruct the evolutionary relationships between organisms, whereas phylodynamic inferences reveal the dynamics that lead

to the observed relationships. These two fields have many practical applications in disciplines such as epidemiology, developmental biology, paleontology, ecology and even linguistics. However, phylogenetics and phylodynamics are complex and fast-evolving fields. As such, inference tools are not easily accessible to researchers who are not from a computational background.

Taming the BEAST is a summer school focusing on the BEAST2 software and consisting of a mix of invited talks, lectures and hands-on tutorials by leading and renowned experts in the field (including several of the core developers of BEAST2). The aim of this summer school is to equip participants with the skills necessary to confidently perform their own phylogenetic and phylodynamic inferences in Bayesian settings, while providing them with a firm grasp of the theory behind those inferences. Participants are also highly encouraged to bring their own datasets along and to engage with the organizers and speakers to address any problems specific to their own datasets/analyses.

REGISTRATION IS NOW OPEN. We welcome applications from graduate students and early-career scientists in the life sciences. Preference will be given to applicants who are not from a computational background and applicants who have already collected/assembled a dataset that they need to analyze.

Invited speakers: Alexei Drummond (University of Auckland) Vladimir Minin (University of California, Irvine) Alexandra Gavryushkina (University of Otago) Tanja Stadler (ETH Zurich) Sebastián Duchêne (University of Melbourne)

Dates: June 17th to June 22nd (Deadline for registration is March 25th).

Place: Oberägeri, Switzerland

Registration Fee: 900 CHF (Registration fee includes accommodation and meals).

For more information please visit the summer school website: <https://www.bsse.ethz.ch/cevo/taming-the-beast/overview-2018.html> For information on previous workshop programs, tutorials etc. please visit <https://taming-the-beast.github.io/> We hope to see you there, the Taming the BEAST organizing team

Tim Vaughan <timothy.vaughan@bsse.ethz.ch>

Portugal 2 EvolBiol Apr

Subject: Portugal-cE3c-Course: two advanced courses with deadlines April 2018

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the two courses with closer deadlines. Additional informations at: <http://ce3c.ciencias.ulisboa.pt/training/?cat>

Course Nature-Based Design Frameworks

organized by Gil Penha-Lopes and Hugo Oliveira | May 14th-18th 2018 @ Lisbon, Portugal

Objectives: This course will introduce all participants to different Nature-based design frameworks such as Biomimicry, Permaculture, Biophilic Design, Regenerative Design and Resilient Design. Providing many examples of how they are applied, from city farms, to rooftopgardens, to river and watershed regeneration, to educational approaches, to food production and ecosystems and landscape regeneration, within rural and urban contexts.

Course instructors

Gil Penha-Lopes (Invited Assistant Professor at FCUL, Leader of the Subgroup 'and Sustainability', CCIAM, cE3c)

<http://ce3c.ciencias.ulisboa.pt/member/gilpenhalopes> and

Hugo Oliveira (PhD student, CCIAM, cE3c)

<http://ce3c.ciencias.ulisboa.pt/member/hugooliveira>

Intended audience: This five days intensive course will be open to a maximum number of 24 participants, being directed to PhD or MSc students in Biology, Environmental studies, Geography or related areas, and postdocs and other professionals working in related topics.

Minimal formation of students: Bachelor in Biology, Geography or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL; UP), Biology and Ecology of Global Changes (BEAG UL; UA) and Climate Change and Sustainable Development Policies (UL). For information of fees for other participants see the programme details.

Candidates should send a short CV and motivation letter to Gil Penha-Lopes (email gpenha-lobes@fc.ul.pt) and Ângela Antunes (email amantunes@fc.ul.pt).

For additional details about the programme of the course, fees and to know how to register, click here, and access the specific course

<http://ce3c.ciencias.ulisboa.pt/training/?cat> For more information about the course, please contact:

gpenha-lobes@fc.ul.pt

.....

Course Applied Methods in Community Ecology and Functional Ecology by Paulo A. V. Borges and François Rigal - June 18th -22nd 2018 @ Lisbon, Portugal

Objectives: This five-days intensive course is mostly a practical course offering an overview on different community ecology and macroecological methods and software. These will include all steps of a research project, from the optimal sampling of communities to process inference from large-scale patterns of taxon, phylogenetic and functional diversity. Specific topics will be: (1) alpha, beta and gamma diversity; (2) estimating diversity from incomplete sampling; (3) partitioning taxonomic beta diversity; (4) community-assembly rules, (5) functional and phylogenetic diversity, (6) null models, (7) rarity and species abundance distribution. Finally, students will be asked to present own data and case studies.

See the PROGRAMME at:

<http://ce3c.ciencias.ulisboa.pt/training/?cat> Course INSTRUCTORS:

Paulo A. V. Borges (Assistant Professor at Azores University, researcher at cE3c) (<http://gba.uac.pt/team/-IBBC>; <http://ce3c.ciencias.ulisboa.pt/member/paulo-a-v-borges>)

and

François Rigal (Assistant Professor at Environment and Microbiology Team, MELODY group, University of Pau and external collaborator of cE3c -IBBC, Azorean Biodiversity Group) (<http://ce3c.ciencias.ulisboa.pt/member/francoisrigal>)

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 Biol-

ogy and Ecology of Global Changes (BEAG UL, UA). For information of fees for other participants see the programme details.

Deadline for applications: April 27th 2018

— / —

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>

Reminder MexicoCity PCMs Jun26-29

This is a reminder that today (March 1st) is the last day to apply for the free, NSF-sponsored workshop that I will be co-teaching with my colleagues Mike Alfaro (UCLA), Ricardo Betancur (UPR-Río Piedras), Alejandro Gonzalez-Voyer (UNAM), & Luke Harmon (U. Idaho). More information about the workshop (in Spanish & English), as well as how to apply, can be seen at the following URL: <http://www.phytools.org/mexico2018/ad/>. – 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/> “Liam.Revell@umb.edu” <Liam.Revell@umb.edu>

Seattle StatGenetics Jul9-27

Register now for the 22nd Summer Institute in Statistical Genetics, to be held in Seattle, July 9 - 27. Twenty modules, including the new “Conservation Genetics” and “Computational Pipelines”. Scholarships are available to students, with an application deadline of March 31. Learn more and watch the video from 2017 at <http://www.biostat.washington.edu/suminst> Bruce

Bruce Weir Professor, Department of Biostatistics Director, Institute for Public Health Genetics University of Washington Seattle, WA 98195-9461

bsweir@uw.edu

Sweden Bioinformatics with R Jun11-21

RaukR Summer School: Advanced R for Bioinformatics 11-21 June 2018. Visby, Gotland, Sweden Registration deadline: April 15, 2018

We are excited to announce a brand new international Summer School in R for Bioinformatics! The Summer School is beautifully located in the middle of the UNESCO World Heritage city of Visby, Sweden, and during 2 weeks you will get the opportunity to learn R from internationally renowned R wizzards and senior bioinformatics staff from NBIS/SciLifeLab. We believe that RaukR will take your bioinformatics R analysis and visualization skills to a new level, so don't miss out on this unique opportunity!

Register today at <https://nbisweden.github.io/-workshop-RaukR-1806/> NBIS/SciLifeLab www.nbis.se, www.scilifelab.se

Note: A “Rauk” is a characteristically shaped stone formation, common on the Island of Gotland, Sweden. See for example https://sv.wikipedia.org/wiki/Rauk#/media/File:Gotland-F%C3%A5r%C3%B6_Raukar-Gamlehamn.jpg Bjorn Nystedt, PhD Joint head of facility Bioinformatics Long-term Support (WABI) National Bioinformatics Infrastructure Sweden at SciLifeLab www.nbis.se, www.scilifelab.se/platforms/bioinformatics

BMC E10:3206, entrance C11 Husargatan 3, SE-752 37 Uppsala

Phone: 018 - 471 4413 E-mail: bjorn.nystedt@scilifelab.se

Björn Nystedt <bjorn.nystedt@scilifelab.se>

Turin EvolGameTheory Jul16-19

Conflict, Competition, Cooperation and Complexity: Using Evolutionary Game Theory to model realistic populations, July 16-19, 2018 at the University of Torino.

<https://www.city.ac.uk/departments/mathematics/-mathematical-biology/FourC-Modelling> This is the

third workshop of the European Union's Horizon 2020 research and innovation programme FourCmodelling (No 690817) under the Marie Skłodowska-Curie grant agreement. The workshop will consist of talks, discussion, and break out sessions that focus on the following aspects of evolutionary game theory: 1. Multiplayer games in structured populations, 2. Complex foraging games and time constraints, 3. Modelling pandemics as complex systems, 4. Modelling cancer as a complex adaptive system.

This event is open to researchers whose areas of expertise complement these themes. A limited number of positions is reserved for PhD students and junior researchers working/interested in evolutionary game theory and their applications within the scope of this project. The workshop fee is 250 and the reduced fee is 125 including lunch and coffee/tea during the day.

If you want to be a part of this exciting event, send a short motivation e-mail (indicating whether you want to present a talk/poster) to Prof. Mark Broom at Mark.Broom.1@city.ac.uk not later than April 30, 2018. Selected candidates will be notified shortly after.

Yours,

Maria Luisa Sapino and Mark Broom (workshop organisers)

“Broom, Mark” <Mark.Broom.1@city.ac.uk>

UK
Phylogenetic Comparative Methods
Oct22-25

“Phylogenetic comparative methods for studying diversification and phenotypic evolution (PCME01)”

Full details can be found at the link below.

<http://bit.ly/2FFjB6s> **PHYLOGENETIC_COMPARITIVE_METHODS_PHENOTYPIC_EVOLUTION**

This course will run from the 22nd - 25th October 2018 in Glasgow City Centre and will be delivered by Dr. Antigoni Kaliontzopoulou.

Course Overview: Phylogenetic comparative methods are commonly used nowadays to investigate how species diversification occurs and to 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 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.

Monday 22nd DAY 1: Introduction 9:00 'V 9:30: Introductions 9:30 'V 10:30: Why do we need PCMs? A short history of the field 11:00 'V 12:00: Testing for phylogenetic signal 13:00 'V 14:00: Ancestral character reconstruction 14:30 'V 17:30: PRACTICALS

Tuesday 23rd DAY 2: Testing hypotheses on phenotypic evolution 9:00 'V 10:30: Phylogenetic independent contrasts and phylogenetic GLS 11:00 'V 12:30: Phylogenetically-informed ordination 14:30 'V 17:30: PRACTICALS

Wednesday 24th DAY3: Tempo and mode of evolutionary change 9:00 'V 10:30: Evolutionary rates: estimation and tests 11:00 'V 12:30: Models of phenotypic evolution 14:30 'V 17:30: PRACTICALS

Thursday 25th DAY 4: Miscellanea 9:00 'V 10:30: Modelling lineage diversification 11:00 'V 12:30: Future perspectives: multivariate extensions to PCMs 14:30 'V 17:30: PRACTICALS

Please feel free to share this anywhere you see fit.

Email oliverhooker@prstatistics.com with any questions.

Check out our sister sites, www.PRstatistics.com (Ecology and Life Sciences) www.PRinformatics.com (Bioinformatics and data science) www.PSstatistics.com (Behaviour and cognition)

1. March 12th - 16th 2018 ECOLOGICAL NICHE MODELLING USING R (ENMR02) Glasgow, Scotland, Dr. Neftali Sillero <http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr02/> 2. March 19th 'V 23rd 2018 BEHAVIOURAL DATA ANALYSIS USING MAXIMUM LIKLIHOOD IN R (BDML01) Glasgow, Scotland, Dr William Hoppitt <http://www.psstatistics.com/course/behavioural-data-analysis-using-maximum-likelihood-bdml01/> 3. April 9th 'V 13th 2018 NETWORK ANALYSIS FOR

ECOLOGISTS USING R (NTWA02 Glasgow, Scotland, Dr. Marco Scotti www.prstatistics.com/course/network-analysis-ecologists-ntwa02/ 4. April 16th 'V 20th 2018 INTRODUCTION TO STATISTICAL MODELLING FOR PSYCHOLOGISTS USING R (IPSY01) Glasgow, Scotland, Dr. Dale Barr, Dr Luc Bussierre <http://www.psstatistics.com/course/introduction-to-statistics-using-r-for-psychologists-ipsy01/> 5. April 23rd 'V 27th 2018 MULTIVARIATE ANALYSIS OF ECOLOGICAL COMMUNITIES USING THE VEGAN PACKAGE (VGNR01) Glasgow, Scotland, Dr. Peter Solymos, Dr. Guillaume Blanchet www.prstatistics.com/course/multivariate-analysis-of-ecological-communities-in-r-with-the-vegan-package-vgnr01/ 6. April 30th 'V 4th May 2018 QUANTITATIVE GEOGRAPHIC ECOLOGY: MODELING GENOMES, NICHES, AND COMMUNITIES (QGER01) Glasgow, Scotland, Dr. Dan Warren, Dr. Matt Fitzpatrick

— / —

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 QuantModellingGenomes Apr30-May4

Quantitative geographic ecology using R: modelling genomes, niches, and communities (QGER01)

Delivered by Dan Warren and Matt Fitzpatrick, this course will take place in Glasgow city centre from 30th April - 4th May

Full details can be found at

www.prstatistics.com/course/quantitative-geographic-ecology-using-r-modelling-genomes-niches-and-communities-qger01/ Course Overview: Spatial

modelling is increasingly being used in ecology and evolutionary biology for both basic and applied research questions. While emphasis traditionally has been on species-level niche modelling, the increasing availability of genomic and community-level data has increased interest in modelling biodiversity patterns above and below the species level. This 5-day course will provide a thorough introduction to different spatial modelling techniques for quantifying and visualizing patterns of biodiversity across scales of biological organization 'V from population-level genetic variation, to species

ecological niches, to communities. Students will learn about theory, common data types, and statistical techniques used in these different applications.

The course will include introductory lectures, guided computer coding in R, and exercises for the participants, with an emphasis on visualization and reproducible workflows. All modelling and data manipulation will be performed with R. Attendees will learn to use niche modelling algorithms including Maxent, GLM, GAM, and others, and will learn both new and existing methods for conducting comparative studies using ENMs in the new ENMTools R package. Generalized Dissimilarity Modelling (GDM) and Gradient Forest (GF) will be taught for modelling genomic and community-level data. The course is intended for intermediate R users with interest in quantitative geographical ecology.

After successfully completing this course students will: 1) Understand the theory underlying ENMs and the critical assumptions necessary to the modelling process. 2) Be able to develop, evaluate, and apply ENMs both in the context of conservation-oriented studies and to study niche evolution. 3) Understand the statistical underpinnings of GDM and GF 4) Be able to develop, evaluate and apply GDM and GF for quantifying and mapping spatial genetic patterns and community-level compositional variation 5) Assess population- and community-level vulnerability to climate change

Check out our sister sites; www.PRstatistics.com (Ecology and life sciences) www.PRinformatics.com (Bioinformatics and data science) www.PSstatistics.com (Behaviour and cognition)

Please share anywhere you see fit.

Email enquiries to oliverhooker@prstatistics.com

Other upcoming courses below

1. February 19th 'V 23rd 2018 MOVEMENT ECOLOGY (MOVE01) Margam Discovery Centre, Wales, Dr Luca Borger, Dr Ronny Wilson, Dr Jonathan Potts www.prstatistics.com/course/movement-ecology-move01/ 2. February 19th 'V 23rd 2018 GEOMETRIC MORPHOMETRICS USING R (GMMR01) Margam Discovery Centre, Wales, Prof. Dean Adams, Prof. Michael Collyer, Dr. Antigoni Kaliontzopoulou <http://www.prstatistics.com/course/geometric-morphometrics-using-r-gmmr01/> 3. March 5th - 9th 2018 SPATIAL PRIORITIZATION USING MARXAN (MRXN01) Margam Discovery Centre, Wales, Jennifer McGowan www.prstatistics.com/course/introduction-to-marxan-mrxn01/ 4. March 12th - 16th 2018 ECOLOGICAL NICHE MODELLING USING R (ENMR02) Glasgow, Scotland, Dr. Neftali Sillero <http://www.prstatistics.com/>

course/ecological-niche-modelling-using-r-enmr02/ 5. March 19th 'V 23rd 2018 BEHAVIOURAL DATA ANALYSIS USING MAXIMUM LIKLIHOOD IN R (BDML01) Glasgow, Scotland, Dr William Hoppitt <http://www.psstatistics.com/course/behavioural-data-analysis-using-maximum-likelihood-bdml01/> 6. April 9th 'V 13th 2018 NETWORK ANAYLSIS FOR ECOLOGISTS USING R (NTWA02 Glasgow, Scotland, Dr. Marco Scotti www.prstatistics.com/course/network-analysis-ecologists-ntwa02/ 7. April 16th 'V 20th 2018 INTRODUCTION TO STATISTICAL MODELLING FOR PSYCHOLOGISTS USING R (IPSY01) Glasgow, Scotland, Dr. Dale Barr, Dr Luc Bussierre

— / —

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>

UPorto ModellingSpeciesEnvAdaptation Apr23-27

MODELLING SPATIAL ECO-EVOLUTIONARY DYNAMICS AND SPECIES' RESPONSES TO ENVIRONMENTAL CHANGES

23-24 & 26-27 April 2018 (CIBIO-UP)

Rapid environmental change threatens biodiversity and exposes species to novel ecological and evolutionary pressures. The scientific community increasingly recognizes the need for dynamic mechanistic models integrating sufficient complexity to forecast the response of natural populations to drivers of global change, such as habitat fragmentation or climate change.

In this Advanced Course hosted by CIBIO-University of Porto (UP) students will first learn fundamental issues to apply spatially-explicit eco-evolutionary models to address biotic responses to anthropic and/or environmental changes. Secondly, we will introduce a novel modelling platform, *RangeShifter v2.0*, which integrates population dynamics, dispersal behaviour and evolutionary processes in a spatially-explicit context. Using some illustrative examples, we will show different functionalities for a wide variety of modelling applications ranging from applied to theoretical questions. Thirdly, we will present new functionalities recently

incorporated into Rangesifter v2.0, namely: *(i)* a genetics module and *(ii)* dynamic landscapes. Finally, we will discuss future potential functionalities to be incorporated into Rangesifter v2.0 including *(i)* the possibility of accommodating plant traits, such as selfing or pollen dispersal kernels and *(ii)* to address eco-evolutionary changes in marine environments.

To take the most of this course, it is highly advisable that participants bring their own spatial datasets (ideally as shapefiles in a projected co-ordinate system) to discuss with the instructors the most suitable way to apply *Rangesifter v2.0* to address their own study issues.

Instructors

Justin Travis (Aberdeen University, UK)

Steve Palmer (Aberdeen University, UK)

Cristina García (CIBIO-Porto University, Portugal)

*Registration deadline: 30th March *

To apply, please send an e-mail accompanied by your short CV (max. one-side A4) to post.graduation@cibio.up.pt.

Fees:

Free for BIODIV students

80 euro non-BIODIV students

150 euro others (postdocs, researchers, managers)

The course will be open to a maximum number of 20 participants.

More info at:

<https://cibio.up.pt/workshops-courses/details/-modelling-spatial-eco-evolutionary-dynamics-and-species-responses-to-environmental-changes>

Virginia ConservationBioinformatics Oct10-19

Bioinformatics Analysis for Conservation Genomics

October 10-19, 2018

Smithsonian-Mason School of Conservation, Front Royal, VA, USA

<https://smconservation.gmu.edu/programs/-graduate-and-professional/professional-training-courses/conservation-genomics/>

This new course is designed to provide attendees at any career stage with a theoretical understanding of the methods used in conservation genomics along with the practical skills necessary to design and carry out the analysis component of a conservation genomics study. While introduction to the theoretical aspects of each of the analytical steps will be given, the emphasis of the course will be on hands-on training, enabling the participants to complete the analysis steps behind a conservation genomics study. Thus, the course will follow the format of short lectures introducing each analytical step, followed by hands-on activities during which students will complete the corresponding analysis. The course will begin with an overview of conservation genomics, comparison of different next generation sequencing platforms, and the analytical factors to consider when beginning a conservation genomics study. The rest of the course will focus on the bioinformatics analysis behind a conservation study including: genome assembly (trimming, assembly techniques, quality assessment), genome annotation, mapping low coverage genome data to a reference genome, SNP calling, demographic analysis, and estimation of genome-wide diversity. These steps will all be accomplished with real data used in a recent conservation genomics study and performed on the Smithsonian High Performance Computing Cluster (SI/HPC). By the end of the course, attendees will have acquired the necessary background and applied knowledge to implement genomic analyses for the conservation of endangered species.

The Smithsonian-Mason School of Conservation is a partnership between George Mason University and the Smithsonian Conservation Biology Institute (SCBI). All courses are intensive residential programs hosted in a sustainably-built Academic Center on the grounds of SCBI in Front Royal, Virginia, USA. All courses offer continuing education credits (CEUs) and some can be taken for graduate credit. Limited scholarships are available for eligible applicants. See our upcoming offerings below and check out our website (<http://SMConservation.gmu.edu>) for more course details and pricing.

Rebecca Dikow (dikowr@si.edu)

“Dikow, Rebecca” <DikowR@si.edu>

Virginia ConservationGenetics Aug19-30 Deadline

Registration Deadline Approaching - Congen2018 Recent Advances in Conservation Genetics ConGen-2018, Front Royal, Virginia, August 19 'V 30, 2018

Dear Conservation Genetics Community:

The American Genetic Association together with the Northern Virginia 4-H Educational Center, Front Royal, Virginia is organizing a 10-day intensive course in methods, interpretation, and applications of molecular genetic analyses for conservation of endangered species, Recent Advances in Conservation Genetics (ConGen-2018) on August 19 'V 30, 2018.

On behalf of The Organizing Committee for ConGen-2018, it is my pleasure and a privilege to invite you to this important international event which will take place in the beautiful Shenandoah Valley village of front Royal, Va. (adjacent to the International Airport Dulles (IAD) outside Washington DC), a hot spot of biodiversity and an up-and-coming site for scientific research, education and communication.

The course will be directed by Dr. Stephen J. O'Â'Brien, and taught by renowned scientists in methods, interpretation, and applications of molecular genetic analyses for conservation of endangered species, who will also share a variety of their personal experiences in this important field. ConGen2018 faculty is an amazing group of people who come from all around the world and will be teaching, sharing their conservation stories and interacting with students during the course. See the full list of faculty at <http://conservationgenetics.org> ConGen-2018 participants will be conservation scientists representing academia, government, NGOs, or industry studying genetics of endangered species. Every day of the course, an open popular science evening lecture will be presented by the internationally renowned faculty to the members of the conservation-minded public, faculty and students from the universities, local businesses, governmental and non-governmental organizations in the area.

Located in beautiful Harmony Hollow, just outside Front Royal, Virginia, the Northern Virginia 4-H Educational Center is a unique, beautiful location that is home to year-round camps and educational programs, as well as providing facilities and services to groups seeking a

relaxed, economical retreat experience. The Center's unique location is easily accessible from major metropolitan areas, and offers a quiet, peaceful respite for your youth group, team or organization to reconnect, regroup and relax. The Northern Virginia 4-H Educational Center is a public recreation area, offering facilities including a public pool, picnic shelters, and multi-use trails that are open to the general public at little to no cost.

Tentative Course Schedule and Topics:

Day 1 Participants arrive Dinner, logistics, introductions
 Day 2 Experimental design: traditional markers and NGS; avoiding pitfalls Overview of NGS approaches Reduced representation sequencing (RADseq, UCEs, exomes), whole genome sequencing/re-sequencing, target enrichment methods, RNAseq Pipelines; QC-filtering; assembly and mapping; storage (use mitogenomes as example) Computer demo/exercises Evening speaker 1
 Day 3 Mining markers from NGS data I (variant discovery) Computer demo/exercises Mining markers from NGS data II (variant interpretation) Computer demo/exercises Evening speaker 2
 Day 4 Genetic diversity and inbreeding I Computer demo/exercises Genetic diversity and inbreeding II Computer demo/exercises Evening speaker 3
 Day 5 Genetic structure/isolation: PCA, STRUCTURE/ADMIXTURE, allele trees Computer demo/exercises Gene flow and admixture Computer demo/exercises Evening speaker 4
 Day 6 Field trip Mid-course dinner & party
 Day 7 Effective population size/Historical demography I Computer demo/exercises Effective population size/Historical demography II Computer demo/exercises Evening speaker 5
 Day 8 Local adaptation: SNPs that matter Computer demo/exercises Local adaptation: genes that matter Computer demo/exercises Evening speaker 6
 Day 9 Estimating relatedness I Computer demo/exercises Estimating relatedness II Computer demo/exercises Evening speaker 7
 Day 10 Phylogenetics: Alignments and Networks Computer demo/exercises Phylogenetics: Trees Computer demo/exercises Evening speaker 8
 Day 11 Phylogenetics: Applications 'V barcoding, metagenomics, eDNA Genetic management of ex situ populations of endangered species Postdoctoral fellowships, careers Course evaluation, group photo Closing party
 Day 12 Participants depart

Who should apply? Applicants should be conservation-minded scientists (advanced graduate students, post-docs, teachers, and researchers with advanced degrees) from academia, government, NGOs, or industry who are studying the genetics of endangered species and who will apply the knowledge gained from this course to the conservation of such species.

Please submit your registration here: <http://->

conservationgenetics.org

— / —

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>

WellcomeUK DrosophilaGenomics Jul30-Aug3

Drosophila Genetics and Genomics 30 July-3 August 2018 Advanced Courses & Scientific Conferences, Wellcome Genome Campus, Hinxton, UK

This popular course, established more than 20 years ago, will provide up-to-date summaries for a range of classical and contemporary, from basic to advanced, topics and techniques in Drosophila genetics and genomics. The course will provide participants with a solid knowledge-base when starting or developing research projects using Drosophila as a model organism.

The course is ideally aimed at faculty, postdoctoral researchers, and graduate students who are currently working in a fly lab, or those who have completed a PhD in another field and starting to work on Drosophila for their postdoctoral studies interested in developing new ideas to transfer to their own research strategy.

Please note: To optimise the impact of the course, attendance is limited to 25 participants.

Learning outcomes After attending this course, participants will be able to:

Describe the latest advances in Drosophila genetics. Appraise the latest cutting-edge techniques used in Drosophila research. Apply CRISPR/Cas9 and other gene replacement or disruption techniques to their own research. Evaluate the various techniques used in advanced genetic analysis. Design and develop a research project using Drosophila. Access an international network of leading Drosophila researchers.

Topics will include: Introduction to Drosophila Advanced genetic analysis Genomics Genetic screens and mosaic analysis CRISPR and genome editing Recombining and imaging RNAi and proteomics Gene regulation and development Behaviour and metabolism Evolutionary and ecological genetics

Lead instructors Casey Bergman University of Georgia, USA Scott Hawley Stowers Institute for Medical

Research, USA

Confirmed speakers Dan Barbash Cornell University, USA Eileen Furlong EMBL, Germany Amanda Laracuate University of Rochester, USA Ruth Lehmann New York University School of Medicine, USA Kate O'Connor-Giles University of Wisconsin-Madison, USA Norbert Perrimon Harvard Medical School, USA Pavel Tomancak Max Planck Institute of Molecular Cell Biology & Genetics, Germany Luis Teixeira Instituto Gulbenkian de Ciência, Portugal

Bursary and Application Deadline: 1 May 2018

Full details: <https://coursesandconferences.wellcomegenomecampus.org/-events/item.aspx?e=699> Treasa Creavin PhD Scientific Programme Manager

Tel: +44 (0)1223 495108 Wellcome Genome Campus Advanced Courses and Scientific Conferences | Wellcome Genome Campus | Hinxton | Cambridgeshire | CB10 1RQ | UK www.wellcomegenomecampus.org/-coursesandconferences Twitter < <https://twitter.com/ACSCevents> > | Facebook < <https://www.facebook.com/ACSCevents/> > | YouTube < <https://www.youtube.com/c/WellcomeGenomeCampusCoursesandConferences> > | LinkedIn < <https://www.linkedin.com/company/-17977124/> >

Wellcome Genome Campus Advanced Courses and Scientific Conferences is part of Connecting Science. Connecting Science enables everyone to explore genomic science and its impact on research, health and society. Please consider the environment before printing this e-mail

Treasa Creavin <treasa.creavin@wellcomegenomecampus.org>

WellcomeUK EvolutionCancer Apr24

Evolutionary Biology and Ecology of Cancer 2018 is open for applications.

This course is aimed at researchers currently working in cancer and/or evolution and ecology. It is particularly suited to evolutionary biologists and ecologists interested in moving into cancer research, and to cancer biologists and oncologists who lack formal training in evolutionary biology.

Applications are invited from early career scientists,

including post-graduate students, postdoctoral fellows and new principle investigators. A limited number of registration bursaries are available to attend this course. Apply by 24 April. For more information please visit the course website: <https://coursesandconferences.wellcomegenomecampus.org/-events/item.aspx?e=710> Course topics * Introduction to the evolution and ecology of cancer * Understanding vulnerability to cancer * The evolution of cancer clones * The cancer ecosystem * Evolutionary prognostics * Thwarting therapeutic resistance

Learning outcomes After attending this course, participants will be able to: * Describe the principles of evolutionary biology as applied to somatic cell evolution in cancer (e.g. generation of diversity, driver mutations, epistasis, selective pressures, cellular co-operation and competition, units of selection). * Describe the principles from ecology relevant to studying tumour microenvironments. * Develop proficiency with the tools for measuring the evolution and ecology of tumours. * Evaluate those tools and metrics used to measure ecosystems and evolution that can be applied to cancer. * Evaluate the strengths and weaknesses of cancer prognostics, particularly evolutionary prognostics * Apply evolutionary and ecological approaches to the problem of therapeutic resistance.

Scientific programme committee Athena Aktipis Arizona State University, USA & Institute of Cancer Research, UK Mel Greaves Institute of Cancer Research, UK Carlo Maley Arizona State University, USA & Institute of Cancer Research, UK

Keynote speaker Charles Swanton University College London, UK

Confirmed tutors Alexander Anderson Moffitt Cancer Center, USA Gerhardt Attard UCL Cancer Institute, UK Amy Boddy University of California Santa Barbara, USA Joel Brown Moffitt Cancer Centre, USA Kit Curtius Barts Cancer Institute, UK Andrea Sottoriva The Institute of Cancer Research, UK Yinyin Yuan The Institute of Cancer Research, UK

Bursary and Application Deadline: 24 April 2018

Full details: <https://coursesandconferences.wellcomegenomecampus.org/-events/item.aspx?e=710> Treasa Creavin PhD Scientific Programme Manager

Tel: +44 (0)1223 495108 Wellcome Genome Campus Advanced Courses and Scientific Conferences | Wellcome Genome Campus | Hinxton | Cambridgeshire | CB10 1RQ | UK www.wellcomegenomecampus.org/-coursesandconferences Twitter < <https://twitter.com/ACSCevents> > | Facebook <

<https://www.facebook.com/ACSCevents/> > science and its impact on research, health and society.
 | YouTube < <https://www.youtube.com/c/-WellcomeGenomeCampusCoursesandConferences>
 > | LinkedIn < <https://www.linkedin.com/company/-17977124/> > Please consider the environment before printing this e-mail
 Wellcome Genome Campus Advanced Courses and Scientific Conferences is part of Connecting Science. Connecting Science enables everyone to explore genomic Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.
 Treasa Creavin <treasa.creavin@wellcomegenomecampus.org>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evol.dir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.