EvolDir

December 1, 2017

Month in Review

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.

—— / ——

Conferences

Aussois France EvolutionaryPhytopathology Jan15-19

Chers collègues,

Les 12e rencontres de Phytopathologie et Mycologie (Journees Jean Chevaugeon, JJC) se tiendront à Aussois (Savoie) du *15 au 19 janvier 2018*

https://colloque.inra.fr/jjc2018/ Au menu, 4 sessions, 5 invites, de la place pour les etudiants, et toujours autant de convivialite !

Attention * le 30 novembre 2017*, date limite des inscriptions et depôt des resumes

Si vous ne connaissez pas les "JJC", venez les decouvrir, et si vous êtes dejà venu, vous êtes toujours les bienvenus !

à bientôt,

Elodie Gaulin, Melanie Roy et Sylvain Raffaele

—

Dear Colleagues,

The 12th meeting of Phytopathology and Mycology (Journees Jean Chevaugeon, JJC) will be held in Aussois (French Alps) from the 15th to the 19th January 2018 Au menu, 4 sessions, 5 invited speakers, a big place for students, and a warm atmosphere! Informations and registrations:* https://colloque.inra.fr/jjc2018/ Save the date - September 30th: Registration opening November 30th: deadline for registration and abstract submission If you have never attended the ≪ JJC ≫ before, please give it a try, and otherwise, you are always welcome ! Note that this year, talks will be in French or English to the choice of the presenter.

best wishes, Elodie Gaulin, Melanie Roy et Sylvain Raffaele

Mela Roy <mela.roy@gmail.com>

Corsica EvolutionPathobiomes Mar18-20

Dear Colleagues,

It is our pleasure to invite you to the Pathobiome Conference 2018 on 18-20 March 2018 in Ajaccio, Corsica (France).

Pathobiome 2018 is the second edition of an international symposium, which gathers the scientific community that investigates the relationship between pathogens, microbiota, and hosts in humans, animals and plants. Abstract submission and registration at https://colloque.inra.fr/pathobiome-2018/ The deadline has been extended to December 8th, 2017.

The pathobiome concept has emerged from the tripartite relationship between the pathogens, the symbionts and the host that can dramatically influence or drive disease processes. This concept applying to a wide range of ecosystems the scientific program will reflect cutting edge of current pathobiome research in mammals, arthropods and plants in various fields (alternatives to antibiotics and pesticides, microbial ecology, epidemiology, microbial evolution, metagenomics, emerging diseases, control strategies, epidemiology, mathematical modelling;). Beside the invited speakers, 18 scientific presentations will be selected to illustrate cutting-edge research in this fast-developing field. Oral communication will be selected among the abstracts submitted. The remaining abstracts will be selected for presentation in the poster sessions.

Click here to submit your abstract: https://colloque.inra.fr/pathobiome-2018/Submission Pathobiome 2018 will include Keynote lectures

Joy Bergelson, University of Chicago, Illinois USA

Brett Finlay, University of British Columbia, Vancouver, Canada

Stephane HACQUARD, Max Planck Institute for Plant Breeding Research, Cologne, Germany

Anna-Liisa LAINE, University of Helsinki, Helsinki, Finland

Otso Ovaskainen, University of Helsinki, Helsinki, Finland

Muriel Vayssier-Taussat, INRA, Maison Alfort, France

"Laine, Anna-Liisa" <anna-liisa.laine@helsinki.fi>

Droushia Cyprus EvolutionaryProtistology May27-Jun1

Dear all,

Apologies if you have already received this email. We are excited to invite you to join us for the XXII meeting of the International Society for Evolutionary Protistology (ISEP), taking place in the scenic and historical Droushia village in Cyprus, between 27th of May until 1st of June 2018.

While we are still organising the meeting, we would like to ask you to visit our webpage (www.isep18.com) and add your name under the "Expression of Interest" section, in order to get a rough idea of how many participants will be attending the meeting.

Both the registration and the abstract submission are open as well.

Below are some Key Dates: - Deadline for Abstracts Submission - 15/2/18 - Notification of Acceptance - 01/3/18 - Early Fee Deadline - 15/3/18

If you request any information, please do not hesitate to contact us.

We are looking forward to see you in Cyprus in May 2018.

Anastasios Tsaousis

on behalf of the organizing committee

Dr. Anastasios D. Tsaousis (PhD) Lecturer in Molecular Parasitology University of Kent, School of Biosciences, Room: Ingram 220 Canterbury, CT2 7NJ, UK tel: +44 (0) 1227 827007

email: tsaousis.anastasios@gmail.com A.Tsaousis@kent.ac.uk

Webpage: http://www.kent.ac.uk/bio/profiles/staff/tsaousis.html Orcid: http://orcid.org/0000-0002-5424-1905 Anastasios Tsaousis <A.Tsaousis@kent.ac.uk>

LakeTahoe EvolutionPlants Jul10-12

Register now for the 42nd New Phytologist Symposium The biology of wood: from cell to trees

10’V12 July 2018

Granlibakken, Lake Tahoe, CA, USA

https://www.newphytologist.org/symposia/42 Wood biology research has traditionally been approached by discipline-specific questions and approaches, but recently the need and power of integrative approaches is becoming apparent. This symposium will bring together diverse researchers from different aspects of wood biology research including anatomists, biochemists, cell biologists, ecologists, geneticist / genomicists, and physiologists.

This symposium aims to facilitate the exchange of ideas and foster new collaborations across disciplines. We will also challenge speakers to put forth their vision for future research, including outstanding questions and interdisciplinary approaches by which they could be addressed.

The symposium will take place over three days at the Granlibakken Resort at Lake Tahoe in California. The symposium will be organised into sessions by research topics, there will be dedicated time for discussions, posters, selected poster talks, a conference dinner and a field trip.

Travel grants are available!

Travel grant deadline: Thursday 5 April 2018

Poster abstract deadline: Thursday 3 May 2018

More details and registration at https://www.newphytologist.org/symposia/42 Kind regards, Mike

Dr Mike Whitfield Development Coordinator, New Phytologist

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

The New Phytologist Trust, registered charity number 1154867

2016 Impact Factor 7.33

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

New Phytologist Symposia in 2018 < https://newphytologist.org/symposia > Plant sciences for the future | The biology of wood: from cell to trees

“Whitfield, Mike” <m.whitfield@lancaster.ac.uk>

Madison Wisconsin PopEvolQuantGenet May13-16

The 2018 Population, Evolutionary, and Quantitative Genetics Conference is coming to Madison, Wisconsin from May 13-16.

Featuring keynote speakers Trudy Mackay, Katie Peichel, and Jonathan Pritchard, #PEGQ18 aims to bring together population, evolutionary, and quantitative geneticists to promote cross-disciplinary exchange between those doing theoretical and experimental work in these broad but overlapping fields.

Quantitative and complex traits Population genomics Experimental evolution Adaptation and ecological genetics Statistical genetics Genome evolution Speciation Theoretical population genetics Molecular evolution

The meeting will also feature lightning talks for poster presenters, and presentations by candidates for the James F. Crow Early Career Researcher Award.

Early career attendees, including students and postdocs, will benefit from a wide range of professional development and networking opportunities. These include the New Faculty Forum, opportunities to invite poster viewers, a peer review workshop from GENETICS editors, and other workshops and events.

For more information, visit http://conferences.genetics-gsa.org/peqg/2018/index . Organizers:

Fernando Pardo-Manuel de Villena - Chair University of North Carolina, Chapel Hill

Dmitri Petrov - Co-Chair Stanford University

Matthew Hahn Indiana University

Hopi Hoekstra Harvard University

Lauren M. McIntyre University of Florida

Matt Rockman New York University

Sarah Bay <SBay@genetics-gsa.org>

Montpellier CallForAbstractsEvolution DeadlineJan15

We are happy to inform you that abstract submission is now open for next year's 2^nd Joint Congress on Evolutionary Biology in Montpellier, France (18-22 August 2018). Joint Congresses take place every six years and bring together four of the world's largest academic societies in the field of evolutionary biology: the European Society for Evolutionary Biology < http://-eseb.org >, the American Society of Naturalists < http://-/www.amnat.org/ >, the Society for the Study of Evolution < http://www.evolutionsociety.org/ > and the Society of Systematic Biologists < http://www.systbio.org/ >.

Following the traditional format of ESEB conferences, *all contributed talks and posters will be submitted to specific symposia and selected on the basis of their abstract by symposium organizers*.

The list of symposia is available at:

http://evolutionmontpellier2018.org/symposia You can consult the list and submit an application to give a talk or poster to the symposia of your choice. You can submit applications to *up to two symposia* from the list. Note that if none of the topics covered by the thematic symposia matches your research, you will have the option to submit your abstract to the Open symposium (also in the list).

If you are a graduate student, you will have the opportunity to compete for the Mayr Award and Hamilton Award. These awards, organized respectively by SSB and SSE, will be given to the presenter of an outstanding student talk at the Joint meeting in Montpellier. *If you want to compete for any of these awards, you have to submit an abstract to either the Mayr Award symposium or Hamilton Award symposium through the normal abstract submission procedure*.

In order to allow as many participants as possible to present their work, and in line with ESEB tradition, *participants can submit only one abstract as the presenting author (i.e. the person who will present the talk/poster).* There is no limit, however, to the number of talks/posters a given person may coauthor.

The symposium organizers of both your first and second choice will examine your proposal and make a selection. Symposium organizers will establish a priority list for abstracts accepted as oral communications and will offer the *option of presenting a poster instead of a talk* for the abstracts that do not fit in that list. Abstracts may be rejected if they are of insufficient quality, but our general policy is to accept most poster presentations. You will be chosen to present either a talk or a poster in a maximum of one symposium.

In order to submit an abstract for a talk or a poster click here 'V http://evolutionmontpellier2018.org/call-abstracts *Please note the following important dates: *

November 6^th 2017: Call for abstracts opens

January 15^th 2018: Deadline for abstract submission (i.e. application to present a talk/poster)

February 28^th 2018: Notification of acceptance sent out and pre-registration for presenters (talks and posters) opens

*March 12^th 2018:*Registration for all participants opens **

*March 26^th 2018:*Oral presentations of unregistered participants are cancelled

For further details, please see: http://-evolutionmontpellier2018.org/ Looking forward to meeting you in Montpellier in 2018!**

ronce ophelie <ophelie.ronce@univ-montp2.fr>

Montpellier Evolution2018 Aug18-22

Evolution 2018 and Grad Student Taxation

Two pieces of information from SSB: One relates to the upcoming Evolution 2018 meeting in Montpellier, France: all talks and posters must be accepted into a symposium, and abstracts for these are due Jan. 15. This includes student talks in the Mayr symposium. This policy is common for ESEB meetings but unusual for SSB/ASN/SSE meetings, so we are trying to call attention to it (please tell your colleagues). Actual registration for the meeting happens later (once decisions about talks and posters have been announced). If you do not submit an abstract by Jan. 15, 2018, you will not be giving a poster or talk at Evolution 2018. The other is a letter by the SSE, ASN, and SSB presidents about the effect of a proposed US tax plan on students studying in the United States [see separate posting in the

EvolDir]. SSB has released other statements informing the public about areas relating to our expertise, often in conjunction with other scientific societies. See them all at http://www.systbio.org/letters.html . Evolution 2018: Jan. 15 deadline for talks or posters

Abstract submission is now open for next year's 2nd Joint Congress on Evolutionary Biology in Montpellier, France (18-22 August 2018). This is the Evolution meeting for 2018. Joint Congresses take place every six years and bring together four of the world's largest academic societies in the field of evolutionary biology: the European Society for Evolutionary Biology, the American Society of Naturalists, the Society for the Study of Evolution and the Society of Systematic Biologists. Following the traditional format of ESEB conferences, all contributed talks and posters will be submitted to specific symposia and selected on the basis of their abstract by symposium organizers. The list of symposia is available at: http://evolutionmontpellier2018.org/symposia You can consult the list and submit an application to give a talk or poster to the symposia of your choice. You can submit applications to up to two symposia from the list. Note that if none of the topics covered by the thematic symposia matches your research, you have the option to submit your abstract to the 'Open symposium' (also in the list). If you are a graduate student, you will have the opportunity to compete for the Mayr Award and Hamilton Award. These awards, organized respectively by the SSB and SSE, will be given to the presenter of an outstanding student talk at the Joint meeting in Montpellier. If you want to compete for either of these awards, you have to submit your abstract to either the Mayr Award symposium or Hamilton Award symposium through the normal abstract submission procedure. In order to allow as many participants as possible to present their work, and in line with ESEB tradition, participants can submit only one abstract as the presenting author (i.e. the person who will present the talk/poster). There is no limit, however, to the number of talks/posters a given person may coauthor. The symposium organizers of both your first and second choice will examine your proposal and make a selection. Symposium organizers will establish a priority list for abstracts accepted as oral communications and will offer the option of presenting a poster instead of a talk for the abstracts that do not fit in that list. Abstracts may be rejected if they are of insufficient quality, but our general policy is to accept most poster presentations. You will be chosen to present either a talk or a poster in a maximum of one symposium. In order to submit an abstract for a talk or a poster click here - http://evolutionmontpellier2018.org/call-abstracts Please note the following important dates: November 6th 2017: Call for abstracts opens January 15th 2018: Deadline for abstract submission (i.e. application to present a talk/poster) February 28th 2018: Notification of acceptance sent out and pre-registration for presenters (talks and posters) opens March 12th 2018: Registration for all participants opens March 26th 2018: Oral presentations of unregistered participants are cancelled For further details, please see: http://evolutionmontpellier2018.org/ Looking forward to meeting you in Montpellier in 2018!

Copyright Â© 2017 Society of Systematic Biologists, All rights reserved. Thank you for being a member of the Society of Systematic Biologists. Our mailing address is: Society of Systematic Biologists 446 Hesler Biology University of Tennessee, Knoxville Knoxville, Tn 37996 Add us to your address book

— / —

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

Montpellier SpeciesTheoryEvolution Aug19-22

We are pleased to invite you to submit your abstracts to the symposium "Species in the Theory of Evolution: from Concepts to Methods and Applications" which will be held during the Evolution 2018 meeting in Montpellier, France. The objective of our symposium is to provide a reappraisal of the position of taxonomy in the recent conceptual and methodological advances in evolutionary biology. We wish to gather scientists working on the species level from different perspectives including large taxonomic inventories, speciation -omics and developmental genetics as well as on the theoretical foundations of taxonomy and systematics. Our invited speaker is Prof. Alessandro Minelli who will give a talk on "Evolvability, modularity and innovation: an evo-devo perspective on the evolution of diagnostic characters between closely related species".

Summary of the symposium: Taxonomy the science that divides organisms into taxonomic units is often viewed as a descriptive science based on a very elementary scientific methodology. It is indeed not rare to compare the taxonomists to philatelists rather to researchers providing scientific insights on biological diversity. The aim of the symposium is to provide an opportunity to taxonomists to explain their scientific approach to biological diversity and how this approach is connected to others fields of evolutionary biology. (1) Methodology in taxonomy: or why taxonomists are not philatelists? (2) Taxonomy and systematics in the "omic" era: How taxonomy and systematics integrate new technical and methodological advances? (3) Species inventories: facts or hypotheses about the structure of biodiversity? Impacts on conservation and management issues. (4) How taxonomy and systematics continue to provide new insights in â euro the origin of species"? (5) What is the evolutionary significance of diagnostic characters in the light of the development of Evo-Devo and Eco-Evo-Devo research ?

Abstract submission deadline: January 15th, 2018 http://evolutionmontpellier2018.org/home

Looking forward to meeting you,

Sarah Samadi Amir Yassin

"amir.yassin@mnhn.fr" <amir.yassin@mnhn.fr>

NewYork PopGenMeeting Jan10

Colleagues!

Join us at Cold Spring Harbor Labs on Wednesday, January 10, for the 2018 New York Population Genomics Meeting! The meeting builds on the tradition established in recent years by annual events at the New York Genome Center, Princeton, and Columbia. This is a great venue to meet your neighbors working in evolutionary, population, quantitative, and statistical genetics and genomics.

Registration for this one-day meeting is FREE but required. Registration includes lunch and a wine & cheese reception. The deadline for abstract submission is DECEMBER 3, 2017.

Keynote Speakers: Eimear Kenney, Icahn School of Medicine at Mount Sinai Joshua Akey, Lewis-Sigler Institute for Integrative Genomics, Princeton University

For more information, to register, or to submit an abstract, visit http://meetings.cshl.edu/nypg18 Matt Rockman, NYU, on behalf of the organizers: Casey Brown, University of Pennsylvania Barbara Engelhardt, Princeton University Joseph Pickrell, Gencove.com Molly Przeworski, Columbia University Adam Siepel, Simons Center for Quantitative Biology/CSHL

"mrockman@nyu.edu" <mrockman@nyu.edu>

Philadelphia EvolutionaryBiol Dec16-17

BMC Evolutionary Biology sponsors the following meeting: "Theory and Models Meet Data in Evolutionary Biology and Genomics" Dec. 16-17, 2017 Philadelphia, PA, USA http://igem.temple.edu/bmceb/overview Free Meeting with Registration Required Confirmed Invited Speakers: Arndt von Haeseler (Vienna), Jody Hey (Temple), Kateryna Makova (Penn State), Corina Tarnita (Princeton), Paul Schmidt (UPenn), Blair Hedges (Temple), Peter Andolfatto (Princeton) Poster Session on Dec. 17

We hope you will join us in Philadelphia. David Liberles daliberles@temple.edu

David A Liberles <tuf77157@temple.edu>

Roscoff France EvolutionReproductiveSystems Apr23-27

Dear Colleagues, informations about the upcoming Jacques Monod conference on the evolution of reproductive systems, including instructions for applications are now available online: http://www.cnrs.fr/insb/cjm/2018/Schwander_e.html Hoping to see you there, Tanja Schwander, Thomas Lenormand & Denis Roze

Dear Colleagues We would like to draw your attention to an upcoming Jacques Monod Conference:

SEX UNCOVERED, THE EVOLUTIONARY BIOLOGY OF REPRODUCTIVE SYSTEMS

April 23-27, 2018 in Roscoff (Brittany), France.

Jacques Monod Conferences, organized by CNRS, are known for the high scientific quality of the talks and discussions, in a relaxed atmosphere.The topics covered by the conference include: the advantage of sex and recombination, the biology of sexual and asexual reproduction, the evolution of inbreeding vs. outcrossing, and the evolution of sex chromosomes and sexual differentiation.

The list of invited speakers is given below. Information about the conference and how to register will be available soon at http://www.cnrs.fr/insb/cjm/cjmprog_e.html Symposium Speakers:

AGRAWAL Aneil (Toronto, Canada) ASHMAN Tia-Lynn (Pittsburgh, USA) BECKS, Lutz (Plön, Germany) BILLIARD Sylvain (Lille, France) CHARLESWORTH Brian (Edinburgh, UK) CHARLESWORTH Deborah (Edinburgh, UK) COELHO Susana (Roscoff, France) DUFAY Mathilde (Montpellier, France) GLÃMIN Sylvain (Montpellier, France) HAAG Christoph (Montpellier, France) HAIG David (Harvard, USA) JAQUIERY Julie (Le Rheu, France) KING Kayla (Oxford, UK) KIRKPATRICK Mark (Austin, USA) KOKKO Hanna (Zürich, Switzerland) LENORMAND Thomas (Montpellier, France) LYNCH Michael (Bloomington, USA) MARAIS Gabriel (Lyon, France) OTTO Sarah (Vancouver, Canada) PORCHER Emmanuelle (Paris, France) RENNER Susanne (Munich, Germany) SCHEU Stefan (Göttingen, Germany) SCHWANDER Tanja (Lausanne, Switzerland) TEOTONIO Henrique (Paris, France) VAN DONINCK Karine (Namur, Belgium) VICOSO Beatriz (Klosterneuburg, Austria) WRIGHT Stephen (Toronto, Canada)

We hope to see you there

Tanja Schwander, Thomas Lenormand & Denis Roze

“roze@sb-roscoff.fr” <roze@sb-roscoff.fr>

Sitges Spain EvolutionDiseases Nov6-9

Join us for the 14th International Conference on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID XIV), which will take place on the 6-9 November 2018 in Sitges, Spain.

Special emphasis will be given to health problems of specific interest to the present world: Zika, tuberculosis, AIDS, malaria, cancer and infectious diseases, to name a few. Plenary lectures and symposia will also deal with transversal topics, such as population genetics, evolution, speciation, taxonomy, bioinformatics, whole genome sequencing analysis and -omics analyses.

SUBMIT YOUR ABSTRACT ONLINE AT www.elsevier.com/meegid-conference/ Abstract Submission Deadline: 1 June 2018

Conference Topics: Studies dealing with viruses, bacteria, parasitic protozoa, fungi and helminths of medical, veterinary or agronomical relevance, related to:

* Cancer and infectious diseases * Micro-and macro-evolution * Experimental evolution * Co-evolution between hosts, pathogens and vectors * In-silico evolution * Genetics * Genomics * Mathematical modelling * Molecular diagnosis, epidemiology and taxonomy * Proteomics * Phylogenetics, phylogenomics, phylogeography

Sophie Hayward <sophie.hayward1@btinternet.com>

Sweden AdaptationPhenotypicPlasticity May15-17

’Adaptation and Phenotypic Plasticity in Marine Species as a Response to Global Change’

Conference session @ Marine Evolution Conference 2018, 15-17 May 2018, Stromstad, Sweden.

Session abstract:

Anthropogenic activities are causing the global climate to change at an unprecedented rate. A plethora of studies have suggested that anomalies in ocean temperature can result in severe drawbacks to the ecology and behaviour of marine species. Further, an increase in concentration of atmospheric CO[2] will lead to the disruption of key processes such as calcification, development during larval stages and predator and prey recognition. Most of these studies, however, do not take into account the capacity of marine organisms to acclimate and adapt. Environmental conditions similar to the ones predicted for the near future occur naturally in fractions of a species’ distribution. Recent studies have highlighted the genetic mechanism by which these populations have adapted locally to these exceptional environments. Further, due to standing genetic variation within populations, a subset of individuals can be more resistant to predicted conditions, aiding in their future persistence. Meanwhile, plastic responses that organisms may express under various conditions have been suggested as a mechanism that could enable acclimation and can be passed on across generations. This session will address the interplay of both mechanisms of genetic adaptation and phenotypic plasticity and their role in long-term adaptation of marine organisms to changing environments. The goal is to assemble cross-disciplinary studies from a variety of taxa and biological scales, which is imperative to understand the fate of marine ecosystems in the upcoming decades.

REGISTRATION: http://cemeb.science.gu.se/-activities/marine-evolution-2018 Deadline for abstract submission and early-bird registration: February 1st 2018!

Celia Schunter, PhD

Timothy Ravasi, PhD

Moises Bernal,PhD

King Abdullah University of Science and Technology (KAUST)

Moises Bernal <bernal.moises@gmail.com>

Sweden EvolutionEpigenetics May15–17

EVOLUTION AND EPIGENETICS / NON-GENETIC INHERITANCE

Conference session @ Marine Evolution 2018, 15-17 May 2018, Stromstad, Sweden

We invite abstracts from researchers who tackle the epigenetic mechanisms

behind plastic responses and non-genetic inheritance in marine species

from a theoretical as well as from an experimental approach.

ABSTRACT: Epigenetic and gene-regulatory processes represent a potentially important, but little researched factor in population responses to long-term change, rapid change, or perturbations. Within the same generation, epigenetic mechanisms may allow an organism to create phenotypic variation or to display altered reaction norms in the absence of genetic variation. Additionally, the inheritance of non-genetic information such as hormones, nutrients, proteins, RNAs, DNA methylation patterns, and histone modifications from one generation to the next may allow offspring to cope with unexpected environments in the absence of genetic change, and thus may facilitate rapid adaptation processes. Because of certain experimental and also conceptual challenges, there is no consensus on the prevalence and on the relevance of epigenetic processes in species adaptation. We therefore invite abstracts from researchers who tackle the epigenetic mechanisms behind plastic responses and non-genetic inheritance in marine species from a theoretical as well as from an experimental approach. We ask them to present their approaches and results, and to discuss principles, concepts and challenges related to the topic.

REGISTRATION: http://cemeb.science.gu.se/-activities/marine-evolution-2018 Irene Adrian-Kalchhauser, PhD

+41 61 2070410

University of Basel

Vesalgasse 1

4051 Basel

Switzerland

Irene Adrian-Kalchhauser <irene.adrian-kalchhauser@unibas.ch>

Sweden MarineInvasions May15-17 2

Evolutionary Biology of Marine Invasions Marine Evolution 2018, 15-17 May 2018, Strömstad, Sweden

We are pleased to announce the call for abstracts for the symposium: Evolutionary Biology of Marine Invasions at the Marine Evolution 2018 Conference

Marine invasions represent natural experiments in evolution, as invasive species spread and adapt to novel environments. In addition, the introduction of novel species to marine systems can impact the evolutionary biology of resident species from the population to community to ecosystem levels. Often, these evolutionary changes can be very rapid and may take myriad forms, including physiological adaptation and behavioral changes to exploit new environments. Likewise, resident species may evolve quickly in response to strong selective forces exerted by invaders, leading to changes in resident populations, community interactions, and even their environments. However, the field of invasion processes and interactions has remained a "black-box" for many marine systems. As rates of anthropogenic transport around the globe increase, so do the spread and expansion of a multitude of species that would otherwise be geographically constrained. Discerning sources, timing, and vectors of invasive species are often main objectives in marine genetic studies, while elucidating the adaptive shifts and population dynamics is fundamental for biodiversity conservation and management of stocks. This session aims to advance the understanding of invasion mechanisms, local adaptation processes, and the interactions of introduced species with native populations and marine environments.

Abstract submission deadline: 1 February 2018 For further details: http://cemeb.science.gu.se/activities/-marine-evolution-2018 Contact E-mail: April Blakeslee, East Carolina University blakesleeap14@ecu.edu Katerina Vasileiadou, Hellenic Centre for Marine Research kvasileiadou@hcmr.gr

Katerina Vasileiadou <kvasileiadou@hcmr.gr>

Sweden MarineInvasions May15-17 CallAbstracts

Evolutionary Biology of Marine Invasions Marine Evolution 2018, 15-17 May 2018, Strömstad, Sweden

We are pleased to announce the call for abstracts for the symposium: Evolutionary Biology of Marine Invasions at the Marine Evolution 2018 Conference

Marine invasions represent natural experiments in evolution, as invasive species spread and adapt to novel environments. In addition, the introduction of novel species to marine systems can impact the evolutionary biology of resident species from the population to community to ecosystem levels. Often, these evolutionary changes can be very rapid and may take myriad forms, including physiological adaptation and behavioral changes to exploit new environments. Likewise, resident species may evolve quickly in response to strong selective forces exerted by invaders, leading to changes in resident populations, community interactions, and even their environments. However, the field of invasion processes and interactions has remained a "black-box" for many marine systems. As rates of anthropogenic transport around the globe increase, so do the spread and expansion of a multitude of species that would otherwise be geographically constrained. Discerning sources, timing, and vectors of invasive species are often main objectives in marine genetic studies, while elucidating the adaptive shifts and population dynamics is fundamental for biodiversity conservation and management of stocks. This session aims to advance the understanding of invasion mechanisms, local adaptation processes, and the interactions of introduced species with native populations and marine environments.

Abstract submission deadline: 1 February 2018 For further details: http://cemeb.science.gu.se/-activities/marine-evolution-2018*/ Contact E-mail:—— April Blakeslee, East Carolina University blakesleeap14@ecu.edu, Katerina Vasileiadou, Hellenic Centre for Marine Research kvasileiadou@hcmr.gr

– Katerina Vasileiadou Institute of Marine Biology, Biotechnology and Aquaculture Hellenic Centre for Marine Research (HCMR) P.O. Box 2214 71003 Heraklion Crete Greece

Tel: +30 2810 337741 Fax: +30 2810 337870 email: kvasileiadou@hcmr.gr

Katerina Vasileiadou <kvasileiadou@hcmr.gr>

Sweden SexInTheOceans May

We are delighted to announce that Stefano Mariani, Chiara Benvenuto and Isabella Capellini, will co-chair a symposium on: Sex in the oceans: from molecules to macroevolution at the forthcoming Marine Evolution 2018 meeting in Stromstad, Sweden, next May.

This session aims to bring together an interdisciplinary group of researchers, to showcase the most recent advances in the field and propose syntheses to explain the origin, the evolution, the mechanisms and the success of the remarkable reproductive strategies in the oceans, and the implications they have for the management of marine resources in the anthropocene.

Details can be found here: http://cemeb.science.gu.se/-activities/marine-evolution-2018/sessions/4.-sex-in-the-oceans–from-molecules-to-macroevolution- Very importantly, we can now confirm that a selection of the best papers stemming from the event will be featured in a Special Issue of Evolutionary Applications.

Thus, I hope you will consider participating, and/or circulating this piece of news to any potentially interested colleague.

– Dr Isabella Capellini Senior Lecturer in Vertebrate Zoology School of Environmental Sciences Hardy Building, University of Hull Cottingham Road, Hull HU6 7RX (UK)

Isabella Capellini <isab972@yahoo.co.uk>

Toronto AGA WildQuantGen Mar23-25

Registration is now open for the American Genetic Association Symposium "Evolutionary Quantitative Genetics in the Wild".

STUDENTS: The AGA is offering multiple free registration slots to graduation students who submit an abstract.

Registration includes opening reception, talks, meals, and poster session as well as complimentary membership in the American Genetic Association and subscription to Journal of Heredity.

AGA symposia are small, friendly gatherings, and provide wonderful opportunities for students and researchers to engage with one another and share their science.

The symposium will take place over March 23-25, 2018 at the University of Toronto, Canada at the University's Hart House venue.

The meeting will focus on studies of the quantitative genetics of fitness-related traits in an evolutionary context across diverse species.

We will open with a reception on Friday night, and our Key Distinguished Lecturer, Loeske Kruuk, will lead off a full day of talks on Saturday. A poster session reception is planned for Saturday night. Finally, a half day of talks will be presented on Sunday.

Registration is open! For all details, visit http://www.theaga.org . Best wishes,

Anne Bronikowski, 2017 AGA President

John Stinchcombe, Local Host and Co-Organizer

Speakers:

Wilhemine Key Distinguished Lecture by Loeske Kruuk (Australian Natl U.) ˜ "Quantitative Genetics of Fitness in Wild Populations"

David Coltman, U. Alberta ˜ "Architecture of quantitative traits in bighorn sheep"

Jeff Conner, Mich State ˜ "Mechanisms of rapid adaptation"

Lynda Delph, Indiana U. ˜ "Sex-specific selection drives sexual dimorphism in correlated characters"

Ned Dochtermann, U. N Dakota ˜ "Is behavior fundamentally different from other types of traits: behavioral heritabilities and genetic correlations in crickets"

Kathleen Donohue, Duke U. ˜ "Regulating life-cycle phenology through developmental arrest: Seed dormancy and plant life cycles in seasonal environments"

Fred Janzen, Iowa State ˜ "Evolutionary quantitative genetics of sex determination in freshwater turtles"

Adam Jones, U. Idaho ˜ "Epistasis in the wild"

Emily Josephs, UCDavis & Mich State ˜ "Detecting polygenic adaptation in domesticated and wild plants"

Andrew McAdam, U. Guelph ˜ "Maternal effects in North American red squirrels"

Joel McGlothlin, Virgina Tech ˜ "Quantitative genetics of sexual dimorphism in brown anoles"

Mike Morrissey, U. St Andrews ˜ "Development and non-additive genetic variation"

Leonie Moyle, Indiana U. ˜ "Intraspecific polymorphism for quantitative traits and interspecific isolating barriers in wild tomato"

Annalise Paaby, Georgia Tech ˜ "Hidden variation and the evolution of complex traits"

Julia Saltz, Rice U. ˜ "Gene-environment correlation: implications for evolutionary quantitative genetics"

Jon Slate, U. Sheffied ˜ "Genomic prediction in a wild mammal"

John Stinchcombe, U. Toronto ˜ "Evolutionary genetics in wild and invasive plants"

Cynthia Weinig, U. Wyoming ˜ "Genetic underpinnings of plant-microbe interactions and their role in adaptation"

Jason Wolf, U. Bath ˜ "A genomic perspective on multivariate evolution"

Anjanette Baker <theaga@theaga.org>

abroniko@iastate.edu

UBristol 51stPopulationGenetics Jan3-6 Register

REGISTRATION CLOSING SOON:

Registration for the 51st Population Genetics Group meeting, at the University of Bristol, UK on 3-6th January 2018 will close on 30th November. All talk slots are now filled. However, there is still room to submit posters.

This conference, one of the longest running evolutionary biology meetings in the world, is a great place for researchers at all stages of their career to meet in a supportive atmosphere, and to present and discuss their ideas.

Contributed talks will be accepted on a first-come-first-served basis, and arranged into parallel sessions. The interests of attendees are broad and include all aspects of population and evolutionary genetics, particularly their relevance to genomic architecture, understanding selection on quantitative traits, the evolution of mating systems, and ecological speciation.

Confirmed plenary speakers are: Prof Tracey Chapman (UEA, UK); Prof Daven Presgraves (University of Rochester, USA), Prof Katie Peichel (University of Bern, Switzerland), and Prof Mike Brockhurst (University of Sheffield).

Prof Joe Felsenstein will also be giving the Fisher Memorial Lecture, live via video link up.

Registration and accommodation details are here:

http://populationgeneticsgroup.org.uk We forward to seeing you in Bristol!

Best wishes

Jon Bridle (jon.bridle@bristol.ac.uk)

(On behalf of the Organising Committee)

Jon Bridle <Jon.Bridle@bristol.ac.uk>

UGothenberg MarineEvolution May15-17

Host-Microbe Coevolution in the Sea U of Gothenberg, Stromstad, Sweden, Marine Evolution 2018, 15-17 May

Is this your area of expertise? Or a topic you want to know more about? The call for abstracts is currently open.

Metagenomic surveys have documented marked spatial heterogeneity in the distribution of aquatic microbes, revealing a previously unknown and spatially dynamic microbial landscape. Spatial heterogeneity in marine microbial communities can influence the genetic diversity and population structure of their hosts, an effect that is expected to be especially pronounced at immune loci involved in microbial recognition. While high-throughput sequencing has become a powerful tool for the quantification of cryptic biodiversity, the overwhelming majority of marine microbes can still not be readily cultured, complicating efforts to move beyond association studies to understand the underlying processes regulating host-microbe interactions. Our session will bring together researchers working at the forefront of marine metagenomics, microbiology, and the experimental analysis of host-microbe interactions to discuss strategies for the functional analysis of host-microbe associations in marine environments, and their implications for understanding aquatic biodiversity and evolution.

We are currently recruiting presenters and participants. Please join us! If you have inquiries or interest in this session, contact us:

Tony Wilson, PhD City University of New York Brooklyn College TWilson@brooklyn.cuny.edu

Jimiane Ashe, MS City University of New York Brooklyn College JAshe@brooklyn.cuny.edu

Abstract submission deadline: 1 February 2018 Registration Information: http://cemeb.science.gu.se/activities/marine-evolution-2018 "JAshe@brooklyn.cuny.edu" <JAshe@brooklyn.cuny.edu>

UGothenburg MarineEvolution May15-17

Dear friends,

The abstract submission and registration portal for Marine Evolution 2018, organized by the Linnaeus Centre of Marine Evolutionary Biology, which will take place the 15th through 17th of May 2018 in Strömstad on the West Coast of Sweden, is now open. Deadline for early bird registration is February 1st.

Registration and abstract submission can be done here: http://cemeb.science.gu.se/activities/marine-evolution-2018/registration Marine Evolution 2018 invites students and researchers in the field of Marine Evolutionary Biology. The program will contain plenary presentations by six renowned speakers, followed by 9 sessions on relevant topics. A list of sessions can be found here: http://cemeb.science.gu.se/activities/marine-evolution-2018/sessions The conference will take place over three days in the beautiful Bohuslän region, listed as one of the "ten last great wildernesses in the world" by CNN. It is situated on the Swedish West Coast, strategically located between major international airports in Oslo, Norway and Gothenburg, Sweden. Above the scientific program, the conference will also host excursion events, evening performances and time for discussions and relaxation. The venue is the Strömstad Spa, a modern conference infrastructure with pool and gym facilities. The conference fee is 3600 SEK (1600 SEK for PhD students), excl. VAT.

All the best, The Marine Evolution 2018 organizing committee

Kerstin Johannesson Anders Blomberg Pierre De Wit Eva Marie Rödström Samuel Perini

pierre.de_wit@marine.gu.se

WashingtonDC SexRatioVariation May22-25

Dear colleagues,

My co-organizer Martin Thiel and I would like to invite you to present your research at the symposium "Too few, too many, or just right: Causes and Consequences of Sex Ratio Variation", part of the upcoming International Crustacean Congress IX in Washington DC from May 22-25th 2018. The aim of this symposium is to highlight the importance of sex ratios for evolutionary and population biology. Participants of this symposium might present examples of crustacean species or populations with variable or biased sex ratios, discuss natural and anthropogenic causes of sex ratio variation, and review possible effects on mating interactions, sexual selection and population biology. Scientists at all steps of their career are encouraged to participate!

If you are interested in participating in this symposium, please contact Martin Thiel (thiel@ucn.cl) or Christine Ewers-Saucedo (ewers.christine@gmail.com).

The deadline for abstract submissions is *March 1st 2018.* More information on the conference can be found here: http://www.birenheide.com/ICC2018/index.php *Symposium details*:

Title: Too few, too many, or just right: Causes and Consequences of Sex Ratio Variation

Co-Coordinators: Christine Ewers-Saucedo, Zoologisches Museum der Christian-Albrechts Universität, Kiel, Germany, ewers.christine@gmail.com Martin Thiel, Universidad Católica del Norte, Coquimbo, Chile, thiel@ucn.cl

Symposium summary: While conservation biology concentrates on population size as a measure of extinction risk, sex ratio, especially the operational sex ratio, can also have great impact on a populations' performance. Diverging sex ratios may reduce the effective number of breeding individuals and the effective population size, which can make populations more susceptible to extinction. Moreover, changes in sex ratios affect the competition for access to mates, thereby affecting reproductive behavior, sexual selection and mating systems. While sex ratios vary naturally in some populations, others are biased by human action. Natural causes of sex ratio variation include sex-specific survival (e.g. predation), local mate competition, and feminizing parasites. Anthropogenic causes include masculinizing and feminizing contaminants and sex-biased fisheries. Shifts in climate and temperature (whether along natural gradients or human-caused) can also impact sex ratios. Sex ratio variation and bias has the potential to play an important role in many crustacean taxa, which therefore provide opportunities to compare and contrast causes and consequences of operational sex ratios using experimental, observational and comparative approaches. Participants of this symposium will present examples of species and populations with variable or biased sex ratios, discuss natural and anthropogenic causes of sex ratio variation, and review possible effects on reproductive biology, mating interactions, sexual selection and population biology.

We plan to publish a special issue in Invertebrate Reproduction and Development.

We applied for funding to offset some of the meeting costs for our symposium speakers.

We are looking forward to seeing you in DC, Martin Thiel and Christine Ewers-Saucedo

Christine Ewers <ewers.christine@gmail.com>

GradStudentPositions

BallStateU BehavioralEvolution

Graduate Student Positions in Behavioral Evolution

The Ward Lab at Ball State University is seeking bright and talented MSc students for Fall 2018. Research in our lab seeks to understand the proximate and ultimate factors that control variation in behavior. We work primarily with stream fishes, but projects involving other organisms are possible. Current projects in the lab focus on two non-mutually exclusive lines of inquiry:

1. Communication systems, sensory perception, and information processing

How do organisms perceive and respond to one another and the environment? This line of research focuses on understanding the mechanisms, function and evolution of sensory and communication systems. Questions asked relate to how animals have evolved to perceive, process, and respond to stimuli in the contexts of mate choice, aggression, and predator-prey dynamics, as well as how behavior develops in response to abiotic environmental cues.

2. Ecological and evolutionary consequences of human-driven behavioral change on animals

What drives the behavioral responses of organisms to a changing world? Another focus of our research is to clarify how different forms of human activity (endocrine disrupting chemicals, land-use changes, invasive introductions) modify the behavior of organisms, and the associated ecological and evolutionary implications of these changes.

Interested prospective students should contact Dr. Jessica Ward at jlward4@bsu.edu. Please include (i) a letter of motivation including a maximum 1-page statement of your research interests and relevant technical skills and experience, (ii) a CV, (iii) your GRE scores (if you have them), and (iv) contact information for 3 references.

Funding is available to students through a variety of sources, including teaching assistantships. However, the departmental deadline for applications for assistantships is February 1 2018. Therefore, interested students should contact Dr. Jessica Ward ASAP.

The Department of Biology at Ball State is a collaborative and dynamic research environment with more than 30 faculty members and ~50 MSc and PhD graduate students. Ball State University is located in Muncie, Indiana, on an attractive campus 45 miles northeast of Indianapolis. To learn more about admissions requirements and processes, applicants should visit the university graduate admissions webpage (http://cms.bsu.edu/-academ$B!D(B/collegesanddepartments/gradschool or the Biology Department webpage (http://cms.bsu.edu/-academics/collegesanddepartments/biology).

Ball State University is an Equal Opportunity/Affirmative Action employer that is strongly and actively committed to diversity within its community. Women, minorities, individuals with disabilities and protected veterans are strongly encouraged to apply. All qualified applicants will receive equal consideration without regard to race, color, religion, sex, national origin, age, disability, protected veteran status or any other legally protected status.

For more information, please contact Dr. Jessica Ward Assistant Professor Department of Biology Ball State University jlward4@bsu.edu.

Jessica Ward <jlward4@bsu.edu>

BrighamYoungU EvolutionaryEcol

The Adams lab in the Department of Biology at Brigham Young University (BYU) welcomes applications from students wishing to pursue a PhD in evolutionary ecology, focusing on soil ecosystems, starting Fall of 2018.

Dissertation projects are dynamic, focusing on core hypotheses associated with the McMurdo Dry Valley LTER (http://mcmlter.org), primarily the characterization of soil ecosystem responses to climate variation. Our hypotheses are informed by approaches including community and autecology, ecological genomics, comparative phylogeography, elemental stoichiometry, molecular evolution, and metagenomics/transcriptomics. Successful candidates will be required to carry out challenging fieldwork in the McMurdo Dry Valleys, Antarctica.

BYU is located in Provo, Utah, where opportunities for world-class skiing, snowboarding, fly-fishing, kayaking, hiking, rock climbing, mountain biking, and many other outdoor recreational activities are less than 20 minutes from the lab. There are several festivals during the year in different areas of the county and Provo is home to a vibrant music scene. Salt Lake City is only 45 minutes travel by car or commuter rail.

For full consideration, complete applications should be received by January 15, 2018, but late applications can be considered through the first part of February. Financial support is competitive and comes from a variety of sources, including teaching assistantships, research assistantships, fellowships, and external research funding from the National Science Foundation.

BYU is a private institution run by the Church of Jesus Christ of Latter-Day Saints. Students are required to uphold a standard of personal conduct. For more information on this standard, please visit the Honor Code Office website (https://honorcode.byu.edu/).

Interested students should contact Byron Adams (bjadams@byu.edu), including a current CV and why our research group might be a good fit for your career and educational interests/goals. Application information can be found on the BYU Biology website, http://biology.byu.edu/GradAdmissions Byron Adams Department of Biology Brigham Young University

Google Scholar https://scholar.google.com/-citations?user=oASVdOIAAAAJ&hl=en&oi=ao “byron_adams@byu.edu” <byron_adams@byu.edu>

BrooklynC MicrobeEvolution

Looking for a Ph.D. student to join the Draghi Lab at Brooklyn College. We study evolution in microbes to understand the basic processes and dynamics of adaptation. I currently have Ph.D. student funding from NSF's Systems & Synthetic Biology program for a project modeling metabolism, evolution and epistasis in the bacterium M. extorquens. This is a collaborative grant involving a variety of cutting-edge experimental and computational approaches; we're just getting started with this 3-4 year project, making this a fantastic opportunity for students with interests in evolution, programming, statistics or microbiology.

Students from a variety of disciplines are invited to apply. Potential applicants should first send a CV and a cover letter directly to Dr. Jeremy Draghi at jdraghi@gmail.com. Brooklyn College is part of the City University of New York, and promising applicants will be directed to apply to either the EEB or MCD subprograms at the CUNY Graduate Center, with applications due January 1^st. Please see https://www.gc.cuny.edu/-Page-Elements/Academics-Research-Centers-Initia tives/Doctoral-Programs/Biology

for further details.

Jeremy Draghi <jdraghi@gmail.com>

CambridgeU PlantEvolution

*** PhD studentship in Plant Evolutionary Radiations available from Oct 2018 ***

* Background * Predicting the conditions that allow species to proliferate in diversity is a central question in evolutionary biology and has practical implications for modern conservation. In many parts of the world, recent and rapid radiations have accompanied the expansion of habitats due to climatic and geological changes (Hughes et al. 2015). However, the importance of niche-based ecological processes in not only generating diversity, but also influencing evolutionary dynamics, remains poorly understood.

This studentship aims to test how different types of niche formation influence species diversification at micro- and macro-evolutionary scales. The first component involves adapting a widely-used mathematical model of adaptive evolution to track genetic and trait responses of individual plants over thousands of generations in response to different ecological conditions (Gavrilets and Vose 2005). This will generate hypotheses, such as faster rates of niche expansion and contraction promote species diversity, which we might test experimentally in the laboratory by evolving a model organism, such as Pseudomonas fluorescens, under different environmental conditions (e.g. Koeppel et al. 2013). The second part of the project will adopt a synthetic approach to relate features of different biogeographic regions (e.g. climatic stability) to macro-evolutionary dynamics of their corresponding floras.

* What the student will do * The student will code the theoretical model in a programming language and refine the modelling scenarios that will be tested. They will also design and execute the laboratory experiment, measuring phenotypic responses and genetic variation

among populations. In the second part of the project, they will use phylogenetic comparative methods to reconstruct the evolutionary history of plant lineages in different biogeographic regions. Our group has already identified a number of biogeographic regions and plant lineages for which this analysis would be tractable. In the first instance, the student will estimate phylogenetic trees for different lineages using pre-existing barcode data on GenBank. Speciation and extinction rates will then be estimated using established maximum-likelihood and Bayesian approaches, and associated with regional characteristics using standard regression techniques, e.g. PGLS.

* Eligibility and Funding * The studentship will be awarded as part of a competitive process under the University of Cambridge's NERC-funded Earth System Science Doctoral Training Partnership. UK and EEA students who meet the UK residency requirements will be eligible for a full studentship that covers the cost of all fees and provides the standard NERC maintenance allowance (14,553 pa for 2017/18). Students from EU countries who do not meet the residency requirements may still be eligible for a fees-only award, and can apply for maintenance feeds funded by the various Cambridge Trusts. Overseas students may similarly be able to join the programme but will need to have arranged funding from other sources. Further funding details are available here: https://essdtp.esc.cam.ac.uk/prospective-students/funding-information * How to Apply * Interested applicants should email AJ Tanentzap (ajt65 -at- cam.ac.uk) expressing their interest and attach a CV. Individuals with a Masters in evolutionary biology, phylogenetics, or a related discipline are particularly encouraged to apply.

The deadline for applications is Thursday 4th January 2018. All supporting documentation (e.g. references) must be uploaded within 7 days of submitting your application. Full details of the application process are available at: https://essdtp.esc.cam.ac.uk/prospective-students/how-to-apply * References * Gavrilets, S. & Vose, A. 2005. Dynamic patterns of adaptive radiation. Proceedings of the National Academy of Sciences, vol. 102, pp.10840-10845. DOI: 10.1073/pnas.0506330102 Koeppel, A.F. et al. 2013. Speedy speciation in a bacterial microcosm: new species can arise as frequently as adaptations within a species. ISME, vol. 7, pp.1080-1091. DOI: 10.1038/ismej.2013.3 Hughes, C. E., Nyffeler R., Linder, H.P. 2015. Evolutionary plant radiations: where, when, why and how? New Phytologist, vol. 207, pp.249-253. DOI: 10.1111/nph.13523

AJ Tanentzap (ajt65 -at- cam.ac.uk)

CityU NewYork EvolutionaryBiol

Interested in a PhD in Ecology, Evolutionary Biology and Behavior? The EEB subprogram at the City University of New York is recruiting doctoral students!

EEB faculty research spans diverse topics across ecology, behavior, evolution and systematics to understand the relationships of organisms, populations and communities to their historic and contemporary environments, with particular strengths in using molecular and computational approaches to solving evolutionary questions. Doctoral students conduct research with faculty mentors across eight campuses of the City University of New York and the American Museum of Natural History.

Applications are due January 1, 2018. Please see instructions on our website (gc.cuny.edu/biology/eeb) and contact program chair Dr. Elizabeth Alter (ealter@york.cuny.edu) with any questions. NB: Students applying to work with a faculty mentor at the AMNH must also submit a fellowship application by December 15, 2017.

Please see our website for a full list of faculty (gc.cuny.edu/biology). Faculty recruiting in Fall 2018 include:

Lorenzo Prendini *(AMNH):* Systematics, evolution and biogeography of arachnids. scorpion.amnh.org

Eunsoo Kim *(AMNH):* Evolution, diversity, and symbioses of microbial eukaryotes. https://www.amnh.org/our-research/staff-directory/eunsoo-kim/ *Mark Siddall* *(AMNH):* Protistan parasites. http://research.amnh.org/users/siddall/ *Mande Holford* *(Hunter):* Discovering novel peptides from venomous marine snails. http://www.holfordlab.com/ *Christopher Blair (City Tech):* Phylogenetics, phylogeography and demographic history of amphibians and reptiles. http://www.citytech.cuny.edu/faculty/CBlair *David Gruber (Baruch):* Fluorescence in marine organisms. http://www.baruch.cuny.edu/wsas/academics/natural_science/dgruber.htm *Stefano Ghirlanda (Brooklyn).* Computational models of learning and decision making, e.g. http://rsos.royalsocietypublishing.org/content/3/11/160734 . *Jeffery Bird (Queens):* Belowground C and N cycling in terrestrial and estuarine ecosystems. http://qcpages.qc.cuny.edu/~jbird/Index.html *Paul Forlano (Brooklyn):* Evolutionary/systems neuroscience of fishes. http://forlanolab.com/ *Jeremy Draghi (Brooklyn):* Eco-evolutionary feedbacks in host shifts in viruses and fitness

landscapes in bacterial metabolism. https://jeremydraghi.com/ *Lisa Manne (CSI):* Terrestrial ecology, biogeography and conservation. https://csivc.csi.cuny.edu/Lisa.Manne/files/ *Richard Veit (CSI):* Ecology of birds, including foraging behavior. https://www.csi.cuny.edu/campus-directory/richard-veit *Tony Wilson (Brooklyn):* Evolution of reproductive complexity in aquatic environments. *http://evolution.brooklyn.cuny.edu *Mike Hickerson (CCNY):* Population genetics, community ecology and biogeography. Determinants of community assembly. https://hickerlab.wordpress.com/ *Ana Carnaval (CCNY):* Spatial patterns of biodiversity and their underlying evolutionary and ecological processes. *www.carnavallab.org *Rob Anderson (CCNY):* Biogeography, spatial configuration of environmental suitability for species, and its ecological, evolutionary and practical consequences.

http://www.andersonlab.ccny.cuny.edu/ *Kyle McDonald (CCNY):* Water and carbon cycling. https://www.ccny.cuny.edu/profiles/kyle-mcdonald – S. Elizabeth Alter, Associate Professor Biology, City University of New York/York College Doctoral Program in Ecology, Evolutionary Biology and Behavior, The Graduate Center Research Associate, American Museum of Natural History

Email: sealter@gmail.com, ealter@york.cuny.edu Office: (718) 262-2732 Website: fishfiles.org Twitter: @lizalter

Liz Alter <sealter@gmail.com>

ClarkU EvolutionaryMorphology

Dr. Philip Bergmann's Evolutionary Functional Morphology Lab at Clark University is recruiting a Ph.D. student to begin in Fall 2018. The Bergmann lab studies form-function relationships in an evolutionary and ecological context, primarily using reptile and amphibian locomotion as a study system. The main research foci are (1) how form-function relationships work and are affected by such as ontogeny and substrate, and (2) the evolution of snake-like body shapes from phenotypic, functional, and ecological perspectives. Tools used by the lab to address these questions include high-speed video and X-ray video, force plates, EMG, dissection, behavioral observations, field work, and computational statistics.

Graduate students should be self-motivated and have prior research experience. They will be encouraged to develop their own projects within the context of the lab research. Interested students should contact Dr. Bergmann (pbergmann@clarku.edu) prior to applying with any questions they may have, a cover letter that includes their research interests, CV, and names and e-mail addresses for two references. The Biology Department at Clark University is small but vibrant, providing students the opportunity to gain experience in research, teaching, mentoring, and outreach. Support by way of Teaching Assistantship is guaranteed for five years, and includes tuition waiver. The application deadline is January 15, 2018.

For more information, visit:

Bergmann Lab: http://www2.clarku.edu/faculty/pbergmann/ Biology Department: http://www2.clarku.edu/departments/biology/ Graduate Admissions: http://www.clarku.edu/admissions/graduate-admissions Philip J. Bergmann

Associate Professor

Biology Department

Clark University

950 Main Street

Worcester, MA 01610

United States

Phone: 508-793-7553

E-mail: pbergmann@clarku.edu

Philip Bergmann <PBergmann@clarku.edu>

ClemsonU EvoDevo

The Powder lab at Clemson University is recruiting MS and PhD students to study the genetic and developmental basis of craniofacial evolution of cichlid fishes (Evo-Devo). Positions would start in Fall 2018. We combine approaches including quantitative trait loci (QTL) mapping and population genomics to identify genetic regions in cichlids that contribute to craniofacial variation. We then analyze candidate genes and transcriptional regulators utilizing pharmacological treatments, gene knockdowns, genetic engineering (CRISPR/cas9), genomics, and geometric morphometric shape analysis in either cichlids or zebrafish embryos. See https://urldefense.proofpoint.com/v2/url? u=https-3A__karapowder.wordpress.com&dDwIFaQ&c=Ngdta5yRYsqeUsEDgxhcqsYYY1Xs5o gLxWPA_2Wlc4&r=ZT1TkG3EwmzuEn3nGf_KR1L0G Tuxt-jYayWp54KkQrs&m=nKbk6PrRofe6JvaAR7X aR1vv66baErir0OYRdhuI_Cc&s=9hwMNEJ0eU5IT 0SRx3S6L8ls0z7BsXLhwPuXADiv6Kc&efor more information

Both MS and PhD degrees are available through the Department of Biological Sciences at Clemson University and will be supported through Graduate Teaching Assistantships (GTAs) and Graduate Research Assistantships (GRAs). Detailed information about the graduate program and admissions are available at http://www.clemson.edu/science/departments/biosci/academics/graduate/index.html .The application deadline is Jan 5, 2018.

About the area: Located in Upstate South Carolina, Clemson's picturesque campus is on the shores of Lake Hartwell and in the foothills of the Blue Ridge Mountains.

We are surrounded by lakes, waterfalls, and abundant hiking. Also within a quick drive is the beautiful and thriving Greenville SC, ranked #7 on Lonely Planet's 2015 Best in the US list, as well as Asheville NC, Atlanta GA, and Charlotte NC.

Interested? Contact Kara Powder at kpowder@clemson.edu to talk more before applying.

– *Kara E. Powder | Assistant Professor of Biological Sciences | Clemson University* *864-656-3196 | **karapowder.wordpress.com | **055A LSF | 190 Collings St. | Clemson, SC 29634-0314 * Clemson, SC 29634-0314 *

DurhamU 4 EcologyEvolutionGenetics

Several competitive PhD studentship opportunities are available in evolutionary ecology and genetics at Durham University, UK. These 3.5 or 4-year fellowships provide a full tuition fee waiver, a competitive living stipend, and a considerable research allowance. For more information about these projects and how to apply see https://sites.google.com/site/andreannajwelch/jointhelab/ phd-studentship-opportunities or contact Dr. Andreanna Welch at a.j.welch@durham.ac.uk. Only the best applicants will be asked to submit a full application.

Durham University is consistently rated as one of the top 100 universities in the world. Located in northeast England, the university is situated in a scenic town and lies within a 15-minute train ride of the thriving city of Newcastle. The department of Biosciences offers a supportive research-driven environment with projects ranging from the cellular to the ecosystem level.

AVAILABLE PROJECTS:

1) BIODIVERSITY AND ECOSYSTEM SERVICES: BIRDS, BATS, BEES, AND COCOA TREES

Primary supervisor: Dr. Andreanna Welch (Durham University) Co-supervisors: Dr. Darren Evans (Newcastle University) Eligibility: British citizens or EU citizens who have resided in the UK > 3 years Full Application Deadline: 17 January 2018, but contact Dr Welch by early January to express interest

Human populations are increasing rapidly and consumption is intensifying. At the same time biodiversity, which provides critical ecosystem services, is being lost at an unprecedented rate. Realisation of this crisis has created an urgent need to balance agricultural production with biodiversity. These two objectives are not disjoint, and indeed, biodiversity can play an integral role in increasing agricultural yields'Xsustainably. To achieve balance, we must manage ecosystems for species that provide support for crops ("ecosystem service species'Â, e.g. species that provide pest control) as well as those that encourage biodiversity ("keystone species"), and especially those that provide both functions ("cross-over species").

To truly work towards this balance, we must first understand the food web, because species vary greatly in their value for agriculture and biodiversity services. The student will use state-of-the-art genetics methods to deduce the diets of animals in the food web of plants, birds, bats and arthropods in African cacao plantations (the main ingredient of chocolate). He or she will address:

A) Which member species are most influential in encouraging crop yields and/or increasing biodiversity? B) Do the above insights change depending on the context of the landscape, e.g. at sites near or far from forest? C) How can we use the above insights to manage ecosystems that are both diverse and high-yielding?

˜˜˜

2) RECONSTRUCTING THE EVOLUTIONARY HISTORY OF ECOLOGICAL DYNAMICS AND EXTINCTION RISK IN SEABIRDS

Primary supervisor: Dr. Andreanna Welch (Durham University) Collaborators: Dr Helen James (Smithsonian Institution), Dr Terry Chesser (US Geological Survey), Dr Vincent Bretanolle (Equipe AGRIPOP, CEBC-CNRS) Eligibility: Open to all students Full Application Deadline: 17 January 2018, but contact Dr Welch by early January to express interest

Even though the oceans cover the majority of the Earth'Âs surface, birds have colonized the oceanic realm only a handful of times during evolutionary history. Oceanic seabirds are intimately tied to their habitat and demonstrate many novel morphological and ecological characteristics, from dynamic soaring to pursuit diving for prey to underwater propulsion in flightless species. Unfortunately, they are also one of the most threatened groups of birds in the world. Thus, oceanic birds provide an excellent system for investigation of ecological diversification, as well as the factors associated with extinction risk. In general the molecular phylogeny of oceanic seabirds has been well studied, with the striking exception of the petrels, shearwaters, and albatrosses of the order Procellariiformes, which is the largest and most diverse group. For this project, the student will generate genome-scale mitochondrial and nuclear DNA sequence data sets to build a time-calibrated, species-level phylogeny for this order. This tree will be combined with information about their ecological, morphological, and life history characteristics, to investigate the evolution of ecological traits as well as the factors associated with extinction risk in this unique and highly threatened group. Large-scale analyses such as these will provide a framework for studying the evolutionary ecology and conservation biology of a broad and globally important ecological role, that of oceanic avian predators.

˜˜˜

3) UNDERSTANDING EVOLUTION IN INVASIVE SPECIES THROUGH NATIVE-EXOTIC RANGE COMPARISONS

Primary supervisor: Dr. Wayne Dawson (Durham University,

— / —

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

---

Durham UK ConservationPhylogeography

Competitive Studentships in the Molecular Ecology Group, Durham, UK:

Project 1: Next generation conservation genetics at sea: detecting and conserving adaptive potential Objectives: To test hypotheses about the more specific mechanisms that generate distinct patterns of diversity at functional loci across environmental gradients in the marine environment using high resolution next generation sequencing data and working with reference genomes. The key objectives will be to identify loci or gene systems that reflect diversity requiring conservation management that are not detectable using conventional methods based on neutral loci. At the same time, these data will enhance our understanding of the process of adaptive evolution, providing novel inference about the evolution of diversity in the marine ecosystem.

A more detailed flyer about the project is available on request. All nationalities are eligible for this studentship.

Project 2: Phylogeography of European ungulates from the last interglacial period and their subsequent evolution Objectives: This study will use next generation sequencing methods to explore the genetic diversity of deer and other ungulates from the Eemian interglacial period, ˜120,000 years ago. This will allow us to test hypotheses about the origin and evolution of modern populations, the impact of the last glacial period on the diversity and distribution of these species, and the phylogenetic relationship between ancient and modern populations, and between each and the rest of the cervid lineage. A key aspect of the study will be the integration of environmental data, so that any changes in demography or distribution can be interpreted in the context of changing environments.

A more detailed flyer describing the project is available at: http://www.iapetus.ac.uk/studentships/ Please note that this studentship is fully funded for UK nationals only.

Application materials should include a c.v., academic records and at least two letters of reference sent to a.r.hoelzel@dur.ac.uk . Deadlines are 12 January 2018 for project 1 and 16 January 2018 for project 2. Please contact Rus Hoelzel at the same email address with any questions about either project.

"HOELZEL, RUS A.R." <a.r.hoelzel@durham.ac.uk>

Europe 15 PlantID

Plant.ID is recruiting 15 PhD fellows

The EU H2020-ITN-ETN project Plant.ID on molecular identification of plants is a European training network aimed at providing 15 PhD fellows across nine European host institutions with excellent training through a network of leading academic experts, museums, governmental and industry partners in the field, using an intensive program with network-wide training events, intra-network supervision and secondments.

Who are we looking for? Marie Curie Training Networks offer a unique opportunity to get cutting-edge training in a multidisciplinary environment with a focus on academic and personal development of the PhD fellows. The supervisors in the network each provide specific competences and as part of the network you develop your skills and carry out research both independently and as part of a network of 15 PhD fellows.

The consortium ensures cross-pollination and exchange of ideas through network-wide training events, summer schools and intersectoral secondments. As a PhD fellow in the Plant.ID network, you need to have good social skills and be willing to conduct the planned secondments and importantly be innovative and goal-oriented. All candidates must be fluent in spoken and written English.

Job conditions The PhD student will be appointed under an employment contract with a competitive salary and mobility allowance at the host institution. Fellows are expected to start in April 2018. Additional funding for research and participation in courses, workshops, conferences, etc. is ensured.

Job description Your key tasks as a PhD fellow in Plant.ID are: - Manage and carry through your research project - Take PhD courses within the Plant.ID network - Write scientific articles and your PhD thesis - Participate in international congresses and Plant.ID network meetings - Stay at a research institution abroad for the secondment(s) - Teach and disseminate your research

EU eligibility criteria for candidates The applicant may be of any nationality but in order to be eligible for the positions the following criteria applies to all applicants: - The applicant shall at the time of recruitment be eligible as an Early Stage Researcher (ESR) by being in the first four years of his/her research career and not have been awarded a doctoral degree.

- The applicant must not have resided or carried out his/her main activity in the country of the host institute for more than 12 months in the 3 years immediately prior to the recruitment.

Plant.ID is recruiting 15 PhD students simultaneously and interested candidates are encouraged to apply for multiple projects within the network. Read more about the 15 individual PhD projects on www.plantid.uio.no. The following projects are included: PhD 1 - Polyploid phylogenetics under the multi-species coalescent - University of Gothenburg PhD 2 - Taxon identification and multispecies coalescent biodiversity assessments - University of Oslo PhD 3 - Euphrasia: species delimitation in mega-diverse hemi-parasites - University of Copenhagen PhD 4 - Shotgun sequencing for comparative diet analysis in capercaillie fowl - University of Copenhagen PhD 5 - DNA barcoding and metabarcoding of herbal products for authentication - University of Oslo PhD 6 - Metabarcoding of aquatic flora for fresh water quality monitoring - BaseClear, Degree Awarding University of Leiden PhD 7 - Hayfever and software-automated pollen metabarcoding - Naturalis Biodiversity Center, Degree Awarding University of Oslo PhD 8 - Paleogenomic annotation of historical Cinchona bark samples across time and space - University of Copenhagen PhD 9 - Genomic barcoding of the succulent plant genus Aloe in trade - Royal Botanic Gardens Kew, Degree Awarding University of Copenhagen PhD 10 - Orchid targets: Genomic barcoding to identify and trace traded orchids - University of Oslo PhD 11 - Is mutational meltdown a threat in the mega diverse genus Begonia? - Royal Botanic Gardens Edinburgh, Degree Awarding University of Edinburgh PhD 12 - Genomic barcoding to trace and identify illegally logged African trees - Botanic Garden Meise, Degree Awarding KU Leuven PhD 13 - Bar-HRM traceability of toxic species in food and medicine - Centre for Research & Technology - Hellas, Degree Awarding Aristotle University of Thessaloniki PhD 14 - Species, a taxonomic category distinct from the lineage concept - University of Gothenburg PhD 15 - Logging forensics: mining ebony wood collections as references - Naturalis Biodiversity Center, Degree Awarding University of Leiden

Application deadline January 15, 2018. For more information and how to apply: www.plantid.uio.no Hugo de Boer Natural History Museum University of Oslo P.O. Box 1172 Blindern 0318 Oslo, Norway Phone: +47 22851875 Plant.ID MSCA-ITN project leader Leader of ForBio - Research School in Biosystematics Plant Evolution and DNA Metabarcoding group

— / —

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

FloridaIntlU MarineEvolutionaryBiology

The CRUSTOMICS lab at Florida International University in the Department of Biology and Marine Sciences Program is looking for highly motivated graduate students with an interest in evolutionary biology and marine invertebrates.

Research Interests

The Bracken-Grissom Lab is fundamentally interested in the evolution of marine invertebrates. Many projects investigate the Decapod Tree of Life and use a phylogenetic framework to study various aspects of their diversification, ecology, biogeography, and conservation. More recent projects integrate taxonomic and genomic methods to study evolutionary processes and complex traits in extreme environments including the deep sea, aquatic caves, and habitats exposed to anthropogenic disasters. Current awarded grants target the evolution of bioluminescence in the deep sea, molecular convergence of cave-adapted phenotypes and ecosystem health following the Gulf of Mexico Deepwater Horizon Oil Spill. More information on our research can be found here: *www.brackengrissomlab.com Qualifications

Applicants should have a background in evolutionary biology and molecular methods. Experience with invertebrate zoology, phylogenetics, systematics, next generation sequencing methods and/or bioinformatics is a plus. Students would ideally have a B.S. degree in Biology or related discipline. Student must be proficient in English (both spoken and written). Our work requires good organizational and computational skills and the ability to work collaboratively as part of a team. Occasional physically demanding fieldwork may also be required to support research.

Requirements

The Bracken-Grissom lab is looking for 1 graduate student to start in the Fall of 2018. PhD candidates are preferred but students interested in pursuing an MS degree are welcome to apply. If you are interested in applying for a graduate position in my lab, please send a letter of interest to hbracken@fiu.edu describing your research interests, career goals and rationale for pursuing a graduate degree along with a CV. Graduate students admitted to the program receive guaranteed funding from the Department for up to 4 years. Additional information on my lab's research, the biology department, and marine sciences program can be found here: www.brackengrissomlab.com and http://biology.fiu.edu/ and www.fiu.edu/~marine. More information on the application process and Graduate School at FIU can be found here http://gradschool.fiu.edu/ .Application deadline Jan 5th 2018.

Contact Information

Heather Bracken-Grissom, PhD

Assistant Professor

Dept. of Biological Sciences

Florida International University-Biscayne Bay Campus

3000 NE 151 Street, MSB-353

North Miami, Florida 33181, USA

305 919-4190 (Phone)

email: hbracken@fiu.edu

– Heather Bracken-Grissom, PhD Assistant Professor Dept. of Biological Sciences Florida International University-Biscayne Bay Campus 3000 NE 151 Street, MSB-353 North Miami, Florida 33181, USA 305 919-4190 (Phone) 305 919-4030 (Fax)

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

FordhamU EvolutionaryBiol

Graduate Fellowships in Ecology, Evolution, and Conservation at Fordham University

The Graduate Ecology program at Fordham University has new research opportunities and fellowships available for well-qualified students interested in pursuing a M.S. or Ph.D. starting in Fall 2018. Research opportunities through our graduate program link scientists at our main campus, the Louis Calder Center (our biological field station), the New York Botanical Garden, and the

Wildlife Conservation Society.

Accepted MS and PhD students are eligible to receive competitive stipends, plus full tuition remission. Students may work in many areas of ecology and evolution, as well as applied areas such as conservation of endangered species, ecological and evolutionary effects of urbanization, behavioral ecology, disease ecology, and responses of plants and animals to climate change.

Interested students should contact relevant faculty members or research scientists to discuss mutual research interests via the following websites.

Biology faculty: https://www.fordham.edu/info/-24004/faculty Louis Calder Biological Field Station: http://www.fordham.edu/calder_center Opportunities at the New York Botanical Garden:

https://www.nybg.org/plant-research-and-conservation/tour/graduate-stud ies/

Opportunities at the Wildlife Conservation Society: http://www.wcs.org/ The deadline for applications is January 3, 2018. Online applications are available from: https://gradadmissions.fordham.edu/apply/ For any questions, please contact Dr. J.D. Lewis by email: jdlewis@fordham.edu

J.D. Lewis Professor and Chair Department of Biological Sciences Fordham University 441 E. Fordham Road Bronx, NY 10458 USA

Louis Calder Center, Fordham University

31 Whippoorwill Road, Box 887

Armonk, NY 10458, USA

Steve Franks <franks.steve@gmail.com>

GeorgeWashingtonU FishEvolution

PhD position in systematics, phylogenomics, and trait evolution of fishes. In the framework of a large multi-institutional program (FishLife), we are seeking to recruit a motivated graduate student with interests in ichthyology, phylogenetics, genomics, and bioinformatics.

Learn more about our graduate program in Systematics, Evolution and Ecology at

https://biology.columbian.gwu.edu/graduate The Department is involved in several special graduate programs collaborating researchers, faculty, and facilities at GW and elsewhere in the Washington DC area. Financial support is available on a competitive basis. Applications for the Fall 2018 semester are due December 1, 2017, but late applications also will be considered.

For more information contact Prof. G. Orti (gorti@gwu.edu) . In your email, please include brief description of your research interests, experience, and career goals, and attach a CV or resume.

Guillermo Orti <guilleorti@gmail.com>

ImperialCollege London AvianAdaptation

The current speed at which environmental conditions change is unprecedented, endangering vulnerable populations and species. A novel idea for how organisms can sustainably respond to rapid environmental changes are environmentally induced adaptations that are heritable. Such trans-generational, potentially epigenetic effects can, with high precision mediate evolutionary rescue of populations that experience rapidly changing environments. These advantages put TAGs at the forefront of mechanisms leading to adaptations to global change. This project will use long-term data from a wild population of passerines, and focused experiments on birds in captivity, to disentangle phenotypic plasticity induced during development from epigenetic TAGs, to better understand the epigenetic mechanism, and evolution of TAGs. We will use state-of-the art long-RNA sequencing experiments to pinpoint TAGs in RNA methylation patterns in sparrow sperm, using focused experiments in captive and/or wild birds.

This exciting project will push further the limits of our knowledge on trans-generational effect. It will be conducted in collaboration between Imperial College, the Sanger Institute, the Gurdon Institute University Cambridge, and the University of Sheffield.

Students should be interested in molecular biology, be willing and able to handle birds, and be interested in quantitative data analysis. A BTO ringing license is beneficial.

The Science and Solutions for a Changing Planet (SSCP) Doctoral Training Partnership is a unique and prestigious doctoral training opportunity, funded by NERC and based out of the Grantham Institute.

Please send your CV and a short letter of motivation to Julia.schroeder@imperial.ac.uk before 30 December

2018.

Applicants should meet the UK NERC eligibility criteria: https://www.imperial.ac.uk/grantham/education/science-and-solutions-for-a-changing-planet-dtp/studentship-opportunities/ ** check out our excellent Master course in Ecology, Evolution & Conservation http://www.imperial.ac.uk/life-sciences/postgraduate/masters-courses/masters-in-ecology-evolution–conservation-msc-and-mres/ Dr Julia Schroeder Lecturer Director MSc Ecology, Evolution and Conservation Post-graduate tutor Imperial College London, Silwood Park Campus Buckhurst Road, SL5 7PY Ascot, Berks, UK +44 (0) 20 7594 9086 https://sites.google.com/site/evolbehavecol/home-1 "Schroeder, Julia" <julia.schroeder@imperial.ac.uk>

ImperialCollege London PopGenomicsChytrid

Biomonitoring and controlling amphibian-killing fungi using worldwide genomic data SUPERVISORS: Matteo Fumagalli (Imperial College London, Life Sciences), Matthew Fisher (Imperial College London, Infectious Disease Epidemiology), Richard Everitt (University of Reading, Mathematics and Statistics) PROJECT SUMMARY: The amphibian chytrid fungus Batrachochytrium dendrobatidis (Bd) is responsible for hundreds of species' extinctions. The genetic mechanisms that underpin Bd's virulence are not known yet, although extreme chromosomal plasticity has been suggested to play a role. Large-scale genomic data from worldwide isolates, coupled with appropriate computational methods, will provide us with an opportunity to address how virulent Bd strains spread around the globe.

This project will encompass three main aims: (i) the improvement of computational methods for large-scale high-throughput sequencing data from mixed-ploidy genome, (ii) the development of a comprehensive bioinformatics platform, (iii) the extension of the methods developed in previous aims to genomic data of Bd isolates distributed worldwide.

HOW TO APPLY: This project is suitable for students with either a quantitative or empirical background. Applicants should be meet the UK NERC eligibility criteria (preferably).

To apply, please follow instructions provided at the Centre for Doctoral Training in Quantitative and Modelling Skills in Ecology & Evolution (http://www.imperial.ac.uk/qmee-cdt/).

Funded by NERC, QMEE is led by a consortium of 5 research organisations with complementary expertise in quantitative ecology and evolution, working in partnership with government, industry and charities.

Informal inquiries as well as application for Track I can be addressed to m.fumagalli@imperial.ac.uk

DEADLINE 14 JANUARY 2018

Matteo Fumagalli

Lecturer in Quantitative Evolution Department of Life Sciences Imperial College London Silwood Park Campus Munro Building, N1.6 Ascot, Berkshire SL5 7PY, UK Tel: +44 (0)20 7594 3793 m.fumagalli@imperial.ac.uk https://www.imperial.ac.uk/people/m.fumagalli "Fumagalli, Matteo" <m.fumagalli@imperial.ac.uk>

ImperialCollege London Speciation

3-year PhD IN EVOLUTIONARY BIOLOGY AVAILABLE NOW!

Evolution of species under environmental stress: ecological genomics in island palms

Building on our decade-long evolutionary research on Lord Howe Island (LHI), the student will use this emerging model system to disentangle the genomic underpinning of speciation, with relevance to understanding stress tolerance in plants. Uniquely, we have identified a pair of closely related palm species that have evolved on the minute LHI by adapting to different soil types. One of the species, Howea forsteriana, evolved on calcareous soils deposited by the sea one million years ago, which cause water, salt and metal stresses whilst affecting flowering time. The student will look at the underlying functional genetics of the species split. S/he will use comparative genomics, large controlled environment assays, transformations, and field experiments to validate candidate genes for speciation, stress tolerance and flowering time.

We expect the student to learn advanced quantitative, molecular biology and fieldwork skills, and publish his/her work in high-impact journals. The project is supervised by Professor Vincent Savolainen and Dr Colin Turnbull, and will be mainly based at Silwood Park campus, Imperial College London. The student should have a good Masters degree, and would be able start immediately. Funding is available for a 3-year PhD.

To apply, please send a short CV before 30 November 2017 to v.savolainen@imperial.ac.uk. You can also email me for further information

Interviews will be held early December 2017

UK Research council eligibility applies (UK residency)

Prof. Vincent Savolainen Professor of Organismic Biology Department of Life Sciences Imperial College London, Silwood Park Campus Buckhurst Road, Ascot, SL5 7PY, UK Tel +44 (0)20 7594 2374 v.savolainen@imperial.ac.uk skype vincent.savolainen1 www3.imperial.ac.uk/people/v.savolainen

Distinguished Visiting Professor University of Johannesburg, South Africa

"Savolainen, Vincent" <v.savolainen@imperial.ac.uk>

IndianaStateU EvolutionaryGenomics

Graduate position opportunities in Ecological Genomics

We are looking for motivated students interested in behavioral evolutionary, and ecological genomics to join our laboratory at Indiana State University (ISU). These graduate positions are part of a new interdisciplinary initiative at ISU, The Center for Genomic Advocacy (TCGA), which is focused on the application of genomic technology to the betterment of society. TCGA is developing a state-of-the-art next generation sequencing facility, which is being used to provide hands-on experience for students as well as string infrastructure for modern genomic studies.

Graduate research will be expected to combine traditional behavioral ecology studies with next-generation sequencing technology to examine the evolution of polymorphism in the white-throated sparrow. Student will conduct extensive laboratory work as well as participate in field based data collection during the breeding season. This species exhibits a clear link between phenotype and genotype, making it an ideal system in which to pinpoint the determinants of complex sexual and parental behavior. We have amassed 29 years of detailed data on this species making it possible to identify the genetic, epigenetic, and environmental bases of behavior. Morphs of the white-throated sparrow provide a unique opportunity to study intraspecific genomic differences, which have resulted from two separate, yet linked evolutionary trajectories. Such results can transform our understanding of the evolution of genomes.

To apply, please send a letter of intent and curriculum by January 15, 2018. The subject of the email should mention: WTSP project Graduate Position.

For more information about the positions, please feel free to contact Dr. Rusty A. Gonser (rusty.gonser@indstate.edu), at the Center for Genomics Advocacy (TCGA), Indiana State University, Terre Haute, IN 47809.

For more information about the lab, TCGA, the department, and the university, see:

http://www.indstate.edu/biology/ http://www.indstate.edu/ https://www.indstate.edu/cgps/graduate https://www.indstate.edu/cas/TCGA Dr. Rusty A. Gonser Professor, Department of biology Director of the Center for Genomic Advocacy (TCGA) Indiana State University Terre Haute, IN 47809

Phone: 812.234.9220 Email : rusty.gonser@indstate.edu

Zoe Delefortrie <zdelefortrie@sycamores.indstate.edu>

Inverness Scotland SalmonConservation

Project Description Aquaculture is fast outpacing the production of wild fisheries and there is increasing concern regarding the potential negative impacts of farm escapes on wild populations of conspecifics. Scotland has the second largest Atlantic salmon farming industry in the species' native North Atlantic range, after Norway. In 2015, this encompassed a production of >40 million smolts and > 171,000 tonnes of salmon for market, with increased production planned for coming years. Scotland also has hundreds of rivers with wild salmon stocks that are the mainstay of a vital recreational fishing industry that is a major contributor to the nation's economic wealth.

The project involves the exploitation of diagnostic molecular markers developed by the RLI as part of a UK Research Council aquaculture sector funded international research collaboration with partners in Norway, Scotland, Ireland and Canada to differentiate farm and wild Atlantic salmon. These will be used to assess actual levels of escaped farm salmon in rivers across Scotland, of interbreeding, and of genetic introgression. The lack of understanding of these factors precludes the effective management of the species, risking unacceptable impacts on wild stocks or holding back expansion of the farming industry, or potentially both. In Norway, genetic mixing is highly variable, from 0-47% while in Scotland only a few, ad hoc studies have been carried out on levels of direct genetic interaction and most of these are dated and provide insight into only a few rivers with general, contemporary levels being poorly documented.

Knowledge of the level of interbreeding and introgression can help guide locational development of the farming industry to minimize impacts on wild stocks and fisheries. Where it can be demonstrated to be limited or absent, this will also help to gain Marine Stewardship certification for farmed salmon products. The project will involve collaboration with local fisheries management organisations to collect contemporary samples of salmon in a representative set of Scottish rivers and to genetically screen these fish, along with archived historical samples, with the farm-wild markers. Levels of escapement, interbreeding and introgression will be quantified, mapped and the factors accounting for observed levels investigated. The implications of observed levels will be explored using an existing individual based genetic-demographic reproductive interaction model.

Supervisory Team The student will be supervised by Dr Mark Coulson and Professor Eric Verspoor of the Rivers and Lochs Institute.

Research Facilities and Environment The student will be based in the Rivers and Loch Institute at the University of the Highlands and Islands Inverness College on the new Inverness Campus and part of a small but growing, dynamic team of researchers focused on aquatic biodiversity conservation and management. The RLI is recognized internationally for its expertise in genetic issues related to aquaculture-wild interactions and as well as in the development of molecular genetic markers, applied molecular population genetics, fisheries management, and fish phylogeography. It is also extending its programme of work to encompass eDNA, DNA barcoding, and metabarcoding, across the spectrum of aquatic organisms, with a focus on freshwater ecosystems. The Institute provides a stimulating and vibrant research environment, supported by a state-of-the-art molecular genomics facility encompassing Sanger and NexGen sequencing systems, qPCR, high throughput DNA fragment analysis instrumentation, with technical support, and in-house bioinformatics, computing and statistical support. The student will receive training in manuscript writing and research presentation as well as engage in-house seminars in research skill development and contribute to weekly alternating journal club and work presentation meetings. There will also be opportunities to attend relevant national and international conferences.

Informal project specific enquiries can be made to: eric.verspoor.ic@uhi.ac.uk

Funding Notes Studentship funded by the European Social Fund and Scottish Funding Council as part of Developing Scotland's Workforce in the Scotland 2014-2020 European Structural and Investment Fund Programme.

Studentship covers fees at Home/EU rate only, plus a stipend at RCUK level, for a total of 42 months (including writing-up).

Funding available for students worldwide, however non UK/EU students will be liable for the difference between home/EU and international fees.

Students must be domiciled in the Highlands and Islands transition region during their course of study to be eligible for funding.

Application Deadline: Deadline for applications for this project is Friday 5th January 2018, 12 midday (UK time).

1st February 2018 start date, earlier start would be preferred.

To apply, follow the link:

— / —

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

---

IowaStateU EvolutionaryBiology

The Ecology and Evolutionary Biology (EEB) graduate program at Iowa State University is recruiting outstanding, motivated graduate students to join a large community of ecology and evolutionary biology researchers https://eeb.iastate.edu/. Research assistantships, teaching assistantships, and a variety of fellowship opportunities are open to students. The application deadline for Fall 2018 admission is 15 December 2017.

Research of the EEB faculty spans diverse topics across population genetics, evolutionary ecology, behavior, macroevolution, and systematics with particular strength in using molecular and computational approaches to solve evolutionary questions. Admission through the EEB program provides opportunities for new graduate students to develop multidisciplinary projects by drawing from the expertise of faculty across 10 participating departments with diverse ecology and evolutionary biology interests. Potential students are encouraged to explore the research underway at ISU through the EEB program and contact individual faculty mentors about opportunities in their group (see partial list below):

Dean Adams: Evolutionary theory, macroevolution of vertebrate morphological diversity, morphometrics, biostatistics. http://www.public.iastate.edu/ ˜ dcadams/ Anne Bronikowski: Evolutionary ecology of life histories in reptiles through the study of comparative physiology, demography, and genetics. http://www.eeob.iastate.edu/people/anne-bronikowski Tracy Heath: Statistical phylogenetics - development, implementation, and application of Bayesian methods for inferring phylogenetic trees and macroevolutionary dynamics. http://phyloworks.org/ Matthew Hufford: Evolution and adaptation of maize during initial domestication and subsequent global spread via comparative and population genomic analysis. http://www.public.iastate.edu/ ˜ mhufford/HuffordLab/home.html Fredric Janzen: Ecology and evolution of diverse sex-determining mechanisms, life histories, and population structures in reptiles in light of rapid environmental change. http://www.public.iastate.edu/ ˜ fjanzen John Nason: Coevolutionary dynamics, species specificity, and reproductive isolating mechanisms in fig-pollinator-parasite interactions. http://www.eeob.iastate.edu/faculty/nason/ Kevin J. Roe: Conservation genetics/genomics and phylogenetic of freshwater organisms. https://www.nrem.iastate.edu/people/kevin-roe Haldre Rogers: Plant-animal interactions for terrestrial communities with a focus on seed dispersal, food webs, extinctions, novel ecosystems, evolutionary ecology, invasive species, tropical ecology, and conservation.https://www.eeob.iastate.edu/people/haldre-rogers Jeanne Serb: Evolutionary origin of eyes in molluscs through the study of protein function, comparative genomics, and phylogeny. https://www.eeob.iastate.edu/people/jeanne-serb Nicole Valenzuela: Ecological/Evolutionary/Functional/Conservation genomics of sex determination, sex chromosomes, and genome organization in turtles through comparative transcriptomics/epigenomics/molecular-cytogenetics/phylogenomics. http://www.public.iastate.edu/ ˜ nvalenzu/ Brian Wilsey: Studies biodiversity loss, restoration ecology, and ecosystem processes in grassland ecosystems. http://www.eeob.iastate.edu/faculty/wilsey/ Environment: EEB is an interdepartmental program of 50 faculty embedded in a highly integrative and collaborative campus (https://eeb.iastate.edu/dir/faculty/). Iowa State University is located in Ames, Iowa, a community of nearly 60,000, recently ranked as one of the most livable small cities in the nation. The university enrolls more than 30,000 students and is committed to achieving inclusive excellence through a diverse workforce. Iowa State University values diversity and is an AA/EEO employer with an ADVANCE program

Questions: Please contact the EEB Director (serb@iastate.edu) or any of the faculty in the EEB program with questions about research. For questions about admission, please contact Ms. Lynette Edsall (camelot@iastate.edu)

’X

Jeanne M. Serb, PhD

Associate Professor

Director, Ecology and Evolutionary Biology (EEB) Graduate Program

— / —

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

---

LouisianaStateU FungalMammalCoevolution

Graduate opportunity in fungal / mammal co-evolution

Jake Esselstyn (http://www.museum.lsu.edu/esselstyn/) and Vinson Doyle (http://www.lsu.edu/agriculture/plant/about/faculty-staff/doyle.php) at Louisiana State University are seeking a graduate student to investigate patterns and processes of co-evolution between mammalian hosts and their associated lung fungi. We encourage prospective candidates with interests in fungal or mammal systematics, co-evolution, emerging infectious diseases, and molecular phylogenetics to contact us.

The successful applicant would be enrolled in the Department of Biological Sciences (http://www.lsu.edu/science/biosci/), with likely office space in the Museum of Natural Science (http://www.lsu.edu/mns/). LSU is home to a large, interactive community of evolutionary biologists and is an excellent destination for graduate studies in these fields.

Please contact us for further details: Jake Esselstyn: esselstyn@lsu.edu Vinson Doyle: vdoyle@agcenter.lsu.edu

– Jake Esselstyn Museum of Natural Science Louisiana State University 119 Foster Hall Baton Rouge, LA 70803

phone: (225) 578-3083 fax: (225) 578-3075 http://www.museum.lsu.edu/esselstyn Want to support mammal research at LSU? Donate to the Alfred L Gardner and Mark S Hafner Mammalogy Fund at: https://securelb.imodules.com/s/1585/17/interior.aspx?sid=1585&gid=1&pgid=2214&cid=3784 Jacob A Esselstyn <esselstyn@lsu.edu>

Maryland BatConservationGenomics

Applications are invited for a M.S. or Ph.D. student assistantship at the Appalachian Laboratory (AL < http://www.umces.edu/al >) of the University of Maryland Center for Environmental Science (UMCES < http://www.umces.edu/ >). We seek a highly motivated student to join our research into the migration patterns and population dynamics of migratory bat species experiencing mortality at wind-energy facilities in North America. The position is based at the AL in Frostburg, Maryland, working with Drs. Paul Gugger < http://www.umces.edu/paul-gugger > (population genomics), David Nelson < https://www.umces.edu/david-nelson > (stable isotope ecology), and Ed Gates < http://www.umces.edu/j-edward-gates > (bat biology). There will also be opportunities for interaction with collaborators at Ohio State University. A M.S. student would matriculate through the Biology Department < https://www.frostburg.edu/dept/biol/ > at Frostburg State University. A Ph.D. student would matriculate through the MEES < http://www.mees.umd.edu/ > program.

For more information, please contact Paul Gugger (pgugger@umces.edu). To apply, please email a single PDF containing a statement of interest, CV (including GPA and GRE scores), and contact information for three references to pgugger@umces.edu. Applications will be accepted through December 1, 2017 until the position is filled. The position is available to start in the fall semester of 2018. Outstanding Ph.D. applicants are encouraged to apply for an UMCES Presidential Fellowship (https://www.umces.edu/fellowship-opportunities), which provides up to three years of stipend, health benefits, and tuition remission.

UMCES is an AA/EOE. Individuals with disabilities, veterans, women and minorities are encouraged to apply.

"pgugger@umces.edu" <pgugger@umces.edu>

Maryland EcologicalEvolutionaryGenomics

The Gugger Lab < http://research.al.umces.edu/pgugger > at the University of Maryland Center for Environmental Science (UMCES < https://www.umces.edu/ >) Appalachian Laboratory < http://www.umces.edu/al > is seeking a motivated Ph.D. or M.S. student to develop a thesis project on ecological, evolutionary, or conservation genomics of trees. The lab uses next-generation sequencing approaches to understand how populations of long-lived trees respond evolutionarily to environmental change, the molecular basis of local adaptation, the factors influencing population genetic variation, the role of hybridization in adaptation, and implications for conservation under global change.

The ideal applicant will have prior research experience in population genetics or plant ecology/evolution, molecular laboratory skills, strong quantitative skills, and interest in learning basic bioinformatics.

The graduate student will matriculate through the MEES < http://mees.umd.edu/ > program and will reside in scenic Frostburg (western MD) for the duration of the degree. Three years of support are available through research assistantships, with additional support possible through teaching assistantships and fellowships < https://www.umces.edu/fellowship-opportunities >. Preferred starting date would be no later than Fall 2018.

To apply, please email Paul Gugger (pgugger@umces.edu) a single PDF containing (1) a statement of interest, (2) a CV, and (3) contact information for three references by December 1, 2017. Please indicate "Genomics graduate position" in your subject line.

UMCES is an AA/EOE. Individuals with disabilities, veterans, women and minorities are encouraged to apply.

"pgugger@umces.edu" <pgugger@umces.edu>

MaxPlanck Jena Germany AncientPathogenPhylodynamics

The Transmission, Infection, Diversification & Evolution Group (TIDE) led by Denise Kühnert is offering one PhD and one Postdoctoral position to begin on 01.06.2018.

The project:

Epidemic dynamics of ancient disease outbreaks

Many of the major human infectious diseases likely arose after the origins of agriculture. Much of what we know about ancient disease outbreaks in the past has been written down by chroniclers who were present during the time and have often suffered from the disease themselves. There are concerns that these writings may be exaggerated, incomplete or inconsistent. Thanks to the recent advances in ancient genome recovery, we are now in the position to shed light on the dynamics of past disease epidemics by deciphering the 'footprint' that past disease outbreaks left on the pathogens' genomes. Understanding the origins and demographic dynamics of ancient pathogens may facilitate a broader understanding of disease emergence.

Your tasks:

- Phylogenetic analysis of ancient pathogen genomes in close collaboration with the Department of Archaeogenetics (DAG), led by Professor Dr. Johannes Krause. - Revision and adaptation of methods used for estimation of divergence times and evolutionary substitution rates of ancient pathogens. - Bayesian (if suitable) phylodynamic analysis of ancient disease outbreaks, based on whole genome sequences from the DAG. Development of statistical tools for inference of epidemiological parameters from ancient disease outbreaks.

Your qualifications:

- PhD position: o Master or equivalent in a quantitative discipline such as Computational Biology, Mathematics, Statistics, Computer Science, Physics.

- Postdoc position: o Have or are about to obtain a PhD degree in a quantitative discipline such as Computational Biology, Mathematics, Statistics, Computer Science, Physics. o Experience analyzing genomic data employing phylogenetic methods o Strong research record

- Both: o Strong interest in infectious disease dynamics o Experience in programming o Proficient English skills

The overarching goal of the Max Planck Institute for the Science of Human History is to explore the history of humans using state-of-the-art analytical methods. Scientists from different disciplines, such as genetics, linguistics, archaeology, anthropology and history are working together to answer fundamental questions about the biological and cultural evolution of man from the paleolithic until today, and they jointly develop innovative methods, in particular in the areas of genome sequencing, language documentation, bioinformatics and phylogeography.

We offer an interesting and responsible job in a competitive, dynamic and stimulating international research environment. The PhD position is for 3 years and paid with 50% of E13 TVöD under a Max Planck PhD contract.

The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. The Max Planck Society seeks to increase the number of women in areas where they are underrepresented and therefore explicitly encourages women to apply.

Your application: Please submit your application to kuehnert@shh.mpg.de. Candidates are requested to submit the application in English as a single pdf file including a Cover letter (explaining research experience and reason for interest in this project), curriculum vitae, a list of publications, copies of certificates, and names and contact information (email and phone) for up to three referees. Informal enquiries are welcome.

Information regarding the Max Planck Institute for the Science of Human History can be found at www.shh.mpg.de . Denise Kühnert <denise.kuehnert@gmail.com>

MaxPlanck Jena Germany AncientPathogens

The Transmission, Infection, Diversification & Evolution Group (TIDE) led by Denise Kühnert is offering one PhD and one Postdoctoral position to begin on 01.06.2018.

The project:

Epidemic dynamics of ancient disease outbreaks

Many of the major human infectious diseases likely arose after the origins of agriculture. Much of what we know about ancient disease outbreaks in the past has been written down by chroniclers who were present during the time and have often suffered from the disease themselves. There are concerns that these writings may be exaggerated, incomplete or inconsistent. Thanks to the recent advances in ancient genome recovery, we are now in the position to shed light on the dynamics of past disease epidemics by deciphering the 'footprint' that past disease outbreaks left on the pathogens' genomes. Understanding the origins and demographic dynamics of ancient pathogens may facilitate a broader understanding of disease emergence.

Your tasks:

- Phylogenetic analysis of ancient pathogen genomes in close collaboration with the Department of Archaeogenetics (DAG), led by Professor Dr. Johannes Krause. - Revision and adaptation of methods used for estimation of divergence times and evolutionary substitution rates of ancient pathogens. - Bayesian (if suitable) phylodynamic analysis of ancient disease outbreaks, based on whole genome sequences from the DAG. Development of statistical tools for inference of epidemiological parameters from ancient disease outbreaks.

Your qualifications:

- PhD position: o Master or equivalent in a quantitative discipline such as Computational Biology, Mathematics, Statistics, Computer Science, Physics.

- Postdoc position: o Have or are about to obtain a PhD degree in a quantitative discipline such as Computational Biology, Mathematics, Statistics, Computer Science, Physics. o Experience analyzing genomic data employing phylogenetic methods o Strong research record

- Both: o Strong interest in infectious disease dynamics o Experience in programming o Proficient English skills

The overarching goal of the Max Planck Institute for the Science of Human History is to explore the history of humans using state-of-the-art analytical methods. Scientists from different disciplines, such as genetics, linguistics, archaeology, anthropology and history are working together to answer fundamental questions about the biological and cultural evolution of man from the paleolithic until today, and they jointly develop innovative methods, in particular in the areas of genome sequencing, language documentation, bioinformatics and phylogeography.

We offer an interesting and responsible job in a competitive, dynamic and stimulating international research environment. The Postdoc position is for 2 years with the possibility of extension. Remuneration will follow the public service pay scale (TVöD), according to qualification and experience. In addition, social benefits are paid according to the regulations of the Civil Service. The PhD position is for 3 years and paid with 50% of E13 TVöD under a Max Planck PhD contract.

The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. The Max Planck Society seeks to increase the number of women in areas where they are underrepresented and therefore explicitly encourages women to apply.

Your application: Please submit your application to kuehnert@shh.mpg.de. Candidates are requested to submit the application in English as a single pdf file including a Cover letter (explaining research experience and reason for interest in this project), curriculum vitae, a list of publications, copies of certificates, and names and contact information (email and phone) for up to three referees. Informal enquiries are welcome.

Information regarding the Max Planck Institute for the Science of Human History can be found at www.shh.mpg.de . Denise Kühnert <denise.kuehnert@gmail.com>

MaxPlanck Jena Germany LanguageEvolution

The Transmission, Infection, Diversification & Evolution Group (TIDE) led by Denise Kühnert is offering one PhD and one Postdoctoral position to begin on 01.06.2018.

The project:

The "phylodynamics" of language evolution

There is evidence of infectious diseases having had major effects on the course of history, mostly by directly diminishing population sizes or by causing people to flee from disease. For example, the expansion of Austronesian languages into Remote Oceania has been theorized to have been pushed by one of the plasmodia causing malaria infection. Testing such theories requires both, an understanding of the past pathogen dynamics and the cultural and linguistic evolution. The field of phylolinguistics has so far mainly been using methods that were developed for viruses or other pathogens.

The initial aim of this project is to develop, test and employ mathematical concepts to describe the tree-generating processes appropriate for language evolution. They will be based on birth-death processes, which are suitable to model language evolution as they can incorporate periods of constant growth or decline, stagnation, but also bursts and extinction events.

This project will be performed in close collaboration with the Department of Linguistic and Cultural Evolution, led by Professor Dr. Russell Gray.

Your tasks:

- Development of birth-death process based methods for the reconstruction of language phylogenies in a Bayesian framework. - Analysis of language families, such as the Austronesian and Austroasiatic language families, to test hypotheses about their origins and historic development. - Test dependence of language diversification on demographic dynamics and potential links to ancient infectious disease outbreaks.

Your qualifications:

- PhD position: o Master or equivalent in a quantitative discipline such as Computational Biology, Mathematics, Statistics, Computer Science, Physics.

- Postdoc position: o Have or are about to obtain a PhD degree in a quantitative discipline such as Computational Biology, Mathematics, Statistics, Computer Science, Physics. o Experience with phylogenetic methods o Strong research record

- Both: o Strong interest in language evolution o Experience in programming o Proficient English skills

The overarching goal of the Max Planck Institute for the Science of Human History is to explore the history of humans using state-of-the-art analytical methods. Scientists from different disciplines, such as genetics, linguistics, archaeology, anthropology and history are working together to answer fundamental questions about the biological and cultural evolution of man from the paleolithic until today, and they jointly develop innovative methods, in particular in the areas of genome sequencing, language documentation, bioinformatics and phylogeography.

We offer an interesting and responsible job in a competitive, dynamic and stimulating international research environment. The Postdoc position is for 2 years with the possibility of extension. Remuneration will follow the public service pay scale (TVöD), according to qualification and experience. In addition, social benefits are paid according to the regulations of the Civil Service. The PhD position is for 3 years and paid with 50% of E13 TVöD under a Max Planck PhD contract.

The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. The Max Planck Society seeks to increase the number of women in areas where they are underrepresented and therefore explicitly encourages women to apply.

Your application: Please submit your application to kuehnert@shh.mpg.de. Candidates are requested to submit the application in English as a single pdf file including a Cover letter (explaining research experience and reason for interest in this project), curriculum vitae, a list of publications, copies of certificates, and names and contact information (email and phone) for up to three referees. Informal enquiries are welcome.

Information regarding the Max Planck Institute for the Science of Human History can be found at www.shh.mpg.de . Denise Kühnert <denise.kuehnert@gmail.com>

MaxPlanck Leipzig HumanOrigins

Ph.D. Student Positions in Human Origins

We invite applications for the Leipzig School of Human Origins (www.leipzig-school.eva.mpg.de), an international Ph.D. program of the Max Planck Institute for Evolutionary Anthropology and the University of Leipzig.

This program provides interdisciplinary training and research opportunities for university graduates who wish to work towards a Ph.D. in anthropology, biology, biochemistry, bioinformatics, evolutionary genetics, human behavioral ecology, psychology, and related fields. Candidates may apply with selected research groups from the following three disciplines:

1) Comparative and Molecular Primatology 2) Functional Genomics and Paleogenomics 3) Human Behavioral Ecology and Developmental Psychology

Graduate students will be accepted to only one of these areas but will have the opportunity to take part in courses and seminars in all of them. Our Ph.D. program is open for international students and is designed as a 3-year-program.

We invite applications from all countries. Applicants hold a Masterâ euro s degree, a Diploma or equivalent in one of the above, or related, fields. It is not necessary to hold the degree at the point of application. However, you must have been awarded your degree prior to the start of the program in September 2018.

Candidates have to be fluent in written and spoken English. German is not required but international students will be offered opportunities to take German language courses.

Ph.D. students are supported by Max Planck support contracts (50 percent of Pay Group 13 of the Collective Wage Agreement for the Civil Service, TVoD) which are provided by the Max Planck Institute for Evolutionary Anthropology, by Ph.D. contracts provided by the University of Leipzig; or by third-party funding.

Term of Appointment: September 2018 Application Deadline: 01 December 2017

For more information on the application process, please check out: www.leipzig-school.eva.mpg.de/application/-application.html and hand in your online application at: http://www.eva.mpg.de/positions-available/leipzig-school-of-human-origins.html Visit www.leipzig.de for information on living in Leipzig, Germany, in the center of Europe.

Contact: Sandra Jacob, Program Coordinator Deutscher Platz 6, Leipzig, 04103, Germany Phone: ++493413550122, Email: leipzig-school@eva.mpg.de Web: www.leipzig-school.eva.mpg.de Sandra Jacob Max Planck Institute for Evolutionary Anthropology / The Leipzig School of Human Origins (Ph.D. Programme) Deutscher Platz 6, 04103 Leipzig, GERMANY phone: ++49 (0) 341 3550-122; fax: ++49 (0) 341 3550-119 http://www.eva.mpg.de/ http://www.leipzig-school.eva.mpg.de/

Sandra Jacob <jacob@eva.mpg.de>

McGillU Biodiversity

The NSERC-CREATE on Biodiversity, Ecosystem Services and Sustainability is recruiting PhD and MSc students interested in, but not restricted to, biodiversity, ecology, evolution, conservation, environmental management, and human-environment interactions. The BESS Program provides a multidisciplinary and immersive training experience to help prepare the next generation of environmental scientists to work with industry, environmental consulting firms, governments, NGOs, and universities. BESS training provides students with skills in environmental monitoring, biodiversity surveying, ecological impact assessment, mitigation strategies, the design of restoration projects, statistical analysis, adaptive forest and agricultural management, and mathematical modeling for predictive and prescriptive planning.

The Program has a strong multidisciplinary component and a diverse group of researchers and collaborators Quebec universities, Canadian companies working in Panama, and several Panamanian institutions, particularly the Smithsonian Tropical Research Institute who administer and supervise complementary courses, an internship rotation, and thesis research. BESS also provides students with an immersive experience through courses and internships in Panama, and elsewhere in the Neotropics.

BESS provides funding to students in the form of stipends and travel allowances. There are no citizenship restrictions. Stipends are given on an individual basis and depending on budget availability, but will not surpass $14,000 CAD per year. Students who are holders of a major fellowship (NSERC, NSF, Fullbright, etc.) will receive a $5000 CAD per year top-up. In addition, all students are eligible for up to $1500 CAD per year to travel to internships, conferences, courses and/or fieldwork.

Applicants must first contact a potential supervisor in one of the three partnering universities (McGill, Laval and UQAM). Students must then apply to the supervisor's department. All students must meet the admission criteria of Graduate and Postdoctoral Studies at the university and the entrance requirements of the specific department.

Candidates applying to BESS will be considered by the Program Delivery Committee, who will consider the following criteria:

Academic background Relevance and viability of proposed research Benefits and fit to the Program Proficiency in French, Spanish, or Portuguese is highly desirable

*All applicants are invited to apply but priority will be given to projects related to the core disciplines of BESS: Biology, Natural Resource Sciences, Geography, Environment.

DEADLINE: JANUARY 15TH, 2018. FOR INFORMATION ON HOW TO APPLY VISIT: https://-www.mcgill.ca/bess/apply Felipe

Felipe Pérez-Jvostov CREATE and CICADA Postdoctoral Fellow on Biodiversity, Ecosystem Services and Sustainability, and Program Coordinator http:/-/www.mcgill.ca/bess/bess Stewart Biology Building N3/11A 1205 Avenue du Docteur-Penfield, Montréal, QC.

BESS- NSERC CREATE <bess.redpath@mcgill.ca>

MichiganStateU EvoDevoGeno

PhD Positions in Evolutionary Developmental Genomics at Michigan State University

The Fish Evo Devo Geno Lab (PI Ingo Braasch) at Michigan State University is recruiting highly motivated PhD students interested in working on the genomic basis of vertebrate evolution and development to start in Fall 2018.

The Braasch Lab focuses on genomic and developmental changes that contribute to major transitions during the course of vertebrate evolution and studies evolutionary novelties at the levels of genome structure, gene family evolution, and gene regulation. We combine comparative genomics with analyses of molecular evolution and functional genetic and developmental approaches using a variety of fishes as our model systems (spotted gar, zebrafish, medaka and others).

Possible projects fall within the following broader research areas of the group:

1. Genomic and morphological evolution of fishes: How do changes in gene regulation contribute to evolutionary novelties and key innovations? How do morphological differences among fish lineages arise from diversification of gene repertoires? What is the role of gen(om)e duplications and gene losses in generating phenotypic diversity?

2. Conquest of land and 'fish-out-of-water': We are studying genomic changes and their functional consequences leading to the evolution of tetrapods from fishes and other 'fish-out-of-water' scenarios, including the evolutionary loss of genes at the water-to-land transition and the gene regulatory basis of hatching.

3. Evolutionary analyses of biomedical fish genomes: Combining genomic sequence comparisons, gene expression analyses and epigenomic profiling, we aim to improve connectivity of teleost biomedical fish models such as zebrafish and medaka to human biology and disease. This work is support by the NIH (http://bit.ly/2o8R8c1). For additional information on our research, see also Braasch et al. 2016, Nature Genetics (doi:10.1038/ng.3526) and Braasch et al. 2015, JEZB (doi:10.1002/jez.b.22589).

Our group is part of the Department of Integrative Biology (IBIO; https://integrativebiology.natsci.msu.edu/), the Ecology, Evolutionary, and Behavior Program (EEBB; https://eebb.natsci.msu.edu/), and the Genetics Graduate Program (https://genetics.natsci.msu.edu/) at Michigan State.

MSU IBIO has a strong research commitment to vertebrate biology with a highly collaborative community of groups working on fish evolution, genomics, development, population genetics, neuroscience, behavior, ecology, and conservation, allowing for vibrant exchange among fields, methods and model systems.

Qualifications: Applicants should hold a bachelor's degree in biology, genetics, molecular biology, bioinformatics, zoology or related fields. Suitable candidates should be enthusiastic about fish biology and excited about working in an interdisciplinary manner. Previous research experience in a relevant area is desired.

Admission: Students will be admitted through the MSU IBIO Graduate Program (https://integrativebiology.natsci.msu.edu/graduate-program/) and the MSU Ecology, Evolutionary Biology, and Behavior Group (https://eebb.natsci.msu.edu/). Another possible route of admission is through the MSU Genetics Graduate Program within the MSU BioMolecular Science Gateway (https://biomolecular.natsci.msu.edu/applicants/how-to-apply/).

Application deadlines for both the MSU IBIO and Genetics Graduate Programs are December 1, 2017.

Funding: Financial support is provided through research and teaching assistantships and the PI's external funding. Competitive applicants will be eligible for university fellowships and supported in applying for graduate fellowships from NSF, NIH, and other agencies.

Interested candidates should email Ingo Braasch (braasch@msu.edu) in advance of the application deadlines on December 1.

Please include the following in your email:

1. Description of your research interests and how they align with pursuing a PhD in vertebrate Evo-Devo and genomics

2. Curriculum Vitae

3. Names and email contacts of three references

We are looking forward to your application!

Dr. Ingo Braasch

Assistant Professor Department of Integrative Biology College of Natural Science Michigan State University braasch@msu.edu; phone: +1 (517) 432-3484 https://www.researchgate.net/profile/Ingo_Braasch braasch@msu.edu

MonashU EvolutionaryEcology

Two fully-funded PhD position are available to work in the Hall group (see mattdhall.com) on themes broadly related to evolutionary ecology, health, and fitness. Using species of Daphnia and their associated pathogens as a powerful experimental model, the successful candidates will work closely with Matt and his collaborators to develop projects that explore any one of the following eco-evolutionary processes.

1) Sexual antagonism and the evolution of health and fitness. Exploring how conflict between the sexes arise and influence different aspects of an organism's health. Can blend together both theory and empirical approaches to exploring genetic architecture as interests dictate (together with Tim Connallon at Monash, http://timconnallon.com/).

2) Energy flux and the spread of disease. The rate at which organisms use, transform, and expend energy defines not only an organism's "pace of life", but also how readily that can be exploited by a pathogen. Advances in high-throughput metabolic assays offer opportunities to incorporate energy flux into studies of host-pathogen coevolution (together with Dustin Marshall and the Centre for Geometric Biology at Monash, https://cgb.org.au/).

3) Demography and host-pathogen interactions. Populations are rarely stable and different densities or growth trajectories can feed back into the spread of disease within and between patches. Experimental mesocosms offer opportunities to explore infectious disease in light of different demographic dynamics (Together with Ben Phillips at the University of Melbourne, https://blphillipsresearch.wordpress.com/).

A stipend (living-allowance) scholarship of ~$26,288 per annum is provided tax free (the equivalent of approx. $33,000 before tax) with no teaching requirements for 3.5 years (the length of a PhD in Australia). We also offer travel and establishment allowances to help in your move and our tuition scholarships cover the cost of tuition fees (normally $38,900 per year). Guaranteed funding of project costs and research support, including the costs of attending at least one conference per year, is included.

Project start dates can be any time in first half of 2018 onwards.

To be eligible, applicants must have completed a 4 year degree with a research component or have post-graduate research experience in ecology, genetics, behaviour, or evolution (or will do so by the end of the year). Preference will be given to those with strong quantitative skills and publications in international journals. Interested students should send a CV and a brief statement of interests to Matt via matthew.hall@monash.edu.

Regards,

Matt

– Dr. Matthew D. Hall School of Biological Sciences, G30D, 18 Innovation Walk Monash University, Clayton Campus, Victoria, 3800, Australia

www.mattdhall.com Email: matthew.hall@monash.edu Phone: +61 3 9905 5793 Mobile: +61 478 399 592 twitter: @mattd_hall

"matthew.hall@monash.edu"
<matthew.hall@monash.edu>

NewcastleU PlantEvolution

A competitive PhD studentship is available in evolutionary plant genetics at Newcastle University (UK) consistently rated as one of the top 200 universities in the world. This 4-year fellowships provides a full tuition fee waiver, a competitive living stipend, and a considerable research allowance.

This PhD studentship is a part of IAPETUS which is the North East of England's and Scotland's multidisciplinary Doctoral Training Partnership (DTP) for the environmental sciences funded and accredited by NERC http://www.iapetus.ac.uk/ Project description

Title. Flower power: decoding genetics of flowering for conservation of the South African biodiversity hotspot

Supervisory Team Dr Maxim V. Kapralov, Newcastle University http://www.ncl.ac.uk/nes/staff/profile/maximkapralov.html Dr Adrian C. Brennan, Durham University https://www.dur.ac.uk/biosciences/about/schoolstaff/profile/?id=11637 Prof Andrew J. Young, Liverpool John Moores University https://www.ljmu.ac.uk/about-us/staff-profiles/faculty-of-science/natural-sciences-and-psychology/andrew-young Key Words 1. Conservation of Adaptive Potential and Functional Diversity 2. Genetics of Rapid Evolution and Speciation 3. Succulent Karoo / Cape Floristic Kingdom / South Africa

Overview

Lying within south-western corner of Africa, the Succulent Karoo biome is recognised as one of the World's most important regions of plant diversity [1]. Here members of the plant family Aizoaceae are especially well adapted to the arid desert environment. This is most evident in the speciose genus Conophytum, a Succulent Karoo specialist consisting of dwarf succulent plants that show a remarkable degree of range-restricted endemism [2]. The Succulent Karoo has been identified as being at high risk from the effects of climate change, with preliminary data suggesting that dwarf succulents may be especially vulnerable [3]. However, we still don't know the underlying mechanisms that influence the distribution and associated speciation of these species.

The aim of this project is to better understand the key drivers of the remarkable radiation within Conophytum. Early molecular phylogenetic analyses of the Aizoaceae family suggested that it represents one of the fastest and largest radiation of any plant group [4]. Within the diverse tribe Ruschieae (71 genera) the Conophytum-clade consists of ten closely-related genera. Intriguingly, floral traits in the genus Conophytum are unusually diverse with variations in flower coloration [5], phenology (seasonality of flowering), and in anthesis (timing of flowering). No other member of Aizoaceae displays such diversity. Presence of nocturnal flowers extremely rare within Aizoaceae but account for the quarter of Conophytum taxa and preliminary work showed that this complex trait evolved multiple times [6].

Conophytum is also characterized by having the vast majority of species flower in the austral autumn, in contrast to when majority of plants flower (the austral winter and spring) within the winter-rainfall region of southwestern Africa. Seasonal shifts in flowering is rare within Conophytum. However, recently the existence of several pairs of morphologically similar species that display differences in phenology has been reported [7], with each species within a pair having a highly restricted distribution (point-endemics). This diversity of flowering time found within a group of closely related species gives us a unique opportunity to elucidate genetic controls in charge of activation of flowering within non-model organisms.

Flowering time is an important trait in plants that affects both their life cycles as well as those of pollinator species. Apart from fundamental interest in how this trait evolved, better understanding of it is crucial for both increasing the global crop yield as well as for mitigating the effects of climate change. Despite the important role of flowering time, its underlying pathways are understudied.

The PhD candidate will test if shifts in both the seasonality and timing of flowering have been among the major drivers in the ecologically important and highly successful radiation of the genus Conophytum resulting in rapid speciation of 150+ taxa and permitting range expansion. S(he) will decode structure and evolution of transcriptional regulatory network which regulates flowering time in Conophytum using a tool-box of modern genetics. In doing so we will be better equipped for the development of conservation measures that reduce the extinction risk of these vulnerable taxa and preserve their adaptive potential and functional diversity.

— / —

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

---

NHM Denmark PaleogenomicsCinchona

NaturalHistoryMuseumDenmark.PlantID.PaleogenomicsCinchona.

PhD position in Paleogenomic annotation of historical Cinchona bark samples across time and space.

The Natural History Museum of Denmark, Faculty of Science, University of Copenhagen is offering a fully funded PhD fellowship under the Plant.ID Horizon2020 European Training Network, starting April 2018 or as soon as possible thereafter. http://jobportal.ku.dk/phd/?show=146108 Plant.ID is recruiting 15 PhD fellows The EU H2020-ITN-ETN project Plant.ID that is based around the molecular identification of plants is a European training network aimed at providing 15 PhD fellows across nine European host institutions with excellent training through a network of leading academic experts, museums, governmental and industry partners in the field, using an intensive program with network-wide training events, intra-network supervision and secondments. Read more about the 15 individual PhD projects on www.plantid.uio.no PhD fellowship 8 (PlantID-PHD8) will be based in the Rønsted group at the EvoGenomics section at the Natural History Museum of Denmark. The museum is situated in the Botanical Garden of the University of Copenhagen, and houses Herbarium C with more than 2.9 million specimens, as well as state-of-the-art genomic laboratories, high-throughput sequencing facilities and computational resources. Furthermore, the section offers a highly international and social environment.

Project With the emergence of ancient DNA techniques combined with high-throughput sequencing (paleogenomics), new opportunities for exploring and using natural history collections have emerged. Cinchona bark, the source of quinine for treatment of malaria, is an outstanding time referenced model system. We will use both modern samples across their geographical range, as well as unrivalled historical collections of about 1000 specimens documenting 150 years of collecting and breeding experiments including samples from forests that no longer exist as well as the chemically annotated collections of Howard and Sons. However, botanical and geographical origin of the historical samples was poorly recorded preventing us from utilizing these extensive collections until now. This project will generate paleogenomic data from historic Cinchona bark samples, use high-throughput sequencing to resolve the current phylogeny of the tribe Cinchoneae based on in-house modern geographically annotated samples to produce a framework allowing placing of the historical samples to species and geographical area, providing critical links for determining changes in the distribution of Cinchona forest over 200 years, including hundreds of chemically annotated historical samples of Howards & Sons in environmental correlation analysis, and determine the proportion of adulterated specimens in the historic collections.

Principal supervisor: Nina Rønsted, Natural History Museum of Denmark, University of Copenhagen, nronsted@snm.ku.dk, Mobile: Www.snm.ku.dk/plant_evolutionary_interactions. Co-supervision Alexandre Antonelli (University of Gothenburg, Sweden), Mark Nesbitt (Royal Botanic Gardens, Kew). Collaboration with Carla Maldonado (National Herbarium of Bolivia) and Tinde van Andel (Naturalis). Planned secondments to University of Gothenburg and Royal Botanic Gardens, Kew.

Who are we looking for? Marie Curie Training Networks offer a unique opportunity to get cutting-edge training in a multidisciplinary environment with a focus on academic and personal development of the PhD fellows. The supervisors in the PlantID network each provide specific competences and as part of the network you develop your skills and carry out research both independently and as part of a network of 15 PhD fellows. The consortium ensures cross-pollination and exchange of ideas through network-wide training events, summer schools and intersectoral secondments. As a PhD fellow in the Plant.ID network, you need to have good social skills and be willing to conduct the planned secondments and importantly be innovative and goal-oriented.

Qualifications

* MSc in Biology, with a strong background in systematic botany. * Experience with phylogenetic inference, DNA sequencing, barcoding, and/or preferably high-through-put sequencing and bioinformatics pipelines is prioritized. * Interest in working in a museum environment and with collections is emphasized. * Good communication skills and interest in science communication and popular engagement is emphasized. * Excellent English speaking, reading, and writing skills are required.

Job conditions The PhD student will be appointed under a 3-year employment contract with a competitive salary (minimum DKK 312.879 including annual supplement (+ pension up to DKK 43.219)) and mobility allowance at the host

— / —

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

---

NHM Denmark SpeciesDelimitation

NaturalHistoryMuseumDenmark.PlantID.EuphrasiaSpeciesDelimitatio

Marie Curie PhD position in species delimitation of mega-diverse Euphrasia hemi-parasitic plants

The Natural History Museum of Denmark, Faculty of Science, University of Copenhagen is offering a fully funded PhD fellowship under the Plant.ID Horizon2020 European Training Network, starting April 2018 or as soon as possible thereafter. http://jobportal.ku.dk/phd/?show=146107 Plant.ID is recruiting 15 PhD fellows The EU H2020-ITN-ETN project Plant.ID that is based around the molecular identification of plants is a European training network aimed at providing 15 PhD fellows across nine European host institutions with excellent training through a network of leading academic experts, museums, governmental and industry partners in the field, using an intensive program with network-wide training events, intra-network supervision and secondments. Read more about the 15 individual PhD projects on www.plantid.uio.no PhD fellowship 3 (PlantID-PHD3) will be based in the Rønsted group at the EvoGenomics section at the Natural History Museum of Denmark. The museum is situated in the

Botanical Garden of the University of Copenhagen, and houses Herbarium C with more than 2.9 million specimens, as well as state-of-the-art genomic laboratories, high-throughput sequencing facilities and computational resources. Furthermore, the section offers a highly international and social environment.

Project Euphrasia is a genus of about 350 taxonomic species of hemi-parasitic plants mostly from colder climates and with many red-listed species, but difficult taxonomy partly due to extensive hybridization. Target capture of many unlinked genes from a unique sample set of more than 1000 collections from Atlas Flora Danica of about 9 Danish taxa will be used to untangle patterns of hybridization from incomplete lineage sorting. Morphological traits enabling recognition of genetically supported clusters (potential species) will be identified using morphometry. A time series will be produced of selected red-listed Danish species from historical collections to monitor changes in occurrence data over the past 100 years. Finally the target capture protocol will be used based on historical herbarium collections to build a genus level reference database and phylogenetic hypothesis of all 350 currently recognised species.

Principal supervisor: Nina Rønsted, Natural History Museum of Denmark, University of Copenhagen, nronsted@snm.ku.dk, Www.snm.ku.dk/plant_evolutionary_interactions. Co-supervision: Henrik Ãrenlund Pedersen, Select Nature, Denmark, and Bengt Oxelman, University of Gothenburg, Sweden.

Who are we looking for? Marie Curie Training Networks offer a unique opportunity to get cutting-edge training in a multidisciplinary environment with a focus on academic and personal development of the PhD fellows. The supervisors in the PlantID network each provide specific competences and as part of the network you develop your skills and carry out research both independently and as part of a network of 15 PhD fellows. The consortium ensures cross-pollination and exchange of ideas through network-wide training events, summer schools and intersectoral secondments. As a PhD fellow in the Plant.ID network, you need to have good social skills and be willing to conduct the planned secondments and importantly be innovative and goal-oriented.

Qualifications

* MSc in Biology with a strong background in systematic botany. * Experience with population biology and/or species delimitation is preferred. * Good understanding of and interest in phylogenetic inference and bioinformatics, barcoding and/or high-trough-put sequencing techniques is an advantage but not a requirement. * Interest in working in a museum environment and with herbarium collections is emphasized. * Good communication skills and interest in science communication and popular engagement is emphasized. * Excellent English speaking, reading, and writing skills are required.

Job conditions The PhD student will be appointed under a 3-year employment contract with a competitive salary (minimum DKK 312.879 including annual supplement (+ pension up to DKK 43.219)) and mobility allowance at the host institution. The fellow is expected to start in April 2018. Additional funding for research and participation in courses, workshops, conferences, etc. is ensured. The PhD student will be enrolled in the PhD program of the Faculty of Science, University of Copenhagen, with the specific intent that it results in a PhD degree and scientific publications.

EU eligibility criteria for candidates The applicant may be of any nationality but in order to be eligible for the positions the following criteria applies to all applicants: 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

---

NIOO Wageningen UGroningen EvolutionSeasonalTiming

PhD position on "Evolutionary responses in seasonal timing to a warming world" at the Netherlands Institute of Ecology (NIOO-KNAW) and GELIFES at Univeristy of Groningen

Project information Seasonal timing of reproduction and growth has major fitness consequences. Due to climate change, species are advancing their timing but species within a food chain do not advance at the same rate. This may lead to directional selection on seasonal timing. A better understanding of the genetic variation and selection pressures underlying seasonal timing is essential for predicting the rate at which species adapt to their warming world. The research will be carried out on great tits, part of the well studied food chain of oak, winter moth and great tit.

This PhD project will have three main aspects: (1) measuring selection on seasonal timing during breeding time,

(2) measuring selective pressures during the pre-breeding period, and (3) exploring the effect of dispersal on local evolutionary change. Studying selection during breeding time (1) will make use of already existing selection lines for early and late reproduction in great tits. Offspring of these lines will be introduced in the wild to obtain unbiased fitness measurements of early and late reproducing birds. Selection pressures during the pre-laying period (2) will be studied by quantifying the phenology of food availability during egg laying directly and using satellite data to extrapolate the current data set on this food availability to a longer set of years. Whether individuals dispersing into the study area affect genetic variation and adaptation because they were differently selected than the local birds (3) will be studied by analysing using our long-term data base (1955-present). Combined with other research questions that will be developed by the PhD student, this project should give better insight in the rate and ability at which species can adapt to a warming world.

The Netherlands Institute of Ecology (NIOO-KNAW) has an excellent track record on evolutionary ecology, with ample experience with working with birds in the wild, under controlled conditions and with their genomes. The Chronobiology unit of GELIFES (University of Groningen) has an excellent track record on chronobiology, including seasonal timing. The position is supervised by Prof Dr Marcel E. Visser at the Netherlands Institute of Ecology (NIOO-KNAW) in Wageningen (m.visser@nioo.knaw.nl or +31 317473439) and by Prof Dr Roelof A. Hut (r.a.hut@rug.nl) of the Chronobiology unit of the Groningen Institute for Evolutionary Life Sciences (GELIFES), University of Groningen.

Qualifications - you should have an MSc or equivalent in Biology or a related discipline, preferably with a strong background in Evolutionary Ecology, Ecological Genetics or Evolutionary Physiology - you are expected to have an excellent academic record (list of examination marks from your university study) and be curious, creative and ambitious - you should be able to write scientific articles and reports (to be proven by your graduation thesis or another comparable report) and be fluent in English both in writing and speech.

Conditions of employment The University of Groningen offers an appointment for a period of four years, which should be concluded during this period with a PhD examination. The University of Groningen offers a salary of Â 2,222 gross per month in the first year up to a maximum of Â 2,840 gross per month in the fourth and final year, based on a full-time position (1.0 FTE), excluding a 8% holiday allowance and a 8.3% end-of-the-year bonus. The first year constitutes a probationary period, with an evaluation of the candidate's performance after 9 months. The objective of this evaluation is to establish whether the candidate will be able to finish a PhD thesis in the remaining three years. If the performance evaluation is positive, the candidate's contract will be extended by another 3 years, for a total of 4 years.

The PhD student will be appointed at the University of Groningen but the research will be carried out at the Animal Ecology Department of the Netherlands Institute of Ecology (NIOO-KNAW) in Wageningen (see www.nioo.knaw.nl) in close collaboration with the Chronobiology unit at the University of Groningen.

A training programme within the Graduate School of Science and Engineering at the University of Groningen is part of the agreement. You and your supervisors will make up a plan for the additional education and supervising that you specifically need. This plan also defines your teaching activities.

How to apply: You may apply for this position until 10 December 23:59 h / before 11 December 2017 Dutch local time by means of the application form (click on "Apply" below on the advertisement on the University of Groningen vacancy 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

---

NordU FishEvolutionaryEcol

Dear colleagues,

A (three/four year) PhD fellowship on the evolutionary ecology of fishes is available at the Faculty of Biosciences and Aquaculture, Nord University (Bodø, Norway).

The aim of the PhD project is to investigate the role of ecology, life history and genomic properties in population divergence and species coexistence. The project will use two stickleback fishes, the three-spined and the nine-spined stickleback, as a model system. The research involves a combination of field studies, functional traits analysis, genomics, and experiments to compare the strength of population-level associations between adaptation, adaptive potential and ecological success across species.

The candidate should have an MSc degree (or equivalent) in biology, (aquatic) ecology, environmental sciences or equivalent fields. Profound knowledge and hands-on experience in evolutionary ecology, population genetics and statistical analyses is required. Interest and prior experience with field work, experimental work, and biological trait analyses would be an asset, as would be eagerness to learn bioinformatics.

The Faculty of Biosciences and Aquaculture (FBA) is one of five faculties at Nord University, and is responsible for research and education within animal sciences, aquaculture, ecology, genomics and natural resource management. The successful candidate will join the PhD programme in Aquatic Biosciences. For more information, visit the Faculty's website: www.nord.no/en/fba The PhD project is supervised by Dr. Joost Raeymaekers (www.nord.no/no/Sok/_layouts/15/UiN.Internet/-UserProfilePage.aspx?pid=NORD%5C06023338), and will be carried out in collaboration with Dr. Filip Volckaert (KU Leuven, Belgium) and Dr. Blake Matthews (Eawag, Switzerland).

For further information, instructions to apply and to submit your application, please follow this link:

https://www.jobbnorge.no/en/available-jobs/job/-143984/phd-fellowship-in-the-evolutionary-ecology-of-fishes Please submit your application by Thursday, 30 November 2017. For further information about the position contact Joost Raeymaekers (joost.raeymaekers@nord.no). Questions related to the application process should be addressed to Office manager Irene Stork (e-mail: irene.stork@nord.no)

References

Raeymaekers JAM, Chaturvedi A, Hablützel PI, Verdonck I, Hellemans B, Maes GE, De Meester L & Volckaert FAM (2017). Adaptive and non-adaptive divergence in a common landscape. Nature Communications 8, 267.

Joost Raeymaekers Faculty of Biosciences and Aquaculture Nord University N-8049 Bodø Norway joost.raeymaekers@nord.no

Joost Raeymaekers <joost.raeymaekers@bio.kuleuven.be>

NorthWesternU PlantBiologyConservation

PLANT BIOLOGY AND CONSERVATION 'Vnow accepting applications

The Graduate Program in Plant Biology and Conservation is a partnership between Northwestern University (NU) and the Chicago Botanic Garden (CBG). PhD, MS thesis-based, and MS internship-based degrees are offered. All degree programs offer a unique opportunity to study ecology, evolution, and environmental issues at the interface of basic and applied plant science. Students apply to the program through Northwestern University and take their courses at both NU and CBG with faculty from both institutions. The Plant Conservation and Science Center at CBG is a valuable resource for students, and the Chicago region provides a vibrant community at the forefront of research in conservation and sustainability.

To learn more, contact program director, Nyree Zerega (nzerega@chicagobotanic.org) or visit our website: http://www.plantbiology.northwestern.edu/ Application deadlines: PhD: December 1, 2017 MS (thesis-based): February 15, 2018 MS (internship-based): Applications will be reviewed beginning February 15 and review will continue through April 30, 2018. Admissions are on a rolling basis.

Nyree Zerega <nzerega@chicagobotanic.org>

NTNU Taiwan AposematicInsects

The Systematics & Evolutionary Biology Lab in the National Taiwan Normal University (NTNU) is recruiting a self-motivated and enthusiastic PhD student to study aposematism in insects begin in the Summer of 2018.

Pachyrhynchus weevils are a group of brilliant, metallic-coloured weevils distributed in the Old World tropics. Recent studies showed that the conspicuous colouration of these weevils function as effective warning signals to prevent predacious pursuit by lizards. We are interested in studying the spatio-temporal dynamics of interactions between vertebrate predators and aposematic prey. The PhD student will be encouraged to, but not limited to, evaluate the speciation mechanisms of *Pachyrhynchus*'s aposematism. The students will be expected to develop their own research dissertation projects within the scope of these research projects.

Related articles:

- Tseng, H-Y., W-S. Huang, M-L. Jeng, R.J.T. Villanueva, O.M. Nuñeza and C-P. Lin (2017) Complex inter-island colonization and peripatric founder speciation promote diversification of flightless

Pachyrhynchus weevils in the Taiwan-Luzon volcanic belt.

Journal of Biogeography (early view) (DOI: 10.1111/jbi.13110)

- Chen, Y-T., H-Y. Tseng, M-L. Jeng, Y-C. Su, W-S. Huang* and C-P. Lin (2017) Integrated species delimitation and conservation implications of an endangered weevil *Pachyrhynchus sonani* (Coleoptera: Curculionidae) in Green and Orchid Islands of Taiwan. *Systematic Entomology* 42: 796-813 (DOI: 10.1111/syen.12242)

- Tseng, H-Y., C-P. Lin, J-Y Hsu, D.A. Pike and W-S. Huang (2014) The functional significance of aposematic signals: geographic variation in the responses of widespread lizard predators to colourful invertebrate prey. *PLoS ONE* 9(3):e91777

Funding - The PhD fellowship includes a competitive monthly stipend of NT$34,000 (˜1,133 USD) for up to 3 years through the TIGP (Taiwan International Graduate Program - Biodiversity), a jointed graduate program between NTNU and Academia Sinica. Students are also eligible for on-campus housing during the years of their studies.

Eligibility - The position is open to all applicants that meet TIGP admission criteria, but preference will be given to students with a master degree or prior experiences in animal behaviour, population genetics, and insect ecology and evolution. Criteria/material used to evaluate the applicant's qualifications for the admission: (http://biodiv.sinica.edu.tw/TIGP-BP/index.php?page=admission)

How to apply - perspective students should prepare (1) a CV, (2) a list of prior experience, (3) three references (contact info & emails), (4) a one-page statement of research interests, and (5) a two-page research proposal based on damselfly speciation or weevil's aposematism in one PDF file, and email the file to Chung-Ping Lin (treehopper@ntnu.edu.tw) with the subject line "TIGP application".

Additionally, perspective students should submit a formal online application for admission in TIGP Biodiversity (http://db1x.sinica.edu.tw/tigp/index.php). Deadline for applications through the online portal is March 31st.

The Systematics & Evolutionary Biology Lab

(http://web.ntnu.edu.tw/˜treehopper/index.php?page=home&lang=en)

The Department of Life Sciences

(http://www.biol.ntnu.edu.tw)

National Taiwan Normal University

(http://en.ntnu.edu.tw)

TIGP Biodiversity Program Website

(http://biodiv.sinica.edu.tw/TIGP-BP/)

Biodiversity Research Center, Academia Sinica

(http://biodiv.sinica.edu.tw/en/)

Fusan Botanical Garden

(http://fushan.tfri.gov.tw/en/index.php)

–

Dr Yu-Hsun Hsu (Post-doc research fellow) Department of Life Science National Taiwan Normal University, Taiwan Website: https://sites.google.com/site/yuhsunhsu/ yuhsunhsu@gmail.com

---

NTNU Taiwan DamselflySpeciation

The Systematics & Evolutionary Biology Lab in the National Taiwan Normal University (NTNU) is recruiting a self-motivated and enthusiastic PhD student to study the speciation in damselflies begin in the Summer of 2018.

We focus on a damselfly species, *Psolodesmus mandarinus*, with two subspecies differ in their distribution and wing pigmentations in Taiwan main island, providing a great opportunity to evaluate the relative importance of natural and sexual selection in damselfly divergence. We incorporate a wide range of techniques, including a whole-island field survey, behavioural observation, morphological manipulation experiments, population genetics and genomic analysis to investigate the divergence in damselflies. A description of research projects:

https://sites.google.com/site/yuhsunhsu/research?pli=1 The PhD student will be encouraged to, but not limited to, evaluate the speciation mechanisms between the two subspecies of *Psolodesmus* damselflies. The students will be expected to develop their own research dissertation projects within the scope of these research projects.

Funding - The PhD fellowship includes a competitive monthly stipend of NT$34,000 (˜1,133 USD) for up to 3 years through the TIGP (Taiwan International Graduate Program - Biodiversity), a jointed graduate program between NTNU and Academia Sinica. Students are also eligible for on-campus housing during the years of their studies.

Eligibility - The position is open to all applicants that meet TIGP admission criteria, but preference will be given to students with a master degree or prior experiences in animal behaviour, population genetics, and insect ecology and evolution. Criteria/material used to evaluate the applicant's qualifications for the admission: (http://biodiv.sinica.edu.tw/TIGP-BP/-index.php?page=admission)

How to apply - perspective students should prepare (1) a CV, (2) a list of prior experience, (3) three references (contact info & emails), (4) a one-page statement of research interests, and (5) a two-page research proposal based on damselfly speciation or weevil's aposematism in one PDF file, and email the file to Chung-Ping Lin (treehopper@ntnu.edu.tw) with the subject line "TIGP application".

Additionally, perspective students should submit a formal online application for admission in TIGP Biodiversity (http://db1x.sinica.edu.tw/tigp/index.php). Deadline for applications through the online portal is March 31st.

The Systematics & Evolutionary Biology Lab

(http://web.ntnu.edu.tw/~treehopper/index.php?page=home&lang=en)

The Department of Life Sciences

(http://www.biol.ntnu.edu.tw)

National Taiwan Normal University

(http://en.ntnu.edu.tw)

TIGP Biodiversity Program Website

(http://biodiv.sinica.edu.tw/TIGP-BP/)

Biodiversity Research Center, Academia Sinica

(http://biodiv.sinica.edu.tw/en/)

Fusan Botanical Garden

(http://fushan.tfri.gov.tw/en/index.php)

–

Dr Yu-Hsun Hsu (Post-doc research fellow) Department of Life Science National Taiwan Normal University, Taiwan Website: https://sites.google.com/site/-yuhsunhsu/ yuhsunhsu@gmail.com

---

OhioStateU MultiSpeciesInteractions

Are you (or do you know) a student interested multispecies interactions and/or evolutionary ecology? Dr. Alison Bennett in the Department of Evolution, Ecology, and Organismal Biology (EEOB) at the Ohio State University is looking for one or two PhD students to start in September 2018 with interests in (but not limited to): fungi, plants, insects, evolutionary ecology, mutualistic networks, above-belowground interactions, and molecular ecology. Applications are due Dec 1 (see https:/-/eeob.osu.edu/grad/program-admissions). Please send an email if interested to bennett.1242@osu.edu Bennett lab webpage is still being set-up, so get in touch with any questions.

"Bennett, Alison" <bennett.1242@osu.edu>

OhioStateU PlantGenomicEvolution

The Translational Plant Sciences Graduate Program at OSU Now Accepting Applications

The Translational Plant Sciences Graduate Program (TPSGP) at The Ohio State University is accepting applications for the 2017-2018 academic year. This five-year Ph.D. program offers full remission of tuition and fees, as well as a competitive stipend and support for research expenses. TPSGP leverages the strengths of a powerful, interdisciplinary group of participating faculty to create a dynamic program which prepares students to become the next-generation of leaders in Plant Science. Potential research projects include, but are not limited to, evolution of crop domestication, plant genomic evolution and selection, co-evolution among plants and pests (insects, pathogens, etc.), plant stress adaptation (e.g. climate).

This program is designed for highly motivated students from a variety of undergraduate and masters level programs. The application deadline for domestic students is December 15th, 2017. For additional information, including a list of faculty, please visit our website at https://tpsgp.osu.edu/home . "Michel, Andrew" <michel.70@osu.edu>

OklahomaStateU EvolutionaryBiomechanics

Ph.D. position at Oklahoma State University

I am recruiting a student to pursue a Ph.D. in my lab at Oklahoma State University, starting Fall 2018. This position will be partly supported as a graduate research assistantship (GRA), for which the student will study the evolution of morphology and functional performance in frogs and toads. The GRA involves both laboratory experiments and fieldwork, which will be mostly local but may involve international trips.

Research in the lab addresses macroevolution and evolutionary biomechanics. Most projects involve fieldwork, laboratory experiments, work with museum specimens, and phylogenetic comparative analyses. Please see my lab's website for more information: moenlab.okstate.edu

Students in the lab have the opportunity to work on ongoing projects, develop their own project, or a combination of the two. Some (broad) potential dissertation research topics include: - The mechanics of movement in frogs and the consequences for macroevolutionary patterns of morphological diversity - The effects of modularity and integration on macroevolutionary patterns of diversity in clades - The importance of deep evolutionary history on phenotypic evolution

If interested, please send me an introductory email that includes your research interests (including why you are specifically interested in working on the above topics), research experience, CV, GPA, and GRE scores. Strong candidates will have had at least one substantial independent research experience, such as a summer REU, undergraduate research thesis, or a Master's degree. Ideal candidates will have experience in typical lab projects and methods, including studies of performance and morphology, herpetology, phylogenetic comparative biology, and statistical analyses in R.

Completed applications need to be submitted to OSU by 1 February 2018 to receive full consideration, but if interested you should begin discussing an application with me long before this date.

Daniel Moen Assistant Professor Dept. Integrative Biology, Oklahoma State University email: daniel.moen@okstate.edu ph. 405-744-6815

Daniel Moen <daniel.moen@okstate.edu>

OklahomaStateU PlantBiolEcolEvolution

Multiple opportunities for graduate study in plant ecology and Teaching assistantships are available for study towards an MS in Plant Biology or a PhD in Plant Science. Potential areas of research could include:

- Trade-offs in drought tolerance among tree species at the forest- prairie ecotone - The roles of drought stress, fungal pathogens, and insects in tree mortality - Tree-ring growth response to climate among species at the forest- prairie ecotone - The role of anthropogenic change in shaping plant-pollinator interactions and plant reproductive output - The role of ecological interactions in plant mating system evolution - Comparative plant genomics, evolution, and systematics - Evolution of milkweed-insect interactions - Plant taxonomy and biogeography

Assistantships include tuition waivers and health insurance.

Learn more about the OSU Department of Plant Biology, Ecology, and Evolution at http://plantbio.okstate.edu/. Contact Dr. Henry Adams (henry.adams@okstate.edu, www.henrydadams.com), Dr. Janette Steets (janette.steets@okstate.edu), or Dr. Mark Fishbein (mark.fishbein@okstate.edu) for more information.

In your email, please include brief description of your research interests, experience, and career goals, and attach a CV or resume. Applications are due to the OSU graduate college by 2/28/18, but early application is strongly advised for full consideration and support.

"Fishbein, Mark" <mark.fishbein@okstate.edu>

Paris-Nice EvolutionaryGeneticsOfDevelopment

First call: November 22, 2017

Two PhD positions are available in the context of a research project between the laboratories of Henrique Teotonio (Institut de Biologie, Ecole Nor-male Superieure, Paris; http://www.ibens.ens.fr/-spip.php?rubrique28&lang=en) and Christian Braendle (Institut de Biologie Valrose, Nice; http://-www.braendlelab.net).

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

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

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

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

For relevant background information see: Carvalho et al. 2014. http://doi.org/10.1186/1471-2148-14-117 Poullet— et al. 2016. http://doi.org/-10.1111/evo.13032 Noble et al. 2017. http://-doi.org/10.1534/genetics.117.300406 Teotonio et al. 2017. http://doi.org/10.1534/genetics.115.186288 teotonio@biologie.ens.fr

Prague EvolutionaryBiol

Hello,

Could you please spread in your institutes info on PhD. position in the Institute of Botany, Czech Academy of Science

Natural DNA methylation variation in Fragaria vesca populations along climatological gradient See https://-nioo.knaw.nl/en/rp06-natural-dna-methylation-variation-fragaria-vesca-populations-along-climatological-gradient for details.

Thanks a lot

Zuzana

Zuzana Münzbergová Tel.: +420 221 95 1636 E-mail: zuzmun@natur.cuni.cz orcid.org/0000-0002-4026-6220

Department of Botany; Faculty of Science Charles University Faculty of Science Albertov 6 < https://maps.google.com/?q=Albertov+6&entry=-gmail&source=g >, 128 43 Praha 2 www.natur.cuni.cz

Department of Population Ecology Czech Academy of Science Zamek 1, 252 43 Pruhonice Czech Republic www.ibot.cas.cz Bojana S <bojana.stojanova@gmail.com>

PurdueU ConservationGenetics

The DeWoody lab at Purdue University is actively recruiting new graduate students for admission in the fall of 2018 to work on research near the interface of population genetics, molecular ecology, and conservation biology. Click here < https://web.ics.purdue.edu/-%7Edewoody/DeWoody/wordpress/ > and here < https://web.ics.purdue.edu/%7Edewoody/DeWoody/-wordpress/?page_id=3D33 > for more information about our lab, click here < https://ag.purdue.edu/-fnr/Pages/gradadminguide.aspx > for more info on the admissions process into the Dept. of Forestry & Natural Resources (the academic home of most students in the lab), or here < https://www.bio.purdue.edu/-Academic/graduate/index.html > for admissions into the Dept. of Biological Sciences (which is another possibility). Contact Andrew DeWoody via email (dewoody@purdue.edu) if you would like more information.

"jantonid@purdue.edu" <jantonid@purdue.edu>

QueenMaryU London MicrobeCoevolution

*** PhD position available***

The genomic basis of host-symbiont dependency

*Background *

Organisms across the tree of life form partnerships with microbes for protection, metabolic and nutrition. In some cases, host and symbiont become so tightly associated that dependency evolves and the two organisms integrate both physically and genomically. Dependency on microbes is particularly prevalent among insects and has led them to great success by allowing them to use otherwise unavailable resources and invade inaccessible habitats. Here we explore how dependency on microbes evolves, and how genomes combine to produce the novel functions that have allowed insects to dominate so many habitats.

In this project you will use the symbionts of ants and aphids to rigorously test hypotheses on the evolution of symbiotic dependency. This may include: exploring the early stages of genome integration in hosts that have recently evolved dependency on microbes; reveal how genomes combine to produce novel adaptive functions; and determining how host ecology influences gains and losses of symbionts.

- You will have access to large genetic databases, insect collections, in-house live organisms and cutting-edge research facilitates to fuel your investigation.

- You will gain experience of molecular/experimental biology, comparative/metagenomics, bioinformatics, and statistics (e.g. comparative phylogenetics).

- You will be encouraged to develop your own ideas and hypotheses.

Skills preferred In a multidisciplinary project such as this, candidates are unlikely to have a background in all disciplines involved. The most important qualification is motivation and that the project appeals to you. We can envisage strong candidates coming through various routes including: - evolutionary genomics/bioinformatics - practical molecular biology - evolutionary theory

For informal questions, contact l.henry@qmul.ac.uk

Applications have to be submitted to: https://mysis.qmul.ac.uk/urd/sits.urd/run/-siw_ipp_lgn.login?process=siw_ipp_app&code1=-RFQM-C1ZF-01&code2=0009&code3=GUEST ****Deadline for applications: Nov 27, 2017****

The selected applicant will be expected to start in January 2018

Supervisor Information Dr. Lee Henry Email: l.henry@qmul.ac.uk For more about our lab visit: *http://www.sbcs.qmul.ac.uk/staff/leehenry.html < http://www.sbcs.qmul.ac.uk/staff/leehenry.html >*

Funding Notes

The studentship is fully funded and available to EU, UK and International citizens. It will cover tuition fees as well as provide an annual tax-free maintenance allowance for 3 years at Research Councils UK rates (16,553 in 2017-18).

Applicants must have an excellent academic track record, with a bachelor's degree (1st or high 2.1 UK equivalent) in a relevant degree. An MSc in bioinformatics, evolutionary biology, or ecology is also highly desirable.

References

Henry LM, Maiden MJC, Ferrari J and HCJ Godfray (2015). Insect life history and the evolution of bacterial mutualism. Ecology Letters 18:516-25

Fisher RM, Henry LM, Cornwallis CK, Kiers ET and SA West (2017). The evolution of host-symbiont dependence. Nature Communications vol. 8

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

lee henry <leehenrym@gmail.com>

SGN Frankfurt LichenEvolution

Sehr geehrte Damen und Herren,

gerne möchten wir bei auf Ihrem Jobportal o.g. Ausschreibung veröffentlichen.

Den Ausschreibungstext finden Sie im Folgenden.

Für Rückfragen stehen wir Ihnen gerne zur Verfügung.

Job offer ref. #01-17036

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. SGN conducts natural history research with almost 800 employees and research institutions in six federal states, and is also custodian of the UNESCO World Heritage Site at Messel.

The Senckenberg Research Institute invites applications for a PhD Position in a project funded by the German Science Foundation (DFG).

PhD Position in Molecular Biosystematics (part-time, 65%)

The project "Lecanomics - new ways of species detection and recognition in a ubiquitous group of lichens" aims to connect both ends of the taxonomic work-flow: field exploration and verification of potential new species by genomic methods. Based on reference genomes we want to develop genomic and genetic markers for species identification and delimitation that will be tested on samples from underexplored regions of the world. World-wide sampling and feedback to collectors is organized by a team of, at present, 20 international specialists through a self-developed web-based work-flow management system. The platform also enables participation of amateur (citizen) scientists. Insights from this project are supposed to streamline the taxonomic work-flow for inconspicuous organisms.

The project requires close communication and offers opportunities to cooperate with international team members and amateur scientists. "Lecanomics" is embedded in the DFG priority program "Taxon-Omics" (http://www.taxon-omics.de/projects.html). Lab visits and attendance of workshops held by the 27 currently funded PIs is strongly encouraged. PhD candidates (m/f) also have access to the training program of GRADE, the graduate academy of Goethe-University, Frankfurt.

Specific tasks will include: - generating draft reference genomes and developing novel genetic markers for species delimitation in lichens - using genome-wide datasets to study species delimitation in selected groups of the lichen genus Lecanora - assisting in the administration of our web-based communication and work-flow management system and cooperate with an international team of specialists

Your profile: - a Master's degree or equivalent in a field related to biodiversity research - experience in molecular genetic lab methods (preferably including library preparation and genome reduction techniques) - basic programming skills in and experience with databases (these assets are desirable but not mandatory) - good command of English (oral and written)

Please apply if you like to: - work in the field and in the lab - acquire new skills and methods - develop your own scientific ideas - share and exchange these ideas with scientists and amateurs

Salary and benefits are according to a part-time public service position in Germany (TV-H E 13, 65%). The position is a 3-year fixed-term post, starting April 1st, 2018.

The Senckenberg Gesellschaft für 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 will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

To apply, please e-mail a single PDF file referencing this position (ref. #01-17036) until and including December 14th, 2017.

Please include a cover letter outlining your motivation, a detailed CV, your full transcripts and grades, contact details of two potential references, a summary of your Master/Diploma thesis, and, if available, a list of publications to the address below:

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main E-Mail: recruiting@senckenberg.de, cc to: christian.printzen@senckenberg.de

For scientific enquiries please contact Dr. Christian Printzen, christian.printzen@senckenberg.de.

recruiting <recruiting@senckenberg.de>

StonyBrookU EcolEvolution

GRADUATE OPPORTUNITIES IN ECOLOGY AND EVOLUTIONARY BIOLOGY

The Graduate Program in Ecology and Evolution in the Department of Ecology and Evolution at Stony Brook University is recruiting doctoral and master's level graduate students for Fall 2018. The program trains students in Ecology, Evolution and Biometry. The deadlines for applications are Dec. 1, 2017 for the PhD program and April 15, 2018 for the MA program (see below).

The following faculty are considering graduate students. It is highly recommended that you contact possible advisors before submitting your application.

DEPARTMENTAL FACULTY

Resit Akcakaya - Population and Conservation Ecology http://life.bio.sunysb.edu/ee/akcakayalab/ Stephen B. Baines - Ecosystem Ecology and Biogeochemistry http://life.bio.sunysb.edu/ee/baineslab/ Liliana M. Dávalos - Vertebrate, Phylogenetics, Biogeography and Conservation http://lmdavalos.net/lab/The_Lab.html Jessica Gurevitch - Plant Population and Invasion Ecology http://gurevitchlab.weebly.com/ Brenna Henn - Human Evolutionary Genomics https://ecoevo.stonybrook.edu/hennlab/ Jesse D. Hollister - Plant Evolutionary Genomics and Epigenetics https://genomeevolution.wordpress.com/ Heather Lynch - Quantitative Ecology and Conservation Biology https://lynchlab.com/ Dianna K. Padilla - Invertebrate Aquatic Ecology and Conservation Biology http://life.bio.sunysb.edu/ee/padillalab/ Joshua Rest - Evolutionary Genomics http://life.bio.sunysb.edu/ee/restlab/Home.html Robert Thacker- Systematics, Phylogenetics, and Ecology http://www.stonybrook.edu/commcms/ecoevo/people/faculty_pages/thacker.html John True - Evolutionary Developmental Biology http://life.bio.sunysb.edu/ee/truelab/True_Lab.html Kishna M. Veeramah - Primate Comparative Genomics http://life.bio.sunysb.edu/ee/veeramahlab/ PROGRAM FACULTY IN OTHER DEPARTMENTS

Nolwenn Dheilly - Evolution of Host-Parasite Interactions http://you.stonybrook.edu/dheilly/ Andreas Koenig http://www.stonybrook.edu/commcms/anthropology/faculty/akoenig.html David Matus - Evolution of Cell Invasion http://www.stonybrook.edu/commcms/biochem/research/faculty/matus.html# Janet Nye - Quantitative Fisheries Ecology https://you.stonybrook.edu/jnye/ Alistair Rogers - Plant Physiology and Climate Change www.bnl.gov/TEST Shawn Serbin - Plant Physiology and Remote Sensing www.bnl.gov/TEST Jeroen B. Smaers - Brain Evolution, Phylogenetic Comparative Methodology, Macroevolutionary Morphology https://smaerslab.com/ Leslie Thorne - Ecology and Behavior of Marine Birds and Mammals http://you.stonybrook.edu/thornelab/ Nils Volkenborn - Benthic Ecology and Sediment Biogeochemistry https://you.stonybrook.edu/voll/ Patricia Wright - Tropical Conservation and Primatology http://www.patwrightlab.net/pat-wright.html For more information regarding the Graduate Program in Ecology and Evolution, please see http://www.stonybrook.edu/ecoevo/index.html for general information. For specific information on the PhD and MA programs, please see http://www.stonybrook.edu/commcms/ecoevo/program/index.html and http://www.stonybrook.edu/commcms/ecoevo/program/maprogram.html The deadline for receipt of all application materials for the PhD program is Dec. 1, 2017 although earlier submission is encouraged to ensure full consideration for available fellowships. After that date, applications may be considered on a rolling basis until Jan. 15th, with consideration for

— / —

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

---

TelAvivU EvolutionaryBiology

PhD position in Evolutionary Biology: "The Evolution of Virulence under Conditions of Frequent Multiple Infections"

The position is available from February 1, 2018.

Project Description Interactions between multiple parasite species (infecting the same host) can affect the evolutionary trajectory of virulence, with important ecological and epidemiological consequences. The goal of the proposed work is to elucidate implications of multiple infections on the evolution of (parasite) virulence. The successful candidate will use a combination of experimental evolution and field approaches to generate new and refined predictions regarding the virulence of parasites that spread into new habitats, where they encounter co-infecting parasites. He/she will use a model system consisting of the crustacean Daphnia and their microparasites. The proposed research is a collaboration between Israeli and German scientific teams: Dr. Frida Ben-Ami from Tel Aviv University (http://fridaslab.weebly.com/) and Prof. Justyna Wolinska from IGB and Freie Universität Berlin (http://www.igb-berlin.de/en/profile/justyna-wolinska), financed by the German Science Foundation (DFG). The position is mainly based in Tel Aviv; however, a two-month research stay at the IGB in Berlin is planned. Funding for attending national/international conferences is available.

Duties and responsibilities - laboratory experiments - field work (investigating geographical patterns of co-infections) - statistical analyses of experimental (life history and genomic) and field (environmental and genetic) data

Requirements - MSc degree in biology - creative thinking - strong background in evolutionary biology, population genetics or ecology - hands-on experience with experimental work - experience in molecular or genomic research would be an advantage - excellent analytical skills and very good knowledge in statistics - excellent communication and writing skills in English - good work ethic

Enquiries or questions should be directed to Dr. Frida Ben-Ami (frida@post.tau.ac.il).

Please send your application by email (all material in one PDF please) to Frida Ben-Ami. Applications should include a CV, a list of publications and a statement about research interests (motivation letter). Please give names and email addresses of two persons who are willing to write a letter of recommendation. Application deadline is December 31, 2017.

Dr. Frida Ben-Ami, Department of Zoology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv 69978, Israel http://www.ben-ami.com Frida Ben-Ami <frida@post.tau.ac.il>

TexasAMU EcologyEvolution

The Ecology and Evolutionary Biology Doctoral Program at Texas A&M is currently recruiting PhD students for the Fall 2018 start date.

Why should you consider obtaining a PhD at Texas A&M University? The Ecology and Evolutionary Biology (EEB) Program at Texas A&M is a relatively new doctoral program at one of the largest and best-funded universities in the United States. It has a strong mixture of nationally and internationally recognized junior and senior faculty working across the globe on a diverse range of basic and applied research, spanning physiological, population, community, ecosystem and landscape ecology, genetics, genomics, behavior, and systematics. To learn about our faculty visit: http://eeb.tamu.edu/people/faculty/).

Support for graduate study is available through multiple sources, including teaching assistantships, research fellowships, and internal merit and diversity and other fellowships. Texas A&M University is positioned at the interface of the Neotropics and Nearctic, in Blackland Prairie and Post Oak Savannah habitat, which supports great species diversity and a wealth of research opportunities with great climate during the academic year. Its location also provides a good base for access to a broad range of habitats and research sites. Additionally, its proximity to Austin, Dallas, Houston and San Antonio offers easy air travel and a cultural component to a whole graduate experience.

How to apply? Visit eeb.tamu.edu/graduate-program/prospective-students/ For consideration for internal fellowships, your application needs to be received by December 15, 2017. Prospective students are strongly encouraged to contact potential faculty sponsors among the EEB core faculty eeb.tamu.edu/people/faculty/

Travel grants are available for prospective students to visit our program February 11-13, 2018. For more information, contact Jason Martina, the EEB Program Coordinator (email: jpmartina@tamu.edu ; phone: 979 845-2114)

Sincerely, – Mariana Mateos, Ph.D. Associate Professor Department of Wildlife and Fisheries Sciences (wfsc.tamu.edu) Ecology and Evolutionary Biology PhD. Program (eeb.tamu.edu) Faculty of Genetics (genetics.tamu.edu) Texas A&M University Wildlife, Fisheries and Ecological Sciences Bldg. < http://aggiemap.tamu.edu/?bldg=1537 >(WFES Rm. 270) 534 John Kimbrough Blvd 2258 TAMUS College Station, TX 77843-2258 Fax 979-845-4096 Email: mmateos@tamu.edu http://people.tamu.edu/ ˜ mmateos My ResearcherID: http://www.researcherid.com/rid/B-5235-2008 mmateos@tamu.edu

---

TexasAMU EvolutionaryGenomics

The Blackmon lab at Texas A&M University is recruiting PhD graduate students interested in evolutionary genomics and genetics. My lab studies a variety of questions including genome structure, sex chromosomes, and trait evolution. We use both theoretical and empirical approaches. In our empirical work, we often focus on beetles and other invertebrates.

While the Blackmon lab is in the Department of Biology, graduate students can earn a PhD in Genetics, Ecology and Evolutionary Biology, or Biology through the lab's participation in two interdepartmental programs at Texas A&M. These programs allow students to take courses and interact with faculty from over 19 other departments that share interests in Genetics and EEB.

With approximately 60,000 students Texas A&M is one of the largest universities in the country. It is located in Bryan/College Station which has a population of about 250k. It is within easy reach of Houston and Austin. This part of Southeast Texas is situated close to many distinct biomes and provides excellent opportunities for fieldwork and outdoor recreation. Support for graduate students is provided for five years by a combination of teaching and research assistantships.

Please contact Heath Blackmon directly at coleoguy@gmail.com for more information regarding opportunities and application information. Additional information about the Blackmon lab can be found at http://coleoguy.github.io/ Heath Blackmon <coleoguy@gmail.com>

TrentU Canada BlackBearGenomics

PhD Opportunity in Black Bear Ecology and Genomics ?C Trent University/Ministry of Natural Resources and Forestry

Description Graduate assistantship focused on the ecology and evolution of black bears - we are seeking a highly motivated person to pursue a PhD degree in the Environmental and Life Sciences Program at Trent University in Peterborough, Ontario, Canada. The graduate project will combine ecological and genomic datasets to address basic and applied research questions broadly focused on the distribution, abundance and evolutionary history of black bears in Ontario. The successful applicant will be expected to become familiar with and apply state-of-the-art statistical and genomic approaches and will have considerable responsibility and freedom to formulate and address basic and applied research questions grounded in ecological and evolutionary theory. The successful applicant will be expected to assist in fieldwork to collect samples. Further, this project will have a major lab component that will be directed by the student, under supervision. The research is expected to have direct applied relevance to management of black bears within the province of Ontario. The student will be co-advised by Dr. Christopher Kyle of Trent University and Dr. Joe Northrup, Research Scientist with the Ontario Ministry of Natural Resources and Forestry within the shared Natural Resources DNA Profiling and Forensic Centre (www.nrdpfc.ca) facilities at Trent University.

Requirements M.Sc. degree in ecology, wildlife, biology or related field is required but exceptional past experience may be considered in place of a M.Sc. degree. Applicants must meet the minimum entrance requirements for the Environmental & Life Sciences graduate program. Desired qualifications include a GPA >3.5 (4.0 scale). A strong background in ecology and/or evolutionary biology, demonstrated analytical capabilities, and passion for wildlife research are required. Strong quantitative, writing, and oral communication skills are also required. The strongest applicants will have demonstrated experience with programming languages commonly used for statistical and scientific applications (e.g., R and Python), and familiarity with geospatial software (e.g., ArcMap, QGIS).

Application instructions Initially, all applications are to be sent as follows. Please email a cover letter describing how you meet the above qualifications, current CV, unofficial transcripts, scientific writing sample and contact info for ’Ã3 references as a single attachment to Joe Northrup at joseph.northrup@ontario.ca. The successful applicant is expected to begin in fall, 2018. Application deadline is January 15, 2018 but review of applications will begin immediately and continue until a suitable candidate is found. Once a successful applicant has been determined a formal application to the University is required.

Canadian candidates will be given preference, but qualified international students who are eligible for international funding opportunities should apply. There are also a limited number of international tuition fee waivers available on a competitive basis.

Additional Information: The Natural Resources DNA Profiling and Forensic Centre (NRDPFC) is located within the Trent University’Âs DNA Building (Peterborough, Ontario, Canada). We have separate genomic DNA and DNA cloning laboratories for molecular work and also an automation laboratory for high throughput sample preparation. Our facility also includes access to a bio-containment Level II lab for processing potentially infectious tissues and an Indigenous Pathogen Containment Level III (IPCL 3) laboratory located in the DNA building that is certified for several indigenous pathogens. Peterborough is a vibrant community a 1.5 hour drive from Toronto and the Pearson International Airport (http://www.peterborough.ca/Living.htm).

Christopher Kyle <christopherkyle@trentu.ca>

TuftsU AdaptationSpeciation

The Dopman lab at Tufts University is seeking to recruit Ph.D. students interested in evolutionary genetics. The long-range goal of our work is to understand the evolution of reproductive isolation and ecological adaptation. Projects on reproductive isolation are using hybridizing populations of moths to understand the genetic basis of behavioral and allochronic isolation, and the role of pleiotropy and chromosomal rearrangements for speciation. Current work on adaptation focuses on seasonal rhythms in moths and butterflies, and is addressing the genetic repeatability of phenology, its influence on fitness and population persistence, and connecting phenology change with spatiotemporal gradients in climate.

Students must have the ability to work with others and a sense of humor, both of which are needed to make science fun and worthwhile. An undergraduate background in molecular genetics, genomics, evolution, or ecology is preferred, as is prior research experience. Highly relevant experience includes application of molecular genetic techniques or computational analysis of genome data.

The Dopman Lab is in the Department of Biology (http://ase.tufts.edu/biology/) and is a member of Tufts' Collaborative Cluster in Genome Structure and Developmental Patterning. The Cluster focuses on genome to organism research and is located on the main campus in Medford, MA. With two additional Tufts campuses (Boston and Grafton), other research universities (Harvard, MIT, BU), and the vibrant city of Boston all within reach, Medford and Tufts are ideal places to live and work.

Interested individuals should email Erik Dopman (erik.dopman@tufts.edu) and provide a CV and brief statement of research interests, relevant educational background, and prior research experience. Applications to the graduate program are due on 15 December, with departmental review occurring shortly thereafter. For more information on the graduate program, see http://ase.tufts.edu/biology/graduate/ . Erik Dopman, PhD Associate Professor, Department of Biology Tufts University 200 Boston Avenue, Suite 4700 Medford, MA 02155 t (617) 627-4890 f (617) 627-3805 e erik.dopman@tufts.edu w http://ase.tufts.edu/biology/labs/dopman/ Erik.Dopman@tufts.edu

---

TulaneU EvolutionaryBiology

'Plus One' MS opportunities in Ecology and Evolutionary Biology at Tulane University.

The Department of Ecology and Evolutionary Biology in the School of Science and Engineering at Tulane University encourages applications to our 'Plus One' MS program, a one-year, non-thesis MS program.

The Plus One degree program is designed for students who are interested in seeking employment with environmental agencies of federal, state, and municipal government; non-governmental organizations; and in private industry, including environmental consulting firms. The program also will be useful for students planning to enter more advanced professional degree programs (e.g., law, public health, medicine, veterinary medicine, natural resources management) and for students intent on pursuing additional academic training (e.g., Ph.D. degree programs). Finally, the program is useful for students seeking to strengthen teaching skills and pedagogy for a future career in education.

Students elect to pursue one of three tracks in the program:

(1) Research, in which students work closely with a tenured or tenure-track faculty mentor, with the goal of strengthening research capacity and potentially producing a peer-reviewed publication; these students typically use this track as a stepping stone to a Ph.D. program in Ecology and Evolutionary Biology or a related field.

(2) Pedagogy, in which students work closely with one or more teaching faculty mentors, with the goal of strengthening teaching experience and skills, including the option to serve as an Teaching Fellow in EBIO 1010, Diversity of Life; these students typically go on to teach at the high school or elementary school level or otherwise engage in educational activities.

(3) Knowledge base, in which students work with the Graduate Studies coordinator or other faculty member to identify courses required to bolster transcripts and knowledge base; these students typically go on to apply to professional degree programs such as law, medical, or veterinary schools or join the workforce.

We have established a strong track record of assisting Plus One students to meet their professional and educational goals. Recent graduates from the program are currently in highly regarded PhD programs, law schools, medical schools and vet schools; teaching in high schools; and working in industry and governmental and non-governmental agencies.

Our department houses a strong team of outstanding researchers and educators, with established strengths in coastal and tropical systems. We are committed to promoting diversity in STEM, and particularly welcome applications from members of groups that are traditionally under-represented in the field of Ecology & Evolutionary Biology.

Visit our departmental webpage at: http://www2.tulane.edu/sse/eebio/ To view specific faculty and research interests, see: http://www2.tulane.edu/sse/eebio/faculty-and-staff/faculty/ To find out more about the Plus One program, see: http://www2.tulane.edu/sse/eebio/academics/graduate/plus-one-ms.cfm For any inquiries or more information, please contact Graduate Studies Coordinator Dr. Jordan Karubian at jk@tulane.edu

"Duncan, Charles-Ryan D" <cduncan8@tulane.edu>

TulaneU EvolutionaryEcol

PhD opportunities - behavioral ecology and tropical biology

Ph.D. opportunities in the Karubian Lab

The Karubian Lab (http://karubian.tulane.edu) is seeking applications to begin Ph.D. studies in Fall 2018.

The Karubian lab is based at the Department of Ecology and Evolutionary Biology at Tulane University, in New Orleans LA. We have an accomplished group of students, and take pride in the supportive and diverse environment our lab and department provide. Students receive TA-ships that cover stipend and tuition costs during their time at Tulane, and several students have received competitive National Science Foundation Graduate Research Fellowships and other sources of external support.

The Karubian lab has a strong commitment to linking research to real world conservation outcomes via meaningful engagement with local communities in the areas where we work. Both these projects have important links to contemporary social issues, and incoming students are encouraged to participate in and contribute to these efforts. Please see http://karubian.tulane.edu/engagement/overview/ for more information.

The Karubian lab is committed to increasing diversity in STEM. Students from Latin America and other groups that are traditionally under-represented in ecology and evolution are particularly encouraged to apply.

Prospective applicants should contact Dr. Jordan Karubian (jk@tulane.edu) with a statement of interest and CV.

We are currently recruiting two students, one for each of following projects:

(1) Evolutionary ecology and conservation of South American palms.

The over-arching goal of this project is to better understand the forces that regulate distributions and diversity of palms. This student will develop independent research that combines fieldwork on ecological processes in tropical rainforest (e.g., dispersal, competition, survival) with laboratory-based genetic approaches (e.g., population genetics / genomics, transcriptomics). Students will build upon previous and ongoing NSF-funded work that links behavior of dispersal agents to seed and pollen movement; characterizes ecological and genetic drivers of non-random seedling survival; and documents how naturally occurring environmental variation interacts with human activities to shape patterns of diversity. Please see http://karubian.tulane.edu/research/plant-animal-interactions/ for more information.

(2) Behavioral ecology and effects of lead exposure on Mockingbirds

This student will develop independent research in New Orleans to investigate how exposure to lead, a common contaminant in urban environments, impacts health and behavior of the northern mockingbird Mimus polyglottos. Our pilot work suggests that lead levels in mockingbird adults may be associated with increases in aggressive behavior. The student working on this project will characterize pathways of lead uptake; relate exposure to physiological condition, cognition, aggressive behavior and reproductive success; and explore the mechanistic (genomic and endocrine) underpinnings of these effects. Please see http://karubian.tulane.edu/research/gulf-coast-ecology/ for more information.

Ryan Duncan, MBA, MAR Program Coordinator

Dept. of Ecology and Evolutionary Biology

Tulane University

434 Lindy Boggs Center

New Orleans, LA 70118

Phone (504) 862-8298

FAX (504) 862-8706

Email cduncan8@tulane.edu

http://tulane.edu/sse/eebio Facebook_SMALL twitter-icon SMALL

Please consider our environment before printing this email.

"Duncan, Charles-Ryan D" <cduncan8@tulane.edu>

UAberdeen MicrobialEcologyEvolution

UAberdeen/JHI(UK).MicrobialEcologyEvolution

Impact of N-Fertilizer Sources on Ammonia Oxidizer Niche Differentiation, Evolution and N2O Production

The University of Aberdeen (UK) / James Hutton Institute (Aberdeen) Supervisors: Cecile Gubry-Rangin, School of Biological Sciences, University of Aberdeen Thomas Freitag, James Hutton Institute Leighton Pritchard, James Hutton Institute Application deadline: 5th January 2018

Project Description: Majority of terrestrial N2O emissions contributing to global warming are produced by microbial nitrifiers (ammonia oxidising archaea (AOA) and bacteria (AOB)). Molecular techniques enable study of the diversity and activity of AOA and AOB and have identified characteristics important in determining their ecology and evolution. Given first evidence of differential selection of AOA and AOB depending on the sources of applied fertiliser N, more knowledge are required regarding the evolutionary and ecological ammonia-based niche differentiation in AOA and AOB.

This PhD studentship aims to determine these evolutionary and ecological mechanisms resulting in ammonia-based niche differentiation in AOA and AOB. Soil microcosm experiments will be complemented by amplicon-genome and whole-genome sequencings. Through phylogenetic ancestral reconstructions and comparative genomics approaches, these data will be used to understand niche differentiation and evolution between and within AOA and AOB.

Student training: The University of Aberdeen Nitrification Group, headed by Prof. James Prosser (https://www.abdn.ac.uk/ibes/people/profiles/j.prosser) and Dr C?cile Gubry-Rangin (https://www.abdn.ac.uk/ibes/people/profiles/c.rangin), is a well-established group with world-wide recognised reputation in microbial ecology and evolution and a high-impact track record.

The PhD student will join a dynamic team of researchers within the School of Biological Sciences (http://www.abdn.ac.uk/sbs/). The University of Aberdeen (UoA) was ranked 1st in the UK by the ?Agriculture, Veterinary and Food Science? REF2014 exercise and provides an excellent scientific environment. In addition, the University of Aberdeen provides state-of-the-art technological support facilities with a unique single-cell genomics platform, highly-specialised cytometry and genomic platforms, an exclusive thaumarchaeotal culture collection, molecular and environmental facilities and a High Performance Computing system. The University of Aberdeen also provides diverse training opportunities for all aspects of research and for transferable academic and generic skills.

Funding Notes: The studentship is funded under the James Hutton Institute/University Joint PhD programme, in this case with the University of Aberdeen and is based in Aberdeen. Applicants should have a first-class honours degree in a relevant subject or a 2.1 honours degree plus Masters (or equivalent).Shortlisted candidates will be interviewed in Jan/Feb 2018. A more detailed plan of the studentship is available to candidates upon application. Funding is available for European applications, but worldwide applicants who possess suitable self-funding are also invited to apply.

Formal application should be made as described on: https://www.findaphd.com/search/ProjectDetails.aspx?PJID=91592 Informal enquiries can be directed to c.rangin@abdn.ac.uk.

Dr Cecile Gubry-Rangin, URF Institute of Biological & Environmental Sciences Cruickshank Building, Room 1.13 University of Aberdeen St Machar Drive Aberdeen AB24 3UU

c.rangin@abdn.ac.uk

Tel. +44(0)1224 273662

"Rangin, Cecile" <c.rangin@abdn.ac.uk>

UAdelaide EvolutionReptileVision

PhD Project in Reptile Visual Evolution Department of Genetics and Evolution School of Biological Sciences The University of Adelaide, South Australia

Vertebrate vision has long fascinated evolutionary biologists and is a celebrated example of the power of integrative biology. Snakes and lizards provide an exceptional but under-utilised model group, having extremely diverse and evolutionarily plastic visual systems and ecologies. We are looking for a PhD student to examine the genetic and physiological consequences of ecological transitions in the visual systems of Australian reptiles. The student will gain broad experience in these areas but especially in comparative genomics and transcriptomics. There will also be opportunities to participate in terrestrial and tropical marine fieldwork.

The candidates must have, as a minimum, an excellent honours undergraduate or a MSc degree and meet the English Language Proficiency (ELP) requirement. The call is open to international and domestic (Australian citizens & permanent residents) students with backgrounds in biology, bioinformatics, population/quantitative genetics, or a related field. Publications would be desirable. International candidates from universities that rank lower than 200 in the world will need first author publications.

The successful applicant will need to apply for postgraduate research scholarship at the University of Adelaide. International applications are due by 31st January 2018 (https://international-hdr.adelaide.edu.au/login) and domestic are due by 31st May 2018 (https://www.adelaide.edu.au/graduatecentre/admission/application-rounds/domestic/)

The student will be based at School of Biological Sciences at the University of Adelaide. The supervisory team includes experts in reptile evolution, vision biology and bioinformatics at the University of Adelaide and University of Bristol (UK). This project is funded by the Australian Research Council and a European Union Fellowship.

Interested applicants are encouraged to send a CV and a cover letter to Dr Bruno SimÃμes or Dr Kate Sanders (bruno.simoes@adelaide.edu.au or kate.sanders@adelaide.edu.au)

Dr. Bruno F. SimÃμes

Marie SkÃ^{1}odowska-Curie Global Fellow (Evol-Eyes) University of Adelaide Affiliate Lecturer

THE UNIVERSITY OF ADELAIDE School of Biological Sciences Department of Genetics & Evolution, Darling Building, 212b room, Adelaide, South Australia 5005, Australia M: bruno.simoes@adelaide.edu.au | T: +61 8 83133946 W: http://researchers.adelaide.edu.au/profile/bruno.simoes UNIVERSITY OF BRISTOL School of Earth Sciences Paleobiology Research Group Life Sciences Building, 24 Tyndall Avenue, Bristol, BS8 1TG, United Kingdom M: bruno.fonsecasimoes@bristol.ac.uk W: http://research-information.bristol.ac.uk/en/persons/bruno-fonseca-simoes bruno.simoes@adelaide.edu.au

---

UAntwerp AvianAdaptation

Living on the edge - Lesser black-backed gulls foraging and breeding at a coastal-urban interface

Lesser black-backed gulls once successfully adapted to anthropogenic environments, indicating a high degree of behavioural plasticity. They are also considered to be generalist feeders with a wide ecological niche. But most individuals do not exploit the complete range of habitats and resources that are available, they rather specialize. However, the adaptive significance of such specialization likely depends on the predictability of the environment, which at current becomes increasingly unreliable - among others due to human-induced environmental changes.

The PhD project aims at investigating how reproductive decisions vary with the ability of an individual to respond to environmental and anthropogenic changes, and how the costs and benefits of individual specialisation relate to trade-offs throughout the annual cycle (including migration, nest-site selection and reproduction). This will be studied in field experiments via large scale behavioural observations of individually marked (colour-ringed) birds in collaboration with the Research Institute for Nature and Forest (INBO). This will be combined with the implementation of state-of-the-art GPS tracking devices that collect detailed information about individual movements and behaviour 24h/24h via the high tech sensor network (LifeWatch Infrastructure) in collaboration with Flanders Marine Institute (VLIZ).

We are seeking a highly motivated, enthusiastic and creative person with a Master in Biology or a related field. You must have good communication skills and be able to work in a team. You have a strong interest in Behavioural Ecology and Conservation, previous experience in related research and fieldwork would be helpful. The post is a full-time four-year PhD position from 1 March 2018 onwards (starting date negotiable).

To apply, please send in a single pdf file: (a) a statement of your research interests, motivation and suitability for this position, (b) your CV and (c) the contact details of two references. Please send your application to Wendt.Mueller@uantwerpen.be before 8 January 2018. Interviews will take place in January 2018, and will continue until the position is filled.

For informal enquiries please contact Prof. Wendt Muller Wendt.Mueller@uantwerpen.be, see also https://www.uantwerpen.be/en/staff/wendt-muller/ Wendt Muller

Behavioural Ecology and Ecophysiology Group

University of Antwerp Campus Drie Eiken D 1.30

Universiteitsplein 1 2610 Antwerp (Wilrijk), Belgium

e-mail: Wendt.Mueller@uantwerpen.be web: https://www.uantwerpen.be/en/staff/wendt-mueller/ tel +32 32652288 mobile:+32 473567276

Müller Wendt <wendt.muller@uantwerpen.be>

UArkansas EvolutionAnimalBehaviour

Graduate Student Positions in Integrative Animal Behavior in the Westerman Lab at The University of Arkansas

The Westerman Lab at the University of Arkansas (the flagship campus in Fayetteville, AR) is seeking PhD and MSc students to begin in the Fall of 2018. We study the evolution and mechanisms underlying behavioral diversity and plasticity, with a focus on sensory system development and visual learning in butterflies. Our current research topics include the role of genetics and social environment in mate preference development, behavioral and developmental plasticity, the role of perception and sensory environment in ornament evolution, and sensory biases. We are an intergrative animal behavior group, and integrate a wide range of techniques, including, but not limited to, controlled laboratory experiments, genomics, histology, and field ecology. Our research incorporates both tropical butterflies and those native to Northwestern Arkansas, and takes advantage of an on-campus butterfly facility as well as multiple species-rich field sites within a 30-minute drive. Graduate students will be expected to develop their own research projects within the scope of the lab. For more information, please visit the lab website: http://www.ericawesterman.org . As a technically integrative lab, we embrace creative approaches to studying animal behavior. Students with a strong background in neurobiology, genetics, and development are particularly encouraged to apply, as are candidates from groups historically underrepresented in STEM.

Interested prospective students should contact Dr. Erica Westerman at ewesterm@uark.edu. Please include a brief description of your research interests and how they fit within the scope of the lab, your CV, your GRE scores (if you have them), and contact information for 3 references.

Deadline for applications for the Graduate Program in Biological Sciences at the University of Arkansas is January 15, 2018: http://fulbright.uark.edu/departments/biology/prospective-students/grad uate-programs.php

However, interested prospective students should contact Dr. Erica Westerman before December 10^st 2017, or as soon as possible.

The Department of Biological Sciences fully funds students through teaching assistantships. However, there are additional sources of funding available through the university (i.e., $10,000-$20,000/yr as supplement to TA stipend) that depend on the qualifications of the applicant. Information about these funding sources can be found here: http://fulbright.uark.edu/departments/biology/prospective-students/grad uate-doctoral-fellowships.php

For more information please contact:

Dr. Erica Westerman

Assistant Professor

Department of Biological Sciences

University of Arkansas

ewesterm@uark.edu

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>

UBath EvolutionGeneDuplications

PhD studentship: How have gene family duplications shaped the disparity and diversity of mammal clades? UK, BBSRC SWBio DTP

Supervisory team: Main supervisor: Dr Araxi Urrutia (University of Bath) Co-supervisors: Prof Matthew Wills (University of Bath) and Dr Martin Genner (University of Bristol)

Understanding the forces that shape global biodiversity patterns was identified as one of the 25 greatest challenges for Science in the 21st Century (1, 2). Some mammal clades are enormously diverse, while their sister groups (originating at the same time) are far less so (e.g., 1,500 species of rodents versus 80 species of rabbits, hares and their allies). Why is this, and what might these differences tell us about the likely responses of groups to the present biodiversity crisis? In this strongly inter-disciplinary project, we will investigate the possible role of Small Scale Duplications of genes (SSDs) in shaping patters of diversity, anatomical complexity (3, 4) and morphological disparity (5-7) of mammals in deep time.

As noted by Ernst Haeckel, developmental trajectories tend to become more complex with macroevolutionary time. Increasing interdependencies between genes and systems, coupled with their co-option for multiple functions (pleiotropy), result in more deleterious collateral consequences of mutations. This predicts that aspects of bodyplan design may become arbitrarily 'locked down' (e.g. seven neck vertebrae in most mammals), and that evolutionary innovation will be commonest when genetic redundancy is highest.

Small Scale Duplications of genes (SSDs) increase the number of genes within a given gene family (gene family size, GFS), and are one way in which mammals may circumvent such pleiotropic constraints and facilitate innovation. This project will use a variety of genomic, phylogenetic palaeontological and comparative approaches (8) to investigate the relationship between the timing and phylogenetic placement of SSDs, the diversity (species richness) and disparity (morphological diversity) of clades, and the anatomical complexity (serial differentiation) of the vertebrae and limbs of the species within those clades.

Applicants must have obtained, or be about to obtain, a First or Upper Second Class UK Honours degree (or the equivalent qualifications gained outside the UK) in an appropriate area of science or technology. In addition, due to the strong mathematical component of the taught course in the first year and the quantitative emphasis in SWBio DTP projects, a minimum of a grade B in A-level Maths (or an equivalent qualification or experience) is required.

Candidates should apply using the University of Bath's online application form selecting PhD programme in Biosciences (full-time) https://www.bath.ac.uk/study/pg/-applications.pl#bio-sci./ For more information, please see: http://www.bath.ac.uk/science/postgraduate-study/research-programmes/funding/bbsrc-phds/ Funding Notes BBSRC SWBio DTP studentships provide funding for a stipend (currently 14,553 per annum for 2017/18), research/training costs and UK/EU tuition fees for 4 years.

Applicants from the UK and EU, who have been resident is the UK for 3 years or more immediately prior to the start of their course, are eligible to apply for a full studentship. Applicants who are classed as International for tuition fee purposes are not eligible for funding.

For more information, please see: View Website

Prof Matthew A Wills The Milner Centre for Evolution, Department of Biology and Biochemistry The University of Bath, The Avenue, Claverton Down, Bath BA27AY

Tel: +44 (0) 1225 383504 Fax: +44 (0) 1225 386407

http://www.bath.ac.uk/bio-sci/contacts/academics/-matthew_wills/ http://www.bath.ac.uk/projects/-the-milner-centre-for-evolution/ Matthew Wills <M.A.Wills@bath.ac.uk>

UBath SexRoleEvolution

PROJECT TITLE: Sex role evolution: phylogenetic analyses of mating and parenting in vertebrates

Main Supervisor: Professor Tamás Székely, University of Bath, UK Co-Supervisor: Dr Daniel J Field, University of Bath, UK Co-Supervisor: Prof Innes Cuthill, University of Bristol. UK

Project Enquiries: T.Szekely@bath.ac.uk

Project Background Sex roles (e.g. courtship, mate choice, pair bonding and parenting) are immensely diverse social behaviours. Recent research has uncovered key elements of sex role variation, but significant uncertainties remain. Appropriate sexual behaviour in nature is essential for reproduction, and thus understanding sex roles is critical for evolutionary biology and population biology. Understanding sex roles is also important for biodiversity conservation since disruptions to normal sexual behaviour due to environmental changes may reduce population viability. A general trend in social behaviour is that females tend to be the caring sex, whereas males focus more on mating; however there are illuminating exceptions. This division of sex roles has far-reaching effects on ecology, physiology and life histories of males and females. The causes, however, of sex role differentiation have remained controversial. This PhD project is focused on understanding the causes of sex role evolution in vertebrates using phylogenetic approaches.

Project Aims and Methods This PhD project will focus on vertebrates (i.e. fishes, amphibians, reptiles, birds and mammals) that exhibit particularly well-studied sex role behaviour. The PhD project has three objectives: 1. to investigate the association between key components of sex roles: courtship, competition for mates, pair bonding and parental care; 2. to examine the influence of variation in ecology, life- history and social environment on sex roles; 3. to investigate the multi-way feedbacks between sex roles, environment, life histories and the social environment using phylogenetic tools. These objectives will be addressed using (i) detailed information on courtship, pair bonding and parental behavior collected by Prof Szekely's team from multiple bird populations, and (ii) across vertebrates based on published data in the literature. This will be a challenging and stimulating project that can potentially produce cutting edge results. The student will not only benefit from the excellent facilities at Bath and Bristol, but also from interacting with top international scientists involved in the project. Fieldwork in exotic locations can be negotiated.

Candidate The ideal candidate has a strong interest in evolution, phylogenetic methods and behaviour, and direct experience working with any vertebrate taxon. Excellent quantitative skills are required to perform phylogenetic comparative analyses and run mathematical simulations. Innovative thinking will be necessary to draw links between disparate sources of data.

Training The training will focus on three major skills: 1. Phylogenetic analyses: this includes inferring phylogenies and using trees in a comparative framework for testing macroevolutionary hypotheses. Training in computational and advanced statistical methods will be a focus of this PhD; 2. Fieldwork including experimental design, behavioural observations, estimating ecological and life-history variables in the field; 3. Transferable skills including research planning, statistical analyses, paper writing, presentation and communication skills.

References / Background reading list 1. RemeÂ, V., R. P. Freckleton, J. Tökölyi, A. Liker & T. Székely. 2015. The evolution of parental cooperation in birds. Proceedings of National Academy of Sciences, US 112: 13603-13608. 2. Prum, R. O., Berv, J. S., Dornburg, A., Field, D. J., Townsend, J. P., Lemmon, E. M. and Lemmon, A. R., 2015. A comprehensive phylogeny of birds (Aves) using targeted next- generation DNA sequencing. Nature 526: 569-573. 3. Cuthill, I. C. et al. 2017. The biology of color. Science 357: 470-475. 4. Liker, A., R. P. Freckleton & T. Székely. 2013. The evolution of sex roles in birds is related to adult sex ratio. Nature Communications 4: 1587.

Tamás Székely, Professor of Biodiversity Royal Society Wolfson Research Merit Award Holder Dept of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK 01225 383676 (phone), 01225 386779 (fax), T.Szekely@bath.ac.uk (email)

— / —

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

---

UBern 2 SpeciationGenomics

Two PhD positions:

Speciation genomics of rodents and their microbes

Applications are invited for two PhD positions investigating the genomic processes of evolutionary divergence and hybridization in rodents and their feedback on associated microbes. Research will deepen and extend our comparative analyses of different stages of speciation in Microtus voles. This will contribute to answering fundamental questions in evolutionary biology such as: What is the importance of adaptive and neutral processes during evolutionary divergence? How tight is the association between fast-evolving microorganisms and processes of speciation in their hosts? Does divergence and diversity of hosts limit or expand the evolutionary scope of associated microorganisms? We will address this through comparative analyses of vole and RNA virus genomes and of microbial communities based on high-throughput sequence data from several Microtus hybrid zones with different levels of divergence. The two PhD candidates will focus on different aspects of the system (host, microbiome, virus, selection, demography, population structure, etc.) depending on the specific qualifications and interests.

I am looking for skilled, creative and highly-motivated candidates who are able to work independently and in a team. Candidates must have a solid background in evolutionary biology, and practical experience with bioinformatics applications and analysis methods in population genetics and/or phylogenetics. Much of the work will concern the processing and analysis of large genomic data sets generated by the candidates. Experience with molecular laboratory work or fieldwork on small mammals is a plus but not essential. A Master degree in a relevant field and a valid driver's license is required.

The project includes short periods of fieldwork, and the writing of several manuscripts for leading scientific journals.

We offer a very stimulating, multi-national research community with excellent infrastructure. We are also part of the Swiss Institute of Bioinformatics (SIB) which broadens the opportunities for further training beyond courses in various doctoral programs. The working language in our institute is English. Some knowledge of German or French is beneficial for living in Switzerland but it is not essential. Bern and Switzerland are consistently ranked among the places with the highest quality of life.

The positions are funded by the Swiss National Science Foundation for a maximum of four years. The anticipated starting date is early 2018. Please send your application as a single (!) pdf file to Prof. Gerald Heckel: gerald.heckel@iee.unibe.ch. To be considered, the pdf must include a letter describing your past research experience and particular skills and motivation for these positions (max. 2 pages), the abstract of your Master thesis, a CV, and contact details of 2-3 referees. Review of applications will begin December 7 2017 and will continue until the positions are filled.

Prof. Dr. Gerald Heckel Computational and Molecular Population Genetics (CMPG) Institute of Ecology and Evolution University of Bern Baltzerstrasse 6 CH-3012 Bern, Switzerland Tel: +41 31 631 30 29 Email: gerald.heckel@iee.unibe.ch http://www.cmpg.iee.unibe.ch Swiss Institute of Bioinformatics (SIB) http://www.isb-sib.ch/groups/-Computational_Population_Genetics.htm "gerald.heckel@iee.unibe.ch" <gerald.heckel@iee.unibe.ch>

UBern SexChromosomeEvolution

PhD position in Evolutionary Genomics at the University of Bern A funded, 4-yr PhD position is available in the Division of Evolutionary Ecology (http://-www.ee.iee.unibe.ch/index_eng.html) at the University of Bern, Switzerland to study the evolution of sex chromosomes in stickleback fish.

The student will work on a recently funded SNF project entitled Chromosome evolution: molecular mechanisms and evolutionary consequences.

The aim of the project is to use genome sequencing and transcriptome data to characterize the diversity of sex chromosome systems found in the stickleback family to address the following questions: (1) What factors are associated with the transition between homomorphic and heteromorphic sex chromosomes?; (2) What mechanisms contribute to the maintenance of gene dosage on degenerate sex chromosomes?; (3) Do Y and W chromosomes have different evolutionary trajectories? The Division of Evolutionary Ecology is a dynamic and interdisciplinary group. We are part of the Institute of Ecology and Evolution at the University of Bern in Switzerland. The Institute currently has six research divisions spanning a broad range of research in ecology and evolution including conservation biology, community ecology, behavioural ecology, population and evolutionary genomics, and mechanisms of adaptation and speciation. We host a large international community of graduate students and post-doctoral researchers.

Candidates must be highly motivated and creative, able to work independently and collaboratively, have a strong background in evolutionary genetics, and have prior experience with the analyses of large genomic datasets. Previous experience with molecular cytogenetic methods is a plus. The working language of our division is English.

The starting date for the PhD student is as early as January 2018. A masters degree is required to apply. Starting salary is 47,000 CHF and includes social security contributions.

Please submit your application via email by 30 November 2017 to Prof. Catherine Peichel: catherine.peichel@iee.unibe.ch Applicants must submit one merged PDF file that includes a letter of motivation, a CV, names of two referees who should have sent their recommendation letter separately by email before the deadline, and copies of relevant publications and/or masters thesis. Incomplete or late applications will not be considered.

catherine.peichel@iee.unibe.ch

UBristol ButterflyEvolution

Please post this on the Evoldir announcement section. Many thanks.

Applications are invited for a PhD studentship eligible for NERC funding at the University of Bristol, UK

When and how does adaptation prevent extinction due to climate change? Testing for evolutionary change at contracting range margins of European butterflies

(Supervisors; Dr Jon Bridle, University of Bristol, Dr Rob Wilson, University of Exeter)

We are looking for a highly-motivated student to test the ecological effects of climate change on butterfly communities, and the role of evolution in increasing their resilience. Profound effects on ecosystem function are predicted as climate change generates rapid shifts in species' geographical distributions. Many organisms have already contracted their ranges at equatorial margins to higher altitudes, and expanded their ranges as their poleward margins become increasingly habitable. However, these responses seem limited by rates of evolution. Although most generalist species have shifted their ranges, most specialist species remain trapped in increasingly fragmented habitats, apparently because they cannot adapt to local conditions at their ecological margins. Defining critical levels of environmental change therefore depends on understanding how easily (and how quickly) evolutionary rescue can occur at ecological margins.

This project will explore evolution in European butterflies at their southern (contacting) margins in comparison to that observed at their northern (expanding) margins. Adaptive divergence may be easier at contracting margins because population sizes are initially high, making genetic variation locally available. By contrast, at expanding margins evolution may require the spread of novel mutations from distant populations, or may cause the rapid loss of adaptive variation.

You will: (i) conduct butterfly and host plant surveys in central Spain, and comparing their thermal niches to our previous data; (ii) Use population genomics to test for local adaptation at contracting range margins in comparison to those involved in poleward expansions; (iii) conduct field transplant experiments to test for adaptive divergence in maternal behaviour and larval survival and and by testing larval growth rate at different altitudes.

You will be based at the University of Bristol, and will include two field seasons in Madrid, and time at the University of Exeter. You will receive expert training in population ecology and genomics, spatial ecology, and the application of evolutionary theory to conservation policy.

Please see:

https://nercgw4plus.ac.uk/project/when-and-how-does-adaptation-prevent- extinction-due-to-climate-change-testing-for-evolutionary-change-at-con tracting-range-margins-of-european-butterflies-2/

For more details of this project, and the application procedure.

The deadline for applications is 7th January 2018.

Please contact Jon Bridle (jon.bridle@bristol.ac.uk) or Rob Wilson (R.J.Wilson@exeter.ac.uk) for informal discussion.

Dr Jon Bridle School of Biological Sciences 2A03, Life Sciences Building University of Bristol, BS8 1TQ Tel. (+44) 117 394 1174 (internal 41174) jon.bridle@bristol.ac.uk http://www.bristol.ac.uk/biology/people/jon-r-bridle/ Jon Bridle <Jon.Bridle@bristol.ac.uk>

UCentralFlorida MarinePopulationGenomics eDNA

Ph.D. and M.S. positions in marine population genomics or eDNA.

Fish Ecology and Evolution in the Gaither Lab at UCF The Gaither Lab at the University of Central Florida (UCF) Department of Biology is recruiting highly motivated and independent graduate students in marine population genomics and evolution for Fall 2018. My lab uses RADSeq, whole genome re-sequencing, and targeted capture approaches to study coral reef and deep-sea fishes. We have new projects coming online involving eDNA techniques. Students will have access to a fully equipped genomics lab and a high powered computing cluster.

Applicants should have completed a degree in a biological science. Computational skills or a desire to learn bioinformatics is a must. Ability to pursue independent research and excellent writing and fluency in English is expected. Interested students are encouraged to email Michelle Gaither at michellergaither@gmail.com with the subject line UCF_Graduate_Positions. Please include a brief description of your research interests and experience and a CV in your email. Note that the deadline for applications to UCF Biology is January 15th.

To learn more about UCF Biology graduate programs go to https://sciences.ucf.edu/biology/graduate-program/ Or if you want to learn more about the Genomics and Bioinformatics Cluster at UCF go to https://www.ucf.edu/faculty/cluster/genomics-bioinformatics/. Michelle R. Gaither Fish Ecology and EvolutionAssistant Professor (Start date Dec. 1st 2017)University of Central FloridaGenomics and Bioinformatics ClusterDepartment of Biologyhttps://scholar.google.com/-

citations?user=jPbEa9cAAAAJ&hl=en&oi=ao DIPnet Coordinator/Postdoctoral Researcher Hawaii Institute of Marine Biology P.O. Box 1346 Coconut Island Kaneohe, Hawaii 96744 Webpage < http://www.calacademy.org/scientists/ichthyology/mgaither > Project webpage < http://deepseaevolution.com/ > Google Scholar < http://scholar.google.co.uk/citations?user=3DjPbEa9cAAAAJ&hl=3Den&oi=3Dao >

Michelle Gaither <michellergaither@gmail.com>

UCincinnati ReproductiveCoevolution

The Morehouse Lab at the University of Cincinnati is seeking highly motivated PhD students to join our vibrant research team. Current research foci in the lab include the co-evolution of color vision and color signaling in jumping spiders (https://goo.gl/cyueWW), the influence of female gaze on the evolution of complex courtship displays (also in jumping spiders), and coevolution between male and female reproductive proteins in butterflies (https://goo.gl/2hg44e). I am particularly motivated to recruit students interested in this latter research topic, given the current balance of interests and expertise in the lab, but am also open to applications from students more attracted to our research on jumping spiders.

In addition to these new research initiatives, we have a number of other research projects that could provide opportunities for incoming students. I am currently adding more information about these on the lab website: www.morehouselab.com. Students interested in joining the lab should contact me as soon as possible (nathan.morehouse@uc.edu) to discuss their interests and fit for the lab. Please include a brief statement of your research interests, how they connect with our current research, and your CV, academic transcripts, and GRE scores if available. Research support in the form of a one-year research assistantship is available for highly qualified applicants.

The University of Cincinnati is emerging as an international center of excellence in sensory biology and ecology. With a strong and growing faculty concentration in Sensory Biology, Behavior, and Evolution (http://www.artsci.uc.edu/departments/biology/research/Sbbe.html), UC provides a vibrant intellectual environment for research and student training. Matching research strengths in sensing and sensor technologies in UC's nationally-renowned College of Engineering offer a number of cross-disciplinary training opportunities. Our Department of Psychology is home to the Center for Cognition, Action, and Perception (http://www.uc.edu/cap.html), which adds research dimensions in cognitive science and ecological psychology. In addition, Sensorium, a regional consortium of sensory biologists and ecologists established this fall through efforts of members of our SBBE group (http://www.sensoriumconference.org), offers additional connections to regional labs, including research groups at Purdue and Case Western.

The Department of Biological Sciences offers competitive support packages for qualified students. The University of Cincinnati and the Department of Biological Sciences have a strong commitment to diversity in science and graduate education. Students from underrepresented ethnic or racial minorities will be considered for the new Provost Graduate Fellowship, which provides a 3-year $25,000 stipend plus tuition remission, and the Yates Fellowship, which awards grants to underrepresented minority candidates.

The University of Cincinnati is a top-25 public 'research-intensive' institution and is ranked among the nation's best institutions for undergraduate education. Founded in 1819, our campus boasts award winning, modern architecture and is located in close vicinity to collaborative resources including the UC Medical campus, Cincinnati Children's Hospital, the Cincinnati Zoo and Botanical Garden, and the Environmental Protection Agency.

Cincinnati is a vibrant city on the banks of the Ohio River. The region is home to year-round cultural and entertainment opportunities such as the Cincinnati Symphony Orchestra and National Underground Railroad Freedom Center, as well as numerous annual music and cultural festivals. Cincinnati is also home to major professional sports teams including the Cincinnati Bengals, Cincinnati Reds, and FC Cincinnati - a new professional soccer team which draws over 20,000 fans per game. The city is located within the Hamilton County Parks system which provides extensive green space and opportunities for outdoor activities.

More information about the graduate program in the Department of Biological Sciences can be found here: http://www.artsci.uc.edu/departments/biology/graduate/future.html Graduate applications are due January 1. To apply: http://www.grad.uc.edu/ApplyOnline.aspx Sincerely,

Nate

Nathan Morehouse

Assistant Professor Department of Biological Sciences University of Cincinnati 711H Rieveschl Hall Cincinnati, OH 45221-0006 Office: (513) 556-9757 colorevolution@uc.edu http://www.morehouselab.com

— / —

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

UCincinnati SensoryEvolution

PhD positions in Sensory System Evolution / Vision Science

>From ancient genes to focused eyes: The Buschbeck laboratory uses exciting new tools to probe fundamental and crucial questions of visual system evolution, function and development in invertebrate models. How do deeply conserved genes and gene networks contribute to the development of extraordinary image-forming eyes? One research project utilizes RNAi knockdown and focuses on when, where and what known eye development genes are expressed during the development of highly unusual beetle larval eyes, with complementary experiments in the genetically powerful Drosophila system. Another research direction utilizes a newly developed, unique micro-ophthalmoscope to perform vision tests on the smallest of all eyes. The goal of that project is to investigate how invertebrates coordinate the optical power of the lens and underlying photoreceptors. Do invertebrates, like vertebrates, need visual input to develop and maintain correctly focused eyes? This important question is especially interesting in the light of rapid and dramatic eye growth that often takes place when animals molt. More details on our NSF sponsored research, additional projects, the lab's research community and mentoring are available at: http://www.buschbecklab.com. Students interested in joining the laboratory should contact Elke Buschbeck as soon as possible at elke.buschbeck@uc.edu. Please include a brief description of research interests as well as you CV.

The University of Cincinnati is emerging as an international center of excellence in sensory ecology. With a strong and growing faculty concentration in Sensory Biology, Behavior, and Evolution (http://www.artsci.uc.edu/departments/biology/research/Sbbe.html), UC provides a vibrant intellectual environment for research and training. Matching research strengths in sensing and sensor technologies in UC's nationally- renowned College of Engineering offer a number of cross-disciplinary training opportunities as well as through a regional consortium of sensory biologists, including researchers at Purdue and Case Western.

The department offers competitive support packages for qualified students. The University of Cincinnati and the Department of Biological Sciences have a strong commitment to diversity in science and graduate education. Students from underrepresented ethnic or racial minorities will be considered for the new Provost Graduate Fellowship, and the Yates Fellowship.

More information about the graduate program in the Department of Biological Sciences can be found here: http://www.artsci.uc.edu/departments/biology/graduate/future.html . Graduate applications are due January 1. To apply: http://www.grad.uc.edu/ApplyOnline.aspx . "Buschbeck, Elke (buschbek)" <buschbek@ucmail.uc.edu>

UConnecticut PlantArthropodInteractions

Ph.D. position - plant-arthropod interactions and global change

The laboratory of Interactions and Global Change - University of Connecticut is accepting applications from prospective Ph.D students interested in the study of ecological and evolutionary processes in plant-arthropod interactions and climate change. Successful candidates will explore the ecology and evolution of thermal tolerance from molecular, physiological and demographic perspectives, using interactions between rolled-leaf beetles and Zingiberales as a study system.

How to apply

e-mail the PI - Carlos Garcia-Robledo (carlos.garcia-robledo@uconn.edu), before December 5 a one-page letter of intent describing your research interests and a brief description of the type of research that you would like to pursue in grad. school. Please also include your CV and unofficial transcripts, and if already available, GRE (all students) - TOEFL (only international students) scores.

More information about the lab: http://carlosgarciarobledo.org/UCONN/ Carlos Garcia-

Robledo

—

Carlos Garcia-Robledo

Assistant Professor Department of Ecology and Evolutionary Biology University of Connecticut 75 N. Eagleville Road, Unit 3043 Storrs, CT 06269-3043 USA

Pharmacy/Biology PBB 400A (office) Pharmacy/Biology PBB 217 (lab) 860-486-4027 (office phone) 860-486-0805 (lab phone) 860-486-6364 (fax)

Lab website: http://carlosgarciarobledo.org/ "Garcia-Robledo, Carlos" <carlos.garcia-robledo@uconn.edu>

UConnecticut PlantComputationalGenomics

The Plant Computational Genomics lab in the Department of Ecology and Evolutionary Biology at the University of Connecticut seeks motivated PhD and MS students to join the lab in the Summer/Fall 2018. Our research focuses on the computational analysis of genomic and transcriptomic data generated by next-generation sequencing platforms from non-model forest tree species. We implement this through analysis related to gene finding, gene expression, transcriptome assembly, and conserved element identification, through machine learning and computational statistics. We use these methods to address questions related to genome biology and population genomics. In addition, we develop web-based applications that integrate BIG data across domains to facilitate the forest geneticist or ecologist's ability to analyze, share, and visualize their data (http://treegenesdb.org). Such integration requires the implementation of semantic technologies and ontologies to connect genotype, phenotype, and environmental resources. We actively contribute to the open source Tripal (http://tripal.info) project with these goals in mind.

RESEARCH TOPICS: Potential research topics in our group include 1) development of visualization tools to support genome-wide association studies in forest trees; 2) application of genomic and transcriptomic techniques to evaluate the impact of climate change on tree populations; 3) development of software solutions to improve assembly and characterization of non-model plant transcriptomes; 4) interrogation of natural genetic variation across populations in large, complex conifer genomes; 5) and your ideas here!

TO APPLY: Financial support for M.S. and Ph.D. students is available through research assistantships, teaching assistantships, and university fellowships. To learn more about our research, please visit: http://compgenomics.lab.uconn .edu/. Excellent written and oral communication, as well as strong quantitative skills, are required. Backgrounds in genetics/genomics, evolutionary biology, bioinformatics, and computer science are desired. Interested candidates should send an email with a research interest statement (1-2 pages), a CV, unofficial undergraduate/graduate transcripts, and GRE scores to Jill Wegrzyn (jill.wegrzyn@uconn.edu). Qualified candidates will be contacted directly for Skype interviews following review. Applications will be reviewed on December 20th.

ABOUT UCONN:

The University of Connecticut (UConn) has been one of the nation's leading public institutions since its founding in 1881. Located in Storrs, UConn's main campus is situated in the picturesque rolling forests and fields quintessential of New England, yet is only 30 minutes from Hartford, and has close connections to Providence, Boston and New York. The Department of Ecology and Evolutionary Biology consists of over 30 faculty and 60 graduate students with research spanning nearly all major groups of organisms. The Department maintains close ties with the Departments of Physiology and Neurobiology, Molecular and Cell Biology, Marine Sciences, and Natural Resources Management and Engineering, as well as the Center for Environmental Sciences and Engineering and the Institute for Systems Genomics, which together comprise one of the largest groups of biologists in the Northeast.

Jill L. Wegrzyn Assistant Professor

Department of Ecology and Evolutionary Biology Institute for Systems Genomics: Computational Biology Core University of Connecticut 181 Auditorium Rd Storrs CT 06269-3214

jill.wegrzyn@uconn.edu +1 860-486-8742

Research: http://compgenomics.lab.uconn.edu CBC Core: http://bioinformatics.uconn.edu Office (ESB 306C) / Lab (ESB 315)

jill.wegrzyn@uconn.edu

UConneticut EndosymbiontsInsectPhylogenomics

PhD Student Position Insect Phylogenomics Microbiomes, Endosymbionts, in the Simon Lab, UConn

The Simon lab at the University of Connecticut seeks creative and motivated PhD students interested in phylogenetics, molecular phylogenomics, bioinformatics, and/or symbiont-host interactions (endosymbionts and/or microbiomes) to begin in the fall of 2018. Experience preferred but not required.

Applicants will participate in an NSF sponsored project entitled: Exploring Symbiont Biodiversity and Complexity in the Family Cicadidae to study the codiversification and interaction between cicadas, their primary obligate endosymbionts, their secondary facultative endosymbionts and their gut microbiota.

Cicada obligate endosymbionts have recently been demonstrated to exhibit spectacular and unprecedented genome diversity. Since cicada symbionts are largely unknown our work will result in considerable biodiversity discovery. We hypothesize that gain or loss of host-symbiont consortium members during cicada phylogenetic history will be correlated with internal or external environmental changes. We are most interested in the timing of symbiont consortium changes. For example, does the gain of a secondary (facultative) endosymbiont facilitate the breakdown or loss of primary (obligate) endosymbionts? Or does the breakdown or loss of the obligate endosymbiont allow invasion by a secondary endosymbiont? Broader impacts will involve collaborations with team members in the US, India, NZ, and Fiji.

Senior Personnel and collaborators on the project include: Thomas Buckley (NZ), David Marshall, John Cooley, John McCutcheon, Emily and Alan Lemmon, Chris Owen, Beth Wade, Al Sanborn, Dan Mozgai, Max Moulds (AU), Ben Price (UK), Martin Villet (ZA), Deepa Agashe (IN), Krushnamegh Kunte (IN), Sudhanya Hajong (IN), Cong Wei (CN), Hong He (CN), Daniela Takiya (BR), Tatiana Ruschel (BR), Pablo Pessacq (Argentina), Claudio Veloso (Chile), Peter Lockhart (NZ, FJ), and numerous cicada researchers around the world.

Interested and qualified PhD candidates should send an email describing their motivation, skills, and research experience/interests along with a CV, GPA, GRE and TOEFL (if relevant) scores. Applicants should also arrange to have letters sent letters sent by three referees who are familiar with the candidates work. Strong applicants will be contacted to schedule an informal Skype interview. Applications to UCONN (early admission) are due December 15th with rolling admission thereafter. Financial support for Ph.D. students is available via research assistantships from our NSF award, teaching assistantships, and university fellowships, but applications to outside funding sources are also strongly encouraged. Send all material to chris.simon@uconn.edu The successful candidates will join the EEB Department at the University of Connecticut and also have opportunities to work in the laboratories of collaborators. The EEB department is a diverse, highly collegial and interactive group of scientists. Relevant to these positions, we are particularly strong in Systematics with eight faculty members whose major focus is phylogenetic systematics and half a dozen others who use phylogenetics in their work. We offer three graduate courses in systematics (Principles and Methods of Systematics, Molecular Systematics, and Phylogenetic Systematics) plus numerous relevant grad seminars. There is a strong symbiont group on campus that includes members of EEB and Molecular and Cell Biology. EEB also has strengths in phenotypic plasticity and functional morphology, global change ecology, behavior, and organismal evolution, ecology and conservation.

Chris Simon Professor, Ecology & Evolutionary Biology University of Connecticut, 75 N. Eagleville Rd. Storrs, CT 06269-3043

chris.simon@uconn.edu

Chris Simon <chris.simon@uconn.edu>

UDenver EvolutionaryGenomics

Graduate students can earn degrees in Biological Sciences with a concentration in Ecology and Evolution or Cell and Molecular Biology. Graduate students will be supported through graduate teaching assistantships for up to 2 (MS) to 5 years (PhD).

Denver is a vibrant city just east of the Front Range of the Rocky Mountains. The University of Denver is nestled in a residential neighborhood 8 miles southeast of downtown Denver. The campus is connected via light rail to downtown and the broader Front Range region.

Please contact Erica Larson, erica.larson@du.edu, for more information. Additional information can be found at https://www.larsonlab.space . "Erica.Larson@du.edu" <Erica.Larson@du.edu>

UEastAnglia IslandAvianEvolution

Aim: To understand the temporal evolution of immunogenetic diversity in wild animals.

In the face of changing environments, genetic variation is essential for the survival of individuals and populations, and thus underpins biodiversity. How genetic diversity is generated and maintained in populations is, therefore, an important evolutionary question with ramifications for everything from epidemiology to conservation.

Pathogens are a strong selective force so it is not surprising that immune genes are often extremely polymorphic. However, we lack fundamental understanding of the rate at which host immunogenetic variation changes over time in natural vertebrate populations, how different genetic mechanisms facilitate it, and the relative influence of genetic drift and selection in this.

The student will use genomic capture techniques to screen variation in Berthelot's pipit at 132 already immune identified loci. Using a combination of museum specimens (1820s), previously collected samples (2006) and fieldwork (2019) they will measure changes in immunogenetic variation across time in multiple isolated populations of this species. Our previous work has identified differences between these populations (in population size and pathogen regimes), which provide axes of variation against which to test temporal patterns of immunogentic change.

The student will investigate: 1. The rate of immunogenetic change in a wild-living bird; 2. The role of mutational rates or mechanisms in enabling change at immune genes; 3. The relative importance of drift and pathogen-mediated selection in driving immunogenetic evolution; 4. The role of different selection mechanisms that can act to maintain variation in natural populations.

Research Environment and Training Supervised by Prof David Richardson and Dr Lewis Spurgin (UEA), with Dr Brent Emerson (CSIC), the student will join a dynamic, collaborative research community at UEA, and spend at least 3 months at CSIC, (CASE partner research institute in Tenerife) directly interacting with researchers.

The student will receive specialized training in ecological fieldwork, molecular genetics, bioinformatics and data analysis. They will also receive extensive training from NERC/UEA to increase generic scientific skills and enhance employability.

For further information, please visit http://www.enveast.ac.uk/apply For more information about the supervisor for this project, please go here: http://www.uea.ac.uk/biological-sciences/people/profile/david-richardson David S Richardson Professor in Evolutionary Ecology and Conservation School of Biological Sciences, UEA, Norwich NR4 7TJ, England e-mail: david.richardson@uea.ac.uk https://www.uea.ac.uk/biological-sciences/people/profile/david-richardson "David Richardson (BIO - Staff)" <David.Richardson@uea.ac.uk>

UEastAnglia SexualDetection

PhD on 'Sexual detection: mechanisms underlying adaptive reproductive plasticity.'

Prof Tracey Chapman, School of Biological Sciences, University of East Anglia, UK.

tracey.chapman@uea.ac.uk

http://traceychapmanresearch.com/ https://www.uea.ac.uk/biological-sciences/people/profile/tracey-chapman An exciting opportunity and a unique training opportunity to understand how individuals respond to their social and sexual environment. You will gain research skills in cutting-edge genetic, genomic manipulations, bioinformatics and cellular microscopy and receive excellent training and career development from the thriving Norwich Biosciences Doctoral Training Partnership and from the collaboration with Professor Clive Wilson at the University of Oxford.

An important part of being successful and competitive is to respond to the rapidly changing environments in which we often find ourselves. Fruitfly males are able to show highly precise responses to their social and sexual environment. Following detection of conspecific rivals, males transfer more ejaculate proteins to females and sire more offspring. They are even able to alter the composition of the ejaculate that they transfer. Males can switch their 'rivals responses' on and off with great accuracy and speed.

The overarching aim is to find out how males can do this. Our recent studies support the hypothesis that males can potentially use different mechanisms, to turn genes on / off, remove inhibitors of gene expression and change the way that ejaculate proteins are made and expelled. The student will test this and determine the temporal sequence of events. They will use phenotypic profiling to assess the effect of genetic manipulations of accessory glands, measure changes to gene and non-coding RNA expression using bioinformatics, and profile structural and signaling changes using high resolution microscopy.

For more details and to apply!

http://www.biodtp.norwichresearchpark.ac.uk/-projects/project/sexual-detection -mechanisms-underlying-adaptive-reproductive-plasticity-chapmanu18dtp

"Tracey Chapman (BIO - Staff)" <Tracey.Chapman@uea.ac.uk>

UEdinburgh 2 EvolutionaryGenetics

Dear all,

I would like to advertise two PhD projects on the evolutionary and reproductive genetics of insects in my lab at the University of Edinburgh starting October 2018 https://scholar.google.co.uk/citations?user=-hTtM8jkAAAAJ&hl=en. There are funding options for both UK and international students. If you are interested please contact me directly (laura.ross@ed.ac.uk) to discuss, deadlines vary depending on funding source. Below are the project descriptions:

Sexual conflict and genome evolution in haplodiploid organisms

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=90109 Sexual conflicts result from a clash of interests between the sexes [1]. In many cases, this battle is fought at the level of the gene: males and females may differ with respect to which version of a gene maximizes their Darwinian fitness. Whilst the effects of such intralocus sexual conflicts have been studied intensively in many organisms, the vast majority of studies have focused on species with classical, diploid sexual reproduction. However, as many as 15% of animal species exhibit an alternative, haplodiploid mode of inheritance. In such species, mothers monopolize the production of male offspring, either by asexual production of sons or by producing sons that eliminate their father's genome after the zygote stage [2]. This asymmetrical mode of inheritance is likely to affect the outcome of intralocus sexual conflict. Specifically, as alleles that favour male fitness cannot be passed on directly from fathers to sons, sexual conflicts may be resolved in favour of females [2]. The aim of this project is to study the fate of alleles under intralocus sexual conflict in a range of haplodiploid taxa. Studying such exceptions to the general rules of reproduction provides illumination of the fundamental principles of evolutionary genetics (see [3] for a recent comparable example). This project will combine laboratory experiments, gene expression studies and genome analyses. We will focus particularly on springtails and fungus gnats, as males in these species carry and express their father's genomes, but do not pass them on to their offspring. In addition, these species still retain recognizable sex chromosomes, which enables informative sex chromosome / autosome comparisons (e.g. [3]). These experimental approaches will be combined with comparative phylogenetic analyses and the development of novel evolutionary theory, according to the interests of the student.

The project will be supervised by Dr. Laura Ross (Edinburgh, http://lauraross.bio.ed.ac.uk) and Dr. Andy Gardner (St. Andrews). Ross is an evolutionary biologist who uses a combination of genomic, empirical and phylogenetic approaches to study the evolution and evolutionary consequences of different types of reproduction among the animal kingdom. Gardner is a leading mathematical biologist whose works spans a wide range of topics in theoretical biology and genetics. The proposed project strongly rest upon the collaboration between the supervisors as, on the one hand, formalization of the relevant theoretical hypotheses is currently lacking and, on the other hand, empirical work is required for estimation of key model parameters. The candidate will be based primarily in Edinburgh, as required by the empirical work, but will spend 1-2 days per month in St. Andrews for the duration of the project, as well as two 1-2 month intensive visits to the Gardner lab in years 2 and 3.

[1] Bonduriansky, Russell, and Stephen F. Chenoweth. "Intralocus sexual conflict." Trends in Ecology & Evolution 24.5 (2009): 280- 288. 280-288. [2] De la Filia, Andres G., Stevie A. Bain, and Laura Ross. "Haplodiploidy and the reproductive ecology of Arthropods." Current Opinion in Insect Science (2015). [3] Jaquiéry, Julie, et al. "Masculinization of the X chromosome in the pea aphid." Plos Genet 9 (2013): e1003690

How males lose their father's genes: parent-of-origin specific genomic exclusion in insects

https://www.findaphd.com/search/ProjectDetails.aspx?PJID=89118 For most organisms, the two copies of a gene - one from their mother, the other from their father - are interchangeable. But sometimes this rule is violated. In a process called genomic imprinting the expression of one of the two copies of a gene is privileged, depending on its parental origin. Genomic imprinting is studied extensively in mammals and plants and most biologists consider it exclusive to these groups. In fact imprinting was first discovered in a different group, the insects, in the 1950s, decades before its discovery elsewhere [1]. Since then

— / —

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

---

UEdinburgh ComputationalPhylogeny

Note: This opportunity is only open to UK nationals (or EU students who have been resident in the UK for 3+ years immediately prior to the programme start date) due to restrictions imposed by the funding body.

MASSIVELY PARALLEL PHYLOGENY RECONSTRUCTION FOR THE AGE OF DNA BIG DATA

Supervisors: Dr Daniel Barker, University of Edinburgh, UK, Daniel.Barker@ed.ac.uk Professor Thomas Meagher, University of St Andrews, UK

The goal is to create re-usable, effective, portable parallel algorithms and open-source software for reconstructing large phylogenies. This would represent a step-change for phylogeny reconstruction, which is now central to many areas of life sciences, from biodiversity and conservation to cancer research. Phylogeny research, a central element of many aspects of modern biology, has been transformed by the availability of DNA sequences, with an explosion in generation and use of such data. Moreover, access to extended data platforms and scientific challenges has increased the scale, in terms of numbers of species, over which phylogeny research is conducted. The resulting Big Data is placing a strain on computational phylogeny. To find the optimal tree-like phylogeny according to current criteria, ideally one would evaluate all possible tree topologies. However, the number of topologies increases factorially with the number of extant entities in the tree. For just 54 species 'V a small study by current standards 'V there are more possible topologies than atoms in the universe. The project will address Big Data challenges for phylogeny research through theoretical and computational approaches. These will include use and characterisation of nature-inspired advanced heuristics (e.g. Strobl and Barker 2016), programming and use of massively parallel computer systems, optimisation of algorithms and implementations, and cross-site, distributed machine learning techniques. Research training will be provided in phylogeny reconstruction, programming, software engineering, high performance computing and machine learning. This will be provided through meetings with the supervisors; meetings/visits and discussion with Dr Martyn Winn (STFC Scientific Computing Department); attendance at short courses and conferences; and attendance at local and regional seminars and discussion groups. It is anticipated the successful candidate would gain valuable skills and insight for employment in phylogeny, high-performance computing, life sciences research and/or machine learning in academia or industry.

Further Information:

Project and application details can be found at the website below. You must follow the instructions on the EASTBIO website for your application to be considered.

Deadline for applications: 4 December 2017

This opportunity is only open to UK nationals (or EU students who have been resident in the UK for 3+ years immediately prior to the programme start date) due to restrictions imposed by the funding body.

http://www.eastscotbiodtp.ac.uk/how-apply-0 Best regards,

Daniel

– Dr Daniel Barker Institute of Evolutionary Biology University of Edinburgh Charlotte Auerbach Road The Kings Buildings Edinburgh EH9 3FL United Kingdom

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

BARKER Daniel <Daniel.Barker@ed.ac.uk>

UEdinburgh PlantGenomeDuplication

Genome duplication in parasitic plants: features and consequences

The University of Edinburgh, UK

Supervisors: Mark Blaxter, Institute of Evolutionary Biology.

Alex Twyford, Institute of Evolutionary Biology.

Project background Parasitism is a ubiquitous feature of the natural world, found in every major organismal group, and across every ecosystem. In plants, parasitism is an extremely successful strategy that has evolved independently on at least a dozen occasions. There are over 4000 parasitic species. These parasitic plants include crop pests (Orobanche, Striga) and ecosystem engineers that affect community assembly (Rhinanthus and many hemiparasites). Studies of parasitic plants are essential for improving food security and in understanding ecosystem services, while also providing important insights into the origin of novel evolutionary strategies.

A major goal in parasitic plant biology is to understand the genetic basis of the parasitic habit. Comparative transciptomic analyses identified ~180 genes upregulated in the haustorium (the parasite attachment organ) shared between three divergent taxa (Yang et al., 2015). Many of these genes are the products of gene duplication that has occurred since divergence from non-parasitic relatives. This raises the question of whether genome duplication plays an important role in the origin of plant parasitism.

This project will use genomic tools to investigate the presence and evolutionary fate of duplicate gene copies in parasitic eyebrights (Euphrasia). These generalist parasitic plant species are extremely ecologically diverse, and include a number of recently evolved UK endemics of conservation concern. They are particularly well-suited to genomic analysis because they have small genomes compared to other parasitic plants. The research project will involve:

- assembling the nuclear genome of a diploid Euphrasia species from next generation and single-molecule data - assembling the genome of a tetraploid Euphrasia

- performing gene finding and rich functional annotation using RNA-seq data

- comparing diploid and tetraploid Euphrasia (and related non-parasitic taxa) to identify retained duplicates and explore their functions and evolutionary histories

- using low-coverage and resequencing data from all 19 British native taxa and new lines collected from European populations that may represent independent genome duplication events to explore pattern and process of duplicate evolution across the genus.

These new insights will be essential for understanding the evolution of plant parasitism, and may represent a step towards developing genetic tools for control of devastating crop parasites.

Please see http://e3dtp.geos.ed.ac.uk/projects.html for more details.

TWYFORD Alex <Alex.Twyford@ed.ac.uk>

UExeter EvolutionaryBiol

Dear Students,

I'd like to draw your attention to two PhD studentships, co-supervised by me, which are currently advertised and whose applications concern evolution:

PhD Studentship 1 - mainly experimental: Stefano Pagliara (https://projects.exeter.ac.uk/-biomicrofluidics/) and I are planning to supervise the project 'Developing a Novel and Versatile Approach to Study Populations of Microbes on Surfaces'. The aim is to develop a 'next-generation agar plate' for quantitative experiments. Envision an agar surface on which colonies can be grown for a long time under very well-defined conditions! The device will be used to study evolution of bacteria and bacteriophage over the course of many days. The project, lab-based but with a theory component, is suitable for candidates with different backgrounds, ranging from microbiology to bioengineering. Deadline for applications is 10th January, 2018.

More info: http://www.exeter.ac.uk/studying/funding/award/?id=2918 PhD Studentship 2 - theoretical: Jacopo Bertolotti (http://www.jacopobertolotti.com/) and I are planning to supervise the project 'Random Walks in Inhomogeneous Media and Their Applications in Mesoscopic Physics and Evolutionary Dynamics'. This should be an exciting project with a rather unique opportunity for training across fields. The project is suitable for candidates with a background in the physical sciences. Deadline for applications is 10th January, 2018. More info: http://www.exeter.ac.uk/studying/funding/award/?id=2959 All projects would be based on or be affiliated with the new Living Systems Institute (http://www.exeter.ac.uk/livingsystems/) at the University of Exeter, which I think is a great environment for people who would like to work at the interface of biology, mathematics and the physical sciences. There is ample opportunity to learn by interacting with other groups!

Kind regards,

Wolfram Moebius Research Fellow Living Systems Institute University of Exeter wmoebius@exeter.ac.uk http://moebiuslab.exeter.ac.uk/ "Moebius, Wolfram" <W.Moebius@exeter.ac.uk>

UGeorgia EvolutionaryBiology

The University of Georgia is seeking graduate students to join a large community of ecology and evolutionary biology researchers through the Integrated Life Sciences (ILS) program.

Admission through the ILS program allows new graduate students to explore research across 14 participating Ph.D. graduate programs, including over 50 laboratories with diverse ecology and evolutionary biology interests. Over their first semester in the program, graduate students can choose rotations among laboratories from nearly all life science departments.

The application deadline for Fall 2018 admission to the ILS program is December 1, 2017. To learn more about the ILS program and research at the University of Georgia, please visit the website at:

http://ils.uga.edu

Potential students are encouraged to explore the ecology and evolutionary biology research underway at UGA through the ILS program and to get in contact with faculty whose research they are interested in:

http://evolutionary.genetics.uga.edu/EvoEcol.html Athens, Georgia is a vibrant college town and is consistently ranked one of the top places to live.

Please contact us or any of the faculty in the ILS program with questions.

Michael White Evolution and Ecology ILS Group Representative Assistant Professor of Genetics whitem@uga.edu

Walter Schmidt Graduate Coordinator of the ILS Program Associate Professor of Biochemistry and Molecular Biology wschmidt@uga.edu

"whitem@uga.edu" <whitem@uga.edu>

UGlasgow EvolutionaryParasitology

PhD Studentship: Worms, sheep and environment: integrating ecological perspectives into anthelmintic resistance management.

Where? University of Glasgow and Moredun Research Institute

Supervisory Team: Barbara Mable, Roz Laing (Institute of Biodiversity, Animal Health & Comparative Medicine, University of Glasgow), David Bartley (Moredun Research Institute, Edinburgh)

Funding Source: Natural Environment Research Council Industrial CASE PhD studentship

Project Details: The purpose of this multidisciplinary studentship is to integrate fundamental and applied perspectives on a research problem with direct societal relevance but which also informs key questions in evolutionary ecology and parasitology. The development of resistance to chemical control measures is a key concern in human and veterinary medicine and in agricultural production systems. To increase the efficiency and effectiveness of chemical control measures in the face of resistance, adaptive management approaches have been proposed that customise intervention strategies to the biology and ecology of the particular target pathogens and their hosts. However, these would ideally consider the specific mechanisms of the control agent, genetics of resistance, rates of migration between susceptible and resistant populations, and the strength of selection imposed by the control agents, while taking into account other types of environmental variation, such as the type of pasture that hosts feed on, the community of hosts that share pastures, and how isolated hosts are from new infections. This requires integration of ecology, evolution, genetics/genomics, parasitology, veterinary science, quantitative analyses of "big data", and mathematical modelling, which has not often been achieved.

The overall aim of this studentship is to take a multidisciplinary approach to investigate the nature and consequences of anthelmintic resistance in an important parasite of sheep, the nematode Haemonchus contortus. The project will focus on resistance to ivermectin, which is one of the key anthelmintics for controlling livestock parasites. The student will benefit from support and resources provided by a large UK-wide consortium investigating anthelmintic resistance (https://-bugconsortium.wordpress.com). The project will involve four main elements but there will be flexibility for the student to take the project in different directions: 1) using previously developed crosses between resistant and susceptible parasites to test the genetic basis of resistance; 2) examining 'real life' fitness (e.g. ability to establish infection, competition, mating success) and the influence of mating preferences, by genotyping the adults and progeny resulting from mixed infections; 3) testing the segregation of resistance markers in previously established lines of a free-living nematode model system (Caenorhabditis remanei) that was selected for ivermectin resistance to test whether there is a common basis of resistance and similar phenotypic consequences; and 4) using deep sequencing approaches to genotype individuals from agricultural environments that differ in resistance management practices to test predictions about expected rates of resistance evolution.

The student will spend at least 3 months per year with the Industrial CASE partner (Moredun Scientific), to receive specific training in the requirements of the animal health industry involved in the development and registration of veterinary medicines. The company has a remit to promote animal health and welfare through research and education, with a particular focus on therapeutics and vaccines.

Funding Details - Research Councils UK standard stipend (14,764 pa + full fees). This is one of three NERC CASE studentships to start October 2018 at Glasgow

Duration - 4 years

Who is eligible? The candidate must have been ordinarily resident in the UK throughout the 3-year period preceding the date of application for an award, not wholly or mainly for the purposes of full time education. A 2:1 (B) or equivalent is required at undergraduate level. Students who have not met this but have taken a masters-level course could be considered. We particularly welcome applications from veterinarians interested in pursuing research but candidates with parasitological, genetics or evolutionary backgrounds would also be appropriate.

How to apply - Full CV + contact details of at least 2 referees. Cover letter indicating motives and qualifications for undertaking the project

Who to send applications to - Please initially send a CV and cover letter to Barbara Mable (Barbara.mable@glasgow.ac.uk). Eligible applicants will be asked to submit a formal application to the University.

Deadline: Initial shortlisting for applications received by Jan. 8 but applications will be reviewed until the position is filled.

Selected Publications by the Supervisory Team:

— / —

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

---

UGuelph PDF PhD 2MSc FishGenetics

Positions are available for one postdoc and two MSc and one Ph.D. positions to investigate the foraging ecology and genetics of two cleaner fish species that forage on parasitic lice attached to Atlantic salmon.

The postdoctoral position begins in May 2018 and is funded for two years. The two MSc. positions begin in January or May 2018 and are funded for two years. The Ph.D. position begins in January or May 2018 and is funded for four years.

The project is led by Professor Elizabeth Boulding (Integrative Biology, U. Guelph) with co-investigator Professor Emeritus Larry Schaeffer (Animal Biosciences, U. Guelph). Our industrial collaborators are led by Dr. K.P. Ang of Kelly Cove Salmon Ltd. (KCS) a division of Cooke Aquaculture Inc. (CAI). They include Dr. J.A.K. Elliott, Dr. M. Herlin, F. Powell from KCS, and Dr. T. M. Jonassen from Akvaplan-Niva, Norway.

The objective of this NSERC Strategic Project is to provide a sustainable and pedigreed source of cleaner fish to reduce lice densities found on Atlantic salmon living in marine sea cages in Eastern Canada. This project will develop highly-repeatable methods of measuring the functional responses of two proven cleaner fishes: the lumpfish (Cyclopterus lumpus) and the cunner (Tautogolabrus adspersus). An outcome of this project will be a breeding program for lice-eating performance by lumpfish and by cunners at two existing hatcheries operated by CAI. It will also deepen our understanding of the reciprocal evolution of early mutualisms between facultative cleaner fishes and their clients.

MSc. student position 1 (behavioural ecology of fishes) will help develop methods of predicting lice-cleaning performance of cunners in marine sea cages from observations of their performance in indoor tanks. This will involve comparing condition-dependent performance among different families of cunners from different geographical regions that have been reared in a common environment. Cunner lice-removal performance in marine sea cages will be assessed using video-footage and by examining their stomach contents.

MSc student position 2 (molecular ecology/bioinformatics) will help develop DNA markers to estimate pedigrees for cleaner fish families spawned in the hatcheries. This position will involve high throughput DNA extraction, and bioinformatics using a high-performance computer cluster. This research will identify DNA markers that show larger than expected amounts of genetic divergence among cunner populations and among lumpfish populations from different geographical areas.

Ph.D. student (applied evolution/behavioural ecology of fishes) will help develop methods of predicting lice-cleaning performance of lumpfish in marine sea cages from their performance in tanks. This will involve comparing condition-dependent performance among different families of lumpfish from different geographical regions that have been reared in a common environment. Lumpfish lice-removal performance in marine sea cages will be assessed using video-footage and by examining their stomach contents. Relationships between traditional and DNA barcoding of stomach contents will be compared for lumpfish and for cunners and used to develop non-lethal methods of monitoring the prevalence of lice in their diets. This may lead to a deeper understanding of environmental factors affecting facultative lice-cleaning performance in the field.

Postdoctoral fellow (with experience in fish applied evolution/applied ethology/behavioural ecology) will help the graduate students develop repeatable methods of measuring posing and other co-operative behaviors by client fish that facilitate parasite-removal by cleaner fishes. Their own project will involve assisting with salmon lice tank challenges of pedigreed Atlantic salmon and measuring posing rates near cleaner fish refuges. It will also involve video-assisted field observations of client behavior near cleaner-fish refuges within marine sea cages. The postdoc will be trained to estimate breeding values for lice-cleaning performance by the cleaner fish and for posing performance by their Atlantic salmon clients. Creating a breeding nucleus containing only cleaner fish and client fish with high breeding values for performance traits would be predicted to increase the reciprocal co-evolution of this mutualism in marine sea cages.

Please apply for the postdoctoral, Ph.D. or MSc. positions by sending an email to Dr. Boulding (boulding@uoguelph.ca) with attachments containing: 1) your curriculum vitae/resume, 2) an electronic transcript of all your university grades, 3) a list of referees with their email addresses and telephone numbers, 4) pdf reprints of your scientific publications (if any), and 5) a statement that you are willing to travel from Guelph to New Brunswick and Newfoundland for fieldwork as needed. She will then request references from the referees of qualified applicants.

Applicants for a M.Sc. or Ph.D. position need to be eligible for

— / —

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

---

UHouston EcologyEvolution

GRADUATE OPPORTUNITIES IN ECOLOGY AND EVOLUTIONARY BIOLOGY

The Department of Biology and Biochemistry at the University of Houston (UH) welcomes applications for its graduate program in Ecology & Evolutionary Biology for Fall 2018. The following faculty in the areas of Ecology and Evolutionary Biology have opportunities available for their labs:

Alex Stewart (alex.stewart@ucl.ac.uk): Mathematical biology Blaine Cole (bcole@uh.edu): Evolution and social behavior Dan Graur (dgraur@uh.edu): Molecular evolutionary bioinformatics Diane Wiernasz (dwiernasz@uh.edu): Sexual selection Erin Kelleher (eskelleher@uh.edu): Evolutionary genetics and genomics George Fox (fox@uh.edu): Experimental evolution and origin of life Kerri Crawford (kmcrawford3@uh.edu): Community ecology Rebecca Zufall (rzufall@uh.edu): Evolutionary genetics Ricardo Azevedo (razevedo@uh.edu): Evolutionary genetics Rich Meisel (rpmeisel@uh.edu): Evolutionary genetics and genomics Steve Pennings (spennings@uh.edu): Community ecology Tony Frankino (frankino@uh.edu): Evolution of complex traits

If you are interested, you should look at the relevant faculty members' web sites and then contact them directly for more information:

http://www.uh.edu/nsm/biology-biochemistry/people/faculty/faculty-alpha/ For more information regarding the Evolutionary Biology and Ecology graduate program at UH see:

http://www.bchs.uh.edu/graduate/prospective-students/ http://www.uh.edu/graduate-school/prospective-students/how-to-apply/ If you have any questions regarding the application process, please contact:

Ms. Rosezelia Jackson (biograd@central.uh.edu)

The deadline for application of prospective students is February 1st, 2018, but students are encouraged to apply as early as possible.

Ricardo

Ricardo B. R. Azevedo, PhD Associate Professor Associate Chair for Graduate Affairs Dept. Biology & Biochemistry University of Houston 369 Science & Research 2 Houston, TX 77204-5001 Tel: 713-743 4149 Fax: 713-743 2636 Email: razevedo@uh.edu

"razevedo@Central.UH.EDU"
<razevedo@Central.UH.EDU>

UIllinois SymbiosisEvolution

The Heath lab at the University of Illinois at Urbana-Champaign is looking for motivated graduate students interested in the evolution and genetics of plant-microbe symbioses. The Heath lab uses a variety of approaches (fieldwork, sequencing, quantitative genetics) in a number of plant and microbial systems to answer fundamental questions about how mutualisms evolve in nature, the molecular basis of symbiosis evolution, and plant-microbiome interactions. Find out more about what we do at our website (http://www.life.illinois.edu/heath/Heath_Lab/HOME.html). Students can apply through either the Program in Ecology, Evolution and Conservation (http://sib.illinois.edu/peec/) or the Department of Plant Biology grad program (http://www.life.illinois.edu/plantbio/graduateAdmissions.htm). Applications are due by December 15, 2017 for full consideration for graduate college fellowships.

Champaign-Urbana is a great micro-urban community located midway between three major cities (Chicago, St. Louis, Indianapolis), with great food and drink, abundant culture, and affordable cost of living.

University of Illinois and the Heath lab are committed to a diverse workplace, and prospective students of all races, genders, and sexual orientations are encouraged to apply.

Email Katy Heath (kheath@life.illinois.edu) for more information.

Katy Heath <kheath@life.illinois.edu>

UJyvaskyla EvolChemCommTigerMoths

2 DOCTORAL STUDENTS-EVOLUTION OF CHEMICAL COMMUNICATION IN TIGER MOTHS

The University of Jyväskylä is a nationally and internationally significant research university and an expert on education that focuses on human and natural sciences. The University is Finland's leading expert in teacher education and adult education, as well as the major exporter of education. The Faculty of Sport and Health Sciences is the only one in the country. The University of Jyväskylä is known for its dynamic operating culture and strong commitment to social responsibility.

We are currently seeking to recruit 2 Doctoral Students beginning January 1st 2018 or as agreed, but not later than April 15th 2018, contract length maximum of four years

The Doctoral Students will work within the project "Chemical communication in wood tiger moths" under the topics: "Following the first tracks of speciation: divergence of wood tiger moth populations in the Caucasus, Western Asia" and "Sexual communication and mate preference via pheromones". The student will join Prof. Johanna Mappes' group but the work will be conducted in collaboration with Prof. Astrid Groot (U. Amsterdam). The project broadly explores the drivers of differentiation between wood tiger moths in the Caucasus region and their European counterparts. One student will focus on the role of chemical communication (pheromones) in this ongoing divergence process. The second one will focus on understanding sexual behavior, and explore male and female choice via pheromones, the genetic basis of intraspecific variation in sexual communication, and what are its possible consequences at the population level.

The tasks of a Doctoral Student focus on research concerning doctoral thesis.

The duties, qualification requirements and language skills of doctoral student are stipulated by the University of Jyväskylä Regulations and language skills guidelines < https://www.jyu.fi/en/workwithus/qualifications >. The selected person is required to have a good command of English language.

The ideal candidate will have basic skills in chemical ecology methods, and a good knowledge of evolutionary biology/ecology. Knowledge on pheromone communication would be an asset. He/She is expected to participate in fieldwork, experimental work, behavioural and electrophysiological assays, as well as chemical analyses. We are looking for two motivated, broad-thinking students interested in pursuing question-driven research.

Doctoral Student must have a Master's degree and permission for post-graduate studies in the University of Jyväskylä. If the applicant does not have permission for post-graduate studies in the University of Jyväskylä, it must be applied with a separate application procedure from the proper faculty.

Doctoral Students' job-specific salary component is based on the job demands level 1-4 according to the salary system concerning teaching and research personnel at universities (1.808,42 euro /month - 2.475,31 euro /month). In addition, a personal performance-based salary component amounting to the maximum of 46,3% of the job-specific salary component is also paid.

A trial period of four months will be used when the position is first filled.

For additional information please contact Dr. Bibiana Rojas (bibiana.rojas@jyu.fi) or Prof. Johanna Mappes (johanna.mappes@jyu.fi).

The application (in English) should include:

1) A 1-page cover letter, outlining the motivation for applying for the doctoral student position 2) Contact details of 2 academics who can provide reference letters 3) CV, composed according to good scientific practice and considering when possible the template for researcherÂs curriculum vitae by The Finnish Advisory Board on Research Integrity < http://www.tenk.fi/en > 4) Copy of degree certificates

Please submit your application at latest on December 8th, 2017 using the online application form: https://rekry.saima.fi/certiahome/application_edit_welcome.html?field_id=0&job_name=2+Doctoral+Students%2C+Biological+and+Environmental+Science&
4435&jc=12&lang=en&place_id=23&did=5600 Bibiana Rojas Postdoctoral Researcher Centre of Excellence in Biological Interactions Department of Biology and Environmental Sciences University of Jyväskylä P.O. Box 35 FI-40014 Finland

http://bibianarojas.co Tel: +358 (0) 408054622

"Rojas Zuluaga, Bibiana" <bibiana.rojas@jyu.fi>

UKansas Biodiversity

The Short Lab in the Department of Ecology and Evolutionary Biology at the University of Kansas is seeking a motivated PhD student to join our research group in the Fall of 2018.

Our lab uses a variety of approaches from morphology and fieldwork to next-generation phylogenomics to address questions related to the systematics, diversity, and evolution of aquatic beetles. The specific research project is flexible depending on the interests of the student. Examples include (not an exclusive list): - Patterns of diversification in the Neotropics - Exploring patterns of habitat shifting or biogeography using phylogenies built with molecular or phylogenomic data - Illuminating diverse lineages using integrative taxonomy

KU has a vibrant, diverse program in evolutionary biology, with a particular strength in specimen-based research. Our Biodiversity Institute has 15 faculty-curators that study everything from birds to fossil plants.

Interested students should contact Andrew Short (aezshort@ku.edu), including a current CV and why our research group might be a good fit. Funding in our department for PhD students is guaranteed for 5 years. More information can be found at shortlab.org. Application information at requirements can be found on our department website, here: https://eeb.ku.edu/prospective-students Deadline for applications is December 1.

"aezshort@ku.edu" <aezshort@ku.edu>

UMississippi EvolutionSpeciesInteractions

PhD/MS positions in evolution of species interactions The Zee Lab at the University of Mississippi is seeking enthusiastic and motivated graduate students (Ph.D. and M.S.) with interests in community ecology and evolutionary biology to begin Fall 2018. Using a combination of laboratory experimental ecology/evolution with microbes and theoretical modeling approaches, we are interested in understanding how historical and contemporary evolutionary forces influence outcomes of species interactions in ecological communities. We experimentally evolve multi-trophic communities of the model bacterium E. coli, the social bacterium Myxococcus xanthus, and the roundworm C. elegans. Students will be encouraged to develop and pursue questions centered on their own research interests and strengths.

Graduate students will be fully supported through teaching and research asssistantships with a competitive stipend, tuition waivers, and benefits. Women and underrepresented minorities are encouraged to apply.

The University of Mississippi is a Carnegie R1 institution undergoing an exciting phase of growth. The university is located in Oxford, a vibrant and idyllic college town in northern Mississippi, about 1 hour south of Memphis, TN. More on the Department of Biology: https://biology.olemiss.edu/. More on Oxford, MS: https://biology.olemiss.edu/why-oxford/ Interested students are encouraged to contact Peter Zee (zee at olemiss dot edu) directly with a description of research interests and experiences.

Peter C. Zee Assistant Professor Department of Biology University of Mississippi peterzee.wordpress.com – Peter C. Zee Assistant Professor 406 Shoemaker Hall Department of Biology University of Mississippi

Peter Zee <zee@olemiss.edu>

UMontana PlantEvolutionaryGenomics

The Fishman Lab (http://www.fishmanlab.org) at the University of Montana (UM) is seeking graduate student applicants (PhD or MS) interested in using genetic/genomic approaches to understand plant evolution. We study variation at the individual, population, and species levels, primarily using Mimulus (monkeyflowers) as a model system.

Students interested in the molecular basis of adaptation to extreme environments are particularly encouraged to apply, as we have 3+ years of RA support associated with NSF-funded projects on yellow monkeyflower adaptation in thermal areas of Yellowstone National Park. Other research topics in the Fishman lab include the genetic basis of phenological, mating system, and life history traits, the evolution of hybrid incompatibilities, the role of chromosomal rearrangements in speciation, and the mechanisms and consequences of selfish evolution by centromeres and mitochondria. Outstanding applicants with interests in any area of empirical plant evolutionary genetics are welcome.

The Fishman Lab is part of a strong and highly interactive group of evolutionary genomics labs at UM, and is a core lab in NSF-funded collaborative network focused on the genomics of adaptation (http://www.unveilnetwork.org). PhD applicants from backgrounds traditionally under-represented in STEM fields are eligible for UNVEIL graduate fellowships < https://www.unveilnetwork.org/opportunities/ >, and all evolutionary genomics students are eligible for cross-institutional travel/training support. The Organismal Biology, Ecology & Evolution Program < http://hs.umt.edu/dbs/grad-programs/OBEE/default.php > at UM provides excellent training opportunities for students and unparalleled access to natural areas for both research and recreation. The University of Montana-Missoula is the state university system's liberal arts campus, fostering a rich cultural community, and Missoula regularly appears on best-places-to-live lists.

The official OBEE program application deadline is Dec. 1st (somewhat flexible), but please contact Lila (lila.fishman@mso.umt.edu) directly first if interested in applying.

Lila Fishman Associate Professor Organismal Biology, Ecology & Evolution Program Division of Biological Sciences University of Montana Missoula, MT 59812

Lila Fishman <lila.fishman@mso.umt.edu>

UNewOrleans ComputerSimulations

Graduate positions (M.Sc. and Ph.D.) are available in the Atallah Lab (https://sites.google.com/view/-atallahlab) in the Biological Sciences Department at the University of New Orleans (UNO). We are currently looking for students interested in working on one of the following two projects: 1) Simulating the role of transposable elements in evolution and human disease: In recent years, evidence has accumulated that transposable elements (TEs) play important roles in both evolutionary processes (such as changes in gene regulation) and the progression of diseases such as cancer. We are developing computer simulations of the activity of TEs in both the soma and the germline. Students interested in this project should be familiar with Shell scripting and computer programming.

2) The evolution of the early embryonic transcriptome in Drosophila species: Embryonic transcriptomes from diverse species can be readily compared due to similarities in embryonic stages. We are analyzing transcriptomes from different stages of early embryogenesis in Drosophila species. Students interested in this project should be prepared for molecular lab work, bioinformatic analysis and possible field collection of samples.

Interested students should send an email to jatallah@uno.edu. Please include a brief description of your background (or a CV or resume), and mention which project you're interested in and why you're excited about this project.

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

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

UNotreDame EcologicalSpeciation

The Jeff Feder lab in the Department of Biological Sciences at the University of Notre Dame, in Notre Dame, Indiana has graduate student positions available for studying the genomics of ecological adaptation and speciation in insects. Our research has both laboratory and field components, spanning the realms of ecology and evolution from experimental manipulation studies to high throughput DNA sequencing, focused on discerning the adaptive basis of speciation and its genomic underpinnings. Ideally, we seek individuals with experience in bioinformatics and candidates with past research experience (e.g., in a master's program), for the position. However, all highly motivated students are encouraged to apply. The Department provides graduate students with generous stipend support and benefits. To apply please e-mail a CV, personal statement of interest, and contact information for three references to feder.2@nd.edu.

For additional information about our lab and graduate program, please see http://federlab.nd.edu/- and http://biology.nd.edu/graduate/graduate-studies-overview/, respectively.

– Meredith M. Doellman PhD Candidate, Feder Lab Department of Biological Sciences Arthur J. Schmitt Fellow University of Notre Dame

"mdoellma@nd.edu" <mdoellma@nd.edu>

UNottingham EvolutionGeneticsSnails

Two funded PhD projects in evolution/genetics/genomics/development of snails, Dec 8th deadline

Twitter link to advert if anyone seeing this wishes to advertise more widely: https://twitter.com/-angus_davison/status/927856306014351360 The Davison lab at the University of Nottingham is seeking enthusiastic and well-qualified students to apply for two PhD positions, both funded by the BBSRC DTP.—Full details here: http://angusdavison.org/index.php/-

139-newphdpositions2017. Apply—here: http://-www.nottingham.ac.uk/bbdtp/how-to-apply-to-the-dtp.aspx . I would strongly encourage good candidates to—email me—(angus.davison@nottingham.ac.uk) if you have any queries prior to the application.

In previous research, the Davison-lab led an international team dedicated to finding the gene that determines mirror image development ("chirality") in the pond snail,—Lymnaea stagnalis. More generally, we are using molluscan genomics, with projects dedicated to finding evolutionary interesting genes, whether chiral variation in Japanese—Euhadra—or the colour polymorphism / supergene of—Cepaea. Field work and foreign lab work is always an option - recent students spent 5 months in a German lab or undertook field work in Japan. The lab also has a strong background in—science communication, with a recent science-related story from the lab reaching an estimated 1.9 billion people (!)

Project #1: "The evolution and development of left-right asymmetry in snails"

Project supervisors: Dr Angus Davison and Dr William Brown, University of Nottingham, UK.

While invariant left/right asymmetry appears to be the rule in nearly all animals, until recently it has not been clear if the path to asymmetry is conserved. In recent research we identified the one in a billion base pair change that determines mirror image development ("chirality") in the pond snail. As we also showed that the same gene is similarly involved in setting up asymmetry in the frog, then our work that began in snails ultimately revealed one of the earliest common symmetry-breaking steps across the whole of the Bilateria. The next stage is to 'unravel' symmetry breaking at the molecular and cellular level, in particular to find the set of genes that first establish asymmetry. In this exciting and fast-moving, the student will seek to understand the mechanics of the very earliest symmetry-breaking steps using Lymnaea stagnalis pond snails, or another species. Most likely, this will involve a range of techniques, from micromanipulation to genomics/bioinformatics, and possibly fieldwork - with the balance determined by the interests of the student.

The project is competitively funded through the 'Molecules, Cells and Organisms' stream of the Nottingham—BBSRC DTP.—http://-www.nottingham.ac.uk/bbdtp/index.aspx Applicants should have, or expect to get, a First Class or Upper Second degree or equivalent in a relevant subject. Further experience, including a Masters degree, is likely to be advantageous. Applications are open to UK + EU residents (EU students will be considered and may be eligible for full funding). This project is also advertised—here http://www.nottingham.ac.uk/bbdtp/available-projects/moleculescellsandorganisms.aspx and here on Findaphd. https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=75229 —

Project #2: "Genetic approaches to understanding molluscan crop pests"

Project supervisors: Dr Angus Davison, Dr Chris Wade and Dr Matt Loose, University of Nottingham, UK.

Snails and slugs cause worldwide problems, both in terms of direct damage to crops, and as intermediate vectors for diseases of farm animals. Yet, they are difficult to identify and we have little idea of what influences their distributions, hindering appropriate control measures. Genetic techniques offer a potential solution in that they can be used to understand gene-flow, the relationship and taxonomy of different species, and, ultimately, the genes involved in enabling adaptation to human-affected environments. However, molluscs in general are relatively lacking in genomic resources, partly because they generally have large genomes, but also because there is no single model mollusc to drive research forward. In this project, the student will apply population genetic, phylogenetic and genomic methods (e.g. RAD-seq) to a tropical snail species, with a view to understanding the adaptations

— / —

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 EvolutionEpigenetics

PhD in Epigenetic Theory at University of Otago, Dunedin, NEW ZEALAND

A PhD position is available within the Department of Zoology at the University of Otago in Dunedin, New Zealand. This position in the laboratory of Professor Hamish G. Spencer is funded by the Marsden Fund of the Royal Society of New Zealand. A scholarship covering fees plus a tax-free stipend of NZ$27,500 per year is available for three years.

The project is part of a larger project entitled "Epigenetics and Evolutionary Theory." Just as natural populations exhibit genetic variation, so too do they harbour epigenetic variation, some of which is transmitted from one generation to the next. This project asks how we can explain this transgenerationally inherited epigenetic variation in natural populations and what might be the consequences for evolution. The candidate will construct and analyse novel mathematical models to investigate these matters, validating these models with data from real examples, and using the models to make novel predictions about the properties of epigenetic variation in nature.

The successful candidate will have a strong interest in applying quantitative methods in biology. They will have a degree (e.g., BSc(Hons), MSc) in biology and/or mathematics (or a related field) that included a research component (e.g., a dissertation or a thesis).

Our research group and the wider Department includes world-class research staff, facilities and strong international collaborations, offering excellent opportunities to gain a variety of highly pertinent research and technical skills.

Dunedin, in the South Island of New Zealand, is a great place to live, with a vibrant music culture. It regards itself as the "Wildlife Capital of New Zealand," with breeding albatrosses, penguins, fur seals and sea lions all found within the city limits. For details about living in Dunedin see http://www.otago.ac.nz/humanresources/-join-otago/lifestyle-and-culture/dunedin/index.html As part of your application, please submit a CV, a transcript of your university grades, a personal statement of suitability and the names and contact details of two referees to Professor Hamish Spencer (hamish.spencer@otago.ac.nz).

"hamish.spencer@otago.ac.nz"
<hamish.spencer@otago.ac.nz>

UppsalaU ButterflyEvolutionaryGenomics

PhD-position in butterfly evolutionary genomics at Uppsala University

A 4-year PhD-position in butterfly genomics is available in the research group of Dr. Niclas Backstrom at the Department of Evolutionary Biology in Uppsala, Sweden. Starting date in January 2018 or as agreed upon. The successful applicant will work with population genomic analysis using whole-genome re-sequencing data from several populations and species, gene expression analysis and management of butterfly populations for crossing and linkage mapping experiments.

Project description: Getting detailed understanding about proximate and ultimate causes to formation of reproductive isolation between diverging lineages is one of the major challenges in evolutionary biology. In the group, we use birds and butterflies as model systems and combine experimental work with bioinformatic analyses to investigate the genetic underpinnings of barriers to gene flow and traits that may play a role in species recognition, mate choice and local adaptation. The project will focus on the importance of chromosome rearrangements, recombination and lineage specific adaptation in driving genomic divergence between closely related cryptic butterfly species. Depending on the personal interests and qualifications of the candidate, the project can also be extended to address other fundamental questions in evolutionary genetics. For any further questions, please visit the lab website (http://www.ieg.uu.se/evolutionary-biology/backstrom/) or contact Niclas Backstrim (email: niclas.backstrom[at]ebc.uu.se).

The Evolutionary Biology Centre (http://-www.ebc.uu.se/?languageId=1) is one of the world's leading research institutions in evolutionary biology. It is part of Uppsala University, an international research university with 40,000 students and 7,000 employees which has been ranked very high among all European Universities in the subject of evolutionary biology. Our lab is part of the Program of Evolutionary Biology (Department of Ecology and Genetics, www.ieg.uu.se.) that excels in many aspects of genetics and evolution and offers an inspiring international atmosphere. There are ample opportunities for interaction with PhD-students, PostDocs and researchers working on related topics. We are tightly linked to the Science for Life Laboratory (https://www.scilifelab.se/) and have access to advanced laboratory infrastructure, high performance computing resources and bioinformatics support.

If you are enthusiastic about evolutionary biology, have a good understanding of population genetics and evolution theory, and/or are skilled in bioinformatics you are most welcome to apply for the position. To apply you must hold a master of science (or your national equivalent) in Biology or a related field. Bioinformatic skills will be necessary to carry out the projects. Candidates must be able to express themselves fluently in spoken as well as written English.

Position: The graduate program covers four years of full-time study. The position can be combined with teaching or other duties at the department (maximum 20%), which prolongs the employment with the corresponding time. The salary will be set according to local agreements. More information about postgraduate studies at Uppsala University is available at http://www.teknat.uu.se/education/postgraduate/. Rules governing PhD candidates are set out in the Higher Education Ordinance Chapter 5, 1-7 and in Uppsala university's rules and guidelines http://regler.uu.se/search/?hits=30&languageId=1&search-language_en=English Application: The application should include (1) A cover letter describing your research interests, relevant previous experience and your specific motivation for the position, (2) A short summary of your Master's (or comparable) studies, (3) A CV including potential previous publications and contact details of two scientific professionals, (4) Attested copies of your academic degree(s). The application should be written in English.

Uppsala University aims for gender balance and diversity in all activities in order to achieve a higher quality at all levels of the organization. We therefore welcome applicants of any gender and with different birth background, functionality and life experience.

For further information about the position please contact: Niclas Backstrom, niclas.backstrom[at]ebc.uu.se, +46-18-471 6415.

You are welcome to submit your application no later than December 10, 2017, UFV-PA 2017/3977. Formal applications should be made using our

— / —

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

---

UppsalaU EvolutionaryGeneticsSexualDimorphism

PhD position available to study evolutionary genetics of sexual dimorphism

This is a fully funded 4-year position in the Evolutionary Biology section at the Department of Ecology and Genetics, Uppsala University, Sweden. The PhD program is in evolutionary genetics. The Department is highly international, with evolutionary biology research currently ranked as 7th best in the world (by CWUR). Our research spans from evolutionary ecology and genetics to studies of ecosystems. For more information, please see www.ieg.uu.se . The advertised PhD project seeks answers to one of the fundamental questions in evolutionary biology: how does a single genome produce sexually dimorphic phenotypes? Sexual dimorphism, from morphology and physiology to behaviors, is nearly ubiquitous in nature. Yet, genetic correlations due to the largely shared genome between the sexes impose constraint to independent trait evolution in the sexes. The PhD candidate will investigate fitness consequences and the genetic architecture of evolution of genetic correlations between the sexes, using artificial selection, phenotypic assaying and modern RNA and DNA sequencing technologies. The work will be carried out with Callosobruchus maculatus seed beetles, a highly amenable model system in sexual selection and conflict research. The results from this research program will be important for understanding how genetics can constrain and resolve adaptive evolution in the sexes and thus shape the most notable form of variation within species, i.e. sexual dimorphism. Beyond basic research, understanding the dynamics of sex-specific genetic architecture is important within the context of biomedicine and sex differences in disease.

The lead-supervisor, Ass. Prof. Elina Immonen, focuses on studying sex-specific selection and the genetics of sexual dimorphism, using experimental, genetic and genomic techniques (https://immonenelina.wordpress.com, http://www.ieg.uu.se/evolutionary-biology/immonen/).

A co-supervisor to the candidate will be Prof. Hans Ellegren, whose group studies many key questions in evolutionary biology including the evolution of genetic diversity, using genomic and bioinformatics approaches (http://www.ieg.uu.se/evolutionary-biology/ellegren/).

To be eligible for the PhD-student position the applicant must hold a master degree (or equivalent) in evolutionary biology, genetics, genomics, ecology, behavioral ecology, or other relevant field. The candidate must also be fluent in both spoken and written English.

Experience in conducting laboratory experiments in insects, molecular laboratory and bioinformatics skills, and in-depth knowledge in sexual selection theories are desirable.

We are looking for a highly motivated student, and in addition to scientific skills within the subject area, great emphasis will be placed on personal skills such as communication and collaboration skills, ability to work independently, scientific maturity and creativity.

Please see the full description, list of application requirements and how to apply here: http://www.uu.se/en/about-uu/join-us/details/?positionId=175737 You are welcome to submit your application no later than 15th December 2017.

The starting date for the PhD student is already 1st of February 2018, or soon thereafter.

elina.immonen@ebc.uu.se

Elina Immonen <elina.immonen@ebc.uu.se>

USouthernMississippi MarineInvertFitness

M.S. and Ph.D. STUDENT POSITIONS Marine Invertebrate Behavior, Ecophysiology, and Fisheries Division of Coastal Sciences, The University of Southern Mississippi Ocean Springs, MS

We seek highly motivated students to fill two graduate student positions in the laboratory of Dr. Zachary Darnell at The University of Southern Mississippi's Gulf Coast Research Laboratory in Ocean Springs, MS. Both positions will begin in August 2018. Students selected for these positions will pursue graduate degrees in the Division of Coastal Sciences and will be supported on research assistantships (details below). Both the M.S. and Ph.D. assistantship will include substantial flexibility in research topic, within the general realms of marine invertebrate behavior, ecophysiology, and fisheries.

Our current research focuses on environmental constaints on behavior, performance, and fitness of marine and estuarine invertebrates, and the strategies used by organisms to overcome these constraints. More specifically, this encompasses (1) plastic and adaptive behavioral and physiological responses to environmental change and environmental stress, (2) environmental effects on life histories, distributions, and population dynamics, and (3) anthropogenic impacts on organism-environment interactions. This research also has a strong applied focus, using ecophysiological approaches to address fisheries management and conservation questions. For more information on current research areas, visit http://sites.usm.edu/zdarnell/ . Details on each assistantship are below:

M.S. ASSISTANTSHIP: The M.S. assistantship includes a stipend of $22,800 per year, increasing to $23,400 per year following comprehensive exams. A tuition waiver is also included. Required qualifications include a minimum GPA of 3.5 on all undergraduate coursework and GRE scores exceeding the 50th percentile. Prior research experience is preferred.

Ph.D. ASSISTANTSHIP: The Ph.D. assistantship includes a stipend of $23,400 per year, increasing to $24,000 per year following comprehensive exams. A tuition waiver is also included. Required qualifications include a minimum GPA of 3.5 on all undergraduate or graduate (if entering with a M.S.) coursework and GRE scores exceeding the 50th percentile. Prior research experience is preferred. Priority will be given to applicants with an M.S. degree, but exceptional applicants at the B.S. level will also be considered.

The Division of Coastal Sciences is a research and graduate education unit within the School of Ocean Science and Technology, offering programs leading to the Doctor of Philosophy and Master of Science degrees. The Division is located at Gulf Coast Research Laboratory (Ocean Springs, MS), a marine laboratory featuring comprehensive basic and applied research programs in coastal and marine biological sciences (http://-gcrl.usm.edu). Research program support includes state-of-the-art laboratory facilities and instrumentation; a fleet of small and large research vessels, including the R/V Point Sur; the GCRL Museum collection; the Center for Fisheries Research and Development; NSF I/UCRC Science Center for Marine Fisheries, and aquaculture facilities including the Thad Cochran Marine Aquaculture Center. Additional information on graduate programs in the Division of Coastal Sciences can be found here: http://gcrl.usm.edu/coastal_sciences/-index.php . Interested students should contact Dr. Zachary Darnell (zachary.darnell@usm.edu). Please include a copy of your CV (including GRE scores), unofficial undergraduate and graduate transcripts, and contact information for three professional references. Review of applicants will begin immediately. For full consideration, submit all materials prior to January 2, 2018.

Zachary Darnell <zachary.darnell@usm.edu>

UStAndrews ComputationalBiology

PhD in Probabilistic Modelling of Evolutionary Trajectories

Evolutionary biologists have long been interested in the question how populations adapt to changing environments. In experimental evolution studies replicate populations are allowed to adapt to novel but controlled laboratory environments. The evolved populations are subjected to whole genome re-sequencing (Evolve and Re-sequencing (ER) approach). These new experiments not only use next generation sequencing (NGS) to measure genomic features at one time point but also monitor them changing over time with the aim of detecting significant frequency changes that indicate selection pressures. Previous attempts at analysing data from experimental evolution studies have been limited as they could not simultaneously include data at intermediate time points, replicate experiments and sources of uncertainty specific to NGS such as sequencing depth. In my group, we have developed a Gaussian Process (GP) approach to model the time-series data from evolutionary trajectories measured during experimental evolution studies (Topa et al., 2015) in Drosophila species. In this project, we plan to combine the GP approach with population genetic models to measure parameters such as selection coefficients and the population size. This will allow us to improve the modelling evolutionary trajectories and the understanding of evolutionary processes.

The PhD topic will also be open to modelling evolutionary trajectories for longer time-scales such populations from different Drosophila species, or the development of phylogenetic methods.

Candidates will be expected to have a strong interest in applying quantitative methods and modelling to Biology. They will have a degree in Bioinformatics, Mathematics, Physics, Statistics, Computer Science or a related field. Prior experience with either population genetics or comparative genomics is a benefit. Preferably the candidate will have experience in programming language such as C, C++, Java and a scripting language such as Python or Perl.

For more details see

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=83293 Deadline is the 3rd December 2014.

Please send informal inquires to Carolin Kosiol ck202@st-andrews.ac.at

Carolin Kosiol Lecturer in Bioinformatics Centre for Biological Diversity School of Biology University of St Andrews St Andrews Fife KY16 9TH United Kingdom

Carolin Kosiol <ck202@st-andrews.ac.uk>

USydney VirusEvolution

Funding Body: University of Sydney

Title: Postgraduate Research Scholarship in the Ecology and Evolution of Viruses

Research Areas: Sciences & Engineering

Type Postgraduate Research

Description: A number of full-time postgraduate PhD studentships will be provided by the University of Sydney associated with an ARC Australian Laureate Fellowship recently awarded to Professor Edward C. Holmes.

The Project will employ novel genomic analyses of viruses from Australian fauna to resolve major questions in RNA virus ecology and evolution. This project will also reveal the basic processes that shape the virosphere, determine how viruses jump species to emerge and cause disease in new hosts, and how viruses evolve new levels of virulence. These aims will be achieved by studying meta-transcriptomic data from diverse animal phyla, from prokaryotes and basal eukaryotes, from iconic native mammalian species and their major invasive pests. New bioinformatics tools will be developed to identify and analyse highly divergent genome sequences.

This research will provide a new understanding of how viruses evolve and contribute to global ecosystems.

Eligibility: Applicants must: have an unconditional offer of admission for full-time studies in a PhD within the Faculty of Science at the University of Sydney, and be willing to undertake research in the field of ecology and the evolution of viruses. hold Honours degree (First Class or Second Class upper) or a Master's degree in a related field with a substantial research component (or equivalent). have a background in biological science.

Selection Criteria: The successful applicant will be awarded the Scholarship on the basis of:

academic merit, area of study and research proposal, curriculum vitae, research performance indicators, feedback from two academic references, and a personal statement which demonstrates their interest in the field of research, and background in biological science. Demonstrated experience in evolutionary biology, genomics and/or virology is preferred.

Applicants may be requested to attend a phone interview.

Amount awarded: For a successful domestic student (Australian citizen, Australian resident or New Zealand citizen) the Scholarship will provide an annual stipend allowance of $26,682 per annum (indexed to the RTP rate, 1 January each year) for up to three years, subject to satisfactory academic performance. The recipient may apply for an extension of up to 6 months. A supplementary stipend valued at $6,000 annually per annum (fixed rate) is also payable to a successful domestic student. The supplementary stipend will have the same tenure as the primary stipend amount.

For a successful international student the Scholarship will provide an annual stipend allowance of $26,682 per annum (indexed to the RTP rate, 1 January each year) for up to three years, subject to satisfactory academic performance. The recipient may apply for an extension of up to 6 months. Academic course fees and single overseas health cover are also included for the same duration as the stipend component. No other amount is payable.

Application guide: It is recommended you read either the domestic or international applicant Terms and Conditions of award attached below prior to submitting an application.

Further information on the area of research can be obtained from Professor Eddie Holmes, NHMRC Australia Fellow, Marie Bashir Institute for Infectious Diseases and Biosecurity, University of Sydney.

Email: edward.holmes@sydney.edu.au

Apply Here: https://sydneyuniversity.formstack.com/-forms/ecology_evolution_of_viruses Closing date: 14 November 2017

PROFESSOR EDWARD C. HOLMES FAA FRS NHMRC Australia Fellow

THE UNIVERSITY OF SYDNEY Marie Bashir Institute for Infectious Diseases & Biosecurity, Charles Perkins Centre, School of Life & Environmental Sciences and Sydney Medical School, The University of Sydney | Sydney | NSW | 2006 | Australia T +61 2 9351 5591 E edward.holmes@sydney.edu.au

“edward.holmes@sydney.edu.au”
<edward.holmes@sydney.edu.au>

Vienna PopulationGenetics

The Vienna Graduate School of Population Genetics is looking for PhD students:

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

We invite applications from highly motivated and outstanding students with a background in one of the following disciplines: bioinformatics, statistics, evolutionary genetics, functional genetics, theoretical and experimental population genetics. Students from related disciplines, such as physics or mathematics are also welcome to apply.

Topics include:

§Comparative population genomics in Drosophila species.

§Contribution of transposable elements to adaption during experimental evolution.

§Developing new statistical tools for the identification of adaptive QTLs.

§Evolution of gene expression.

§Evolution of phenotypic plasticity.

§Evolution of sex chromosomes in Drosophila species.

§Evolution of sperm competition in Drosophila.

§Functional characterization of adaptive QTLs.

§Maximum likelihood inference of population genetic parameters using genome-wide data from nearly neutral sites.

§Sex-specific arms race between transposable elements and small RNAs.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by January 14, 2018 will be considered. Two letters of recommendation need to be sent directly by the referees. Accepted PhD students will receive a monthly salary based on currently EUR 2071 before tax according to the regulations of the Austrian Science Fund (FWF).

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at https://twitter.com/-PopGenViennaPhD c/o Institut für Populationsgenetik Veterinärmedizinische Universität Wien (Vetmeduni Vienna) Veterinärplatz 1, 1210 Wien

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

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

VirginiaCommonwealthU NicheEvolution

The Eckert lab located at Virginia Commonwealth University (VCU) is looking to recruit a new doctoral student to study niche evolution in conifers. Students interested in conifers, phylogenetic comparative methods, niche evolution, and the genetic architecture of adaptation are particularly encouraged to apply. The student would be enrolled in the Integrative Life Sciences (ILS) doctoral program. This program has competitive teaching and research assistantships, including tuition waivers, available to qualified applicants. More information about the ILS program is located at: https://lifesciences.vcu.edu/academic-programs/phd-in-integrative-life-sciences/ The Eckert lab is located in the Department of Biology at VCU. Currently, lab members include one postdoctoral scientist, three doctoral students, one M.S. student, and several undergraduate researchers. Members of the lab are encouraged to develop their own projects, attend conferences, and match research and teaching experiences to their career goals. For more information about my mentoring style, please see: http://mentoringphilosophyaje.blogspot.com/ VCU is located in Richmond, Virginia, and is a large, urban campus with an undergraduate enrollment of approximately 32,000 students. Richmond has great art, music, and food scenes, as well as wonderful park systems. It is located along the James River and was recently voted the best river town in the United States.

If you are interested, please contact me via e-mail (aeckert2@vcu.edu). In your e-mail, please provide brief descriptions of your research and career goals, as well as attach your CV. The deadline for applications to the ILS program is January 10, 2018.

Andrew J Eckert <aeckert2@vcu.edu>

Wageningen PlantAdaptation

The Netherlands Institute of Ecology in Wageningen (NIOO-KNAW) invites applications for TWO PHD POSITIONS IN PLANT EPIGENETICS The two PhD positions are part of the EU-funded Marie Curie training network EpiDiverse (www.epidiverse.eu). This is a cross-European network that involves leading research groups from molecular genetics, ecology and computational biology to investigate epigenetic mechanisms and their adaptive significance in wild plant species. The EpiDiverse network provides an excellent opportunity to receive cross-disciplinary doctoral training and to do cutting-edge research in plant epigenetics. A comprehensive training program is offered to learn molecular, bioinformatic and ecological aspects of epigenome analysis, including dedicated summer schools, workshops and extended exchange visits to different groups in the network. Students will be part of a group of 15 PhD students from across Europe that will all work on similar questions, and that will regularly meet and interact.

Projects available at the Netherlands Institute of Ecology are: 1. Life history variation and epigenetic inheritance (https://tinyurl.com/epidiverse-rp9). This 4-year project investigates differences in DNA methylation dynamics (environmental effects, transgenerational stability) between species with different reproductive modes and other life history characteristics.

2. Epigenetic contribution to phenotypic plasticity in Populus nigra (https://tinyurl.com/epidiverse-rp13). This 4-year project investigates environmental effects on DNA methylation in black poplar and evaluates functional consequences, temporal stability, and also stability of epigenetic variants through clonal versus sexual propagation.

Please visit the project website (www.epidiverse.eu) for more information and for instructions on how to apply. For questions on the projects please contact Koen Verhoeven (k.verhoeven@nioo.knaw.nl and www.nioo.knaw.nl/users/kverhoeven).

REQUIREMENTS: We seek two bright and enthusiastic biologists with a background in either (molecular) ecology or genetics, and a keen interest in working at the interface of these two disciplines. Candidates from other relevant programs such as computational biology, with a strong interest in ecology and evolution, are also invited to apply. Experience with NGS technologies is a plus, but comprehensive training in both wet lab and computational aspects of epigenomic analysis will be provided. A high standard of spoken and written English is required, as are good quantitative and analytical capabilities, good interpersonal and communication skills, and the ability to work independently and as part of a team. For these Marie Curie network positions some specific eligibility criteria apply: candidates must be within the first four years after obtaining their MSc degree and may be of any nationality, but must not have spent more than 12 months in the last 3 years in the country of the recruiting host institution (The Netherlands, for these projects). The deadline for applications is 24 November 2017.

Dr. Koen Verhoeven Department of Terrestrial Ecology Netherlands Institute of Ecology (NIOO-KNAW) Tel: +31 (0)317 473624 Web: www.nioo.knaw.nl/users/-kverhoeven Email: k.verhoeven@nioo.knaw.nl

"Verhoeven, Koen" <K.Verhoeven@nioo.knaw.nl>

WashingtonStateU EcolEvolutionaryBiology

Graduate school research opportunities in Ecology and Evolutionary Biology

The School of Biological Sciences at Washington State University invites motivated applicants for graduate training and research in ecology & evolutionary biology.

Research opportunities in both plant and animal systems are diverse. Research focus areas include disease and community ecology, ecosystem ecology, evolutionary genetics, ecological and evolutionary physiology, genomics, evolutionary theory, and phylogenetics and systematics. Our faculty and a brief description of research interests:

Jesse Brunner: Disease ecology Jeremiah Busch: Population genetics, plant evolution Patrick Carter: Quantitative genetics, animal physiology Omar Cornejo: Genomics, host-pathogen evolution Erica Crespi: Animal developmental physiology Wes Dowd: Animal evolutionary physiology Mark Dybdahl: Evolutionary ecology, adaptation, phenotypic plasticity Dave Evans: Ecosystem ecology and nutrient cycling Richard Gomulkiewicz: Evolutionary genetics and theory Joanna Kelley: Genomics, adaptation to extreme environments Eric Roalson: Plant phylogenetics and systematics Elissa Schwartz: Disease dynamics and virus-host interactions Andrew Storfer: Landscape genomics, disease evolution Heather Watts: Animal behavior and physiology

For more information, please visit their websites, available via sbs.wsu.edu

Our graduate training program offers many opportunities for excellence. Every SBS student is fully funded with generous stipends through teaching or research assistantships, accompanying tuition waivers, and health benefits. Plus, SBS endowments provide over $100,000 per year in student awards to facilitate research, training, and professional travel. PhDs receive up to $10,000 in guaranteed support for research-related travel and MS students receive up to $5,000 ?in guaranteed support. The campus houses outstanding facilities, including plant and animal growth chambers, managed field sites, a modern genomics core and a campus-wide computer cluster.

Washington State University is located in Pullman, WA, a friendly mid-sized town on the rolling hills of the unique Palouse region in eastern Washington. The campus is only eight miles from the University of Idaho in Moscow, ID. The two towns and campuses provide an academically and culturally rich community. The area offers great parks, bike paths, restaurants, farmer's markets and unbeatable opportunities for recreation in the adjacent mountains, rivers, and wilderness.

For more information regarding the Graduate School applications at WSU, see: gradschool.wsu.edu

If you have any questions regarding the application process, please contact:

Ms. Jenny Davis (sbs.gradstudies@wsu.edu)

The deadline for application of prospective students is January 10, 2018, but students are encouraged to apply anytime.

"Dybdahl, Mark" <dybdahl@wsu.edu>

Wisconsin FishPopulationGenomics

Master's position in the Larson Lab using genomics to study connectivity and species diversity in the Boardman River, MI

Description and responsibilities: The USGS Wisconsin Cooperative Fishery Research Unit at UW-Stevens Point is looking for a MS student to conduct genomics research on fish populations from the Boardman River near Traverse City, MI. This research is part of the FishPass project, a large collaborative effort to explore fish passage solutions that restore connectivity for native species while blocking invasive species, such as sea lamprey. The Union Street dam on the Boardman River is 150 years old, and fish populations below the dam have been isolated from above dam populations since its completion. The successful candidate will use restriction site-associated (RAD) sequencing to collect genetic data on five fish species sampled above and below the

Union Street Dam to determine if these populations are significantly differentiated and/or show differences in diversity. Additionally, the student will collect eDNA samples from existing monitoring sites and pair these data with traditional surveys to determine the utility of eDNA metabarcoding for investigating species diversity and distribution patterns in this system. Genetic samples from white sucker, smallmouth bass, walleye, yellow perch, and rock bass as well as water samples for the eDNA portion of this project are being collected by the Michigan Department of Natural Resources and other local agencies and fieldwork for the student will be minimal. However, the student will likely be asked to help with sample collection one to two times per summer. Laboratory work will consist of constructing RAD and amplicon sequencing libraries to send out for high-throughput sequencing. Bioinformatic analysis will involve using programs such as STACKS to analyze RAD data and working with Linux based pipelines to analyze eDNA data.

Qualifications: B.S. in biology, fisheries, or a related field, GPA of 3.0+, and GRE of 300+. Background in genetics is preferred but not required. Previous experience with fieldwork and analysis of genomic data is desirable.

Salary: $16,000 per year (2 yr) plus health insurance and tuition waiver. Closing date: March 1, 2018.

Starting date: Position will start in September 2018 but there may be an opportunity to work in the Larson Lab during summer 2018 before the position starts.

Contact: Please send CV, transcript copies, GRE scores, and names and contact information for 3 references to Wes Larson (Wes.Larson@uwsp.edu).

Web Links: https://larsonlab.wordpress.com/ https://www.coopunits.org/Wisconsin_Fish/People/Wes_Larson/index.html http://www.glfc.org/fishpass.php Wes.Larson@uwsp.edu

Jobs

23andMe PopulationGenetics

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

We are seeking colleagues with extensive training and experience in statistical and population genetics to join our highly productive, world-class Ancestry Research & Development team. Our team develops novel algorithms to interpret the ancestry data of individual 23andMe customers and works to publish novel findings regarding human genetics and population history. We are seeking team members who are excited to develop cutting edge features that will reach millions of people.

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

Candidates for senior positions should also have multiple years of experience leadership and of executing independently developed ideas.

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

Enthusiasm for working in a highly collaborative environment.

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

23andMe has over 2 million customers worldwide with ~85 percent consented to participate in research. 23andMe is located in Mountain View, CA. More information is available at www.23andMe.com . At 23andMe we value a diverse, inclusive work force and we provide equal employment opportunity for all applicants and employees. All qualified applicants for employment will be considered without regard to an individual's race, color, sex, gender identity, gender expression, religion, age, national origin or ancestry, citizenship, physical or mental disability, medical condition, family care status, marital status, domestic partner status, sexual orientation, genetic information, military or veteran status, or any other basis protected by federal, state or local laws. 23andMe will reasonably accommodate qualified individuals with disabilities to the extent required by applicable law.

Adam Auton <aauton@23andme.com>

AMNH NewYork EvolutionaryBiolMentoring

Science Research Mentoring Program (SRMP) Manager

Apply HERE: https://careers.amnh.org/applicants/-Central?quickFind=52638 Position Summary

The American Museum of Natural History (AMNH) seeks an individual to manage and advance its exemplary youth science achievement program, the Science Research Mentoring Program (SRMP). SRMP is a competitive, multiyear out of school program that supports high achieving, low-resourced students to realize great advances in their science learning and college & career readiness. The Manager will be responsible for all aspects of the Museum's program which includes recruiting and supporting scientist mentors, educators and youth, developing curricula and implementing preparatory coursework in the fields of science represented by the Museum.

The Manager needs a proven track record of authentic scholarship in the sciences and will serve as a mentor in the program. However, this position is principally managerial. Release time for scientific studies is limited and scientific study must be folded into mentorship duties. The Manager will be also be responsible for collaborating with colleagues across a variety of youth programs, and participate in the larger strategic advancement of the Museum's out-of-school education pipeline. The Manager will need to work select weekend days, work a schedule of 11-7pm on select weekdays and be available during summer months when programs are at their peak.

Specific day-to-day responsibilities: - Serve as a high school science research mentor - Recruit and select students annually for science research placements. - Recruit and select scientists (internally and externally) to serve as research mentors and course instructors. - Co-produce and implement a suite of preparatory courses including an intensive summer institute in which students learn laboratory skills. - Develop and implement protocols and advisory process for culminating student research placement year. - Plan, coordinate and implement student orientations, graduation events and family nights. - Meet regularly with students and scientists to monitor progress and support mentorship. - Develop and maintain program budgets for specific programs. - Conduct administrative duties. - Participate in Youth Initiatives departmental scope of work as required.

Required Qualifications

-Ph.D. in Science. -Experience working in fast-paced environment and multi-tasking. -Experience with creating systems, and maintaining records. -Fluency with writing proposals and reports. Impeccable organization, coordination, and communication skills

Preferred Qualifications

-At least three years of experience working with youth and/or youth serving organizations in an administrative role. -Expertise in developing partnerships with individuals and organizations. -Experience with managing budgets. Familiarity with New York City school systems

Posting Date: 11-01-2017

Closing Date: Open Until Filled

Required Applicant Documents: Resume & Cover Letter

Questions: Contact Mark Weckel; Assistant Director of Youth Initiatives (mweckel@amnh.org)

Mark Weckel, PhD Assistant Director; Youth Initiatives Visiting Scientist; Center for Biodiversity and Conservation American Museum of Natural History Email: mweckel@amnh.org Phone: 212-313-7947 www.srmp4life.com www.gothamcoyote.com Mark Weckel <mweckel@amnh.org>

ArizonaStateU EvolutionaryComputing

Note: Although these jobs are being posted through the ASU School of Computing, , Informatics, and Decision Systems Engineering, a major emphasis of our center is evolution, and recruits specializing on evolution or ecology would likely be affiliated with the ASU School of Life Sciences.

BIODESIGN IN COMPUTER SCIENCE FACULTY POSITIONS 'V Job #12147

The School of Computing, Informatics, and Decision Systems Engineering (SCIDSE), part of the Ira A. Fulton Schools of Engineering at Arizona State University (ASU), and the new Biodesign Center focused on Security and Robustness in Adaptive Computation invite applications for multiple tenured or tenure- track faculty positions. Areas of interest include: biological modeling (especially immunology, evolution, or ecology), cybersecurity, software engineering, and intelligent systems. Originality, fit with the Center, and the potential impact of the candidate are higher priorities than specific research area.

We seek applicants who will contribute to our programs and expend collaborations between the Biodesign Institute and SCIDSE. Faculty members are expected to develop an internationally recognized and externally funded research program, adopt innovative educational practices in graduate and undergraduate education, develop and teach graduate and undergraduate courses, advise and mentor graduate and undergraduate students, and undertake service activities within the university, in the professional community and at a national level.

Required qualifications include an earned doctorate in computer science, software engineering, biological sciences, or related field and demonstrated research and teaching excellence appropriate to the candidate'Âs rank. The Ira A. Fulton Schools of Engineering value demonstrated commitment to interdisciplinary research and teaching, history of extramural funding, and record of significant publications.

Appointments will be at the assistant, associate or full professor rank commensurate with the candidate'Âs experience and accomplishments, starting August 2018. Although tenure home may be in any of the Fulton Schools of Engineering, the School of Computing, Informatics, and Decision Systems Engineering is currently the most involved in the interest areas of the search. Teaching responsibilities will be to the School and research program closely tied to the new Biodesign Center.

Review of applications will begin November 30, 2017; if not filled, reviews will occur on the 1st and 15th of every month thereafter until the search is closed. Apply at http://engineering.asu.edu/hiring/ candidates will be asked to submit the following through their

Interfolio Dossier: Cover Letter Current CV Statement describing research interests Statement describing teaching interests Contact information for three references

For further information or questions about this position please contact the search committee chair Professor Stephanie Forrest, email to Stephanie.forrest@asu.edu

Arizona State University is a VEVRAA Federal Contractor and an Equal Opportunity/Affirmative Action Employer. All qualified applicants will be considered without regard to race, color, sex, religion, national origin, disability, protected veteran status, or any other basis protected by law. Please see ASU'Âs full non-discrimination statement (ACD 401) at https://www.asu.edu/aad/manuals/acd/acd401.html and ASU'Âs Title IX policy can be located at https://www.asu.edu/titleIX . Carlo C. Maley, Ph.D. Associate Professor Biodesign Institute School of Life Sciences Arizona State University

Cell: +1-480-326-0428

Carlo Maley <maley@asu.edu>

AuburnU EvolutionaryAdaptation

Faculty Position in Global Change Biology

Department of Biological Sciences, College of Sciences and Mathematics

Auburn University

The Department of Biological Sciences at Auburn University invites applications for a tenure-track faculty position beginning Fall 2018 at the rank of Assistant Professor in Global Change Biology of Marine Systems and/or Plant Systems. The successful candidate is expected to establish an extramurally funded, internationally recognized research program focused on local, regional, or global impacts of anthropogenic environmental changes. We seek candidates who will complement a University initiative focused on climate change and who will position us to address problems of global anthropogenic changes as they relate to biotic diversity. The newly hired faculty member will be able to participate in University-wide initiatives including the Climate, Human, and Earth Systems (CHESS) Cluster

The University has formal ties to Dauphin Island Sea Lab, which offers opportunities for new faculty to build research connections. The candidate will have teaching responsibilities in undergraduate Ecology and will be expected to develop or contribute to a graduate course in their research specialty.

Applicants must have a Ph.D. in Biological Sciences or a closely related discipline, and may have relevant postdoctoral experience. The successful candidate must demonstrate excellent written and interpersonal communication skills and collegiality. Desired qualifications include a strong record of publication, teaching experience, and demonstrated (or potential) ability to acquire extramural funding. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin and to continue to work legally for the proposed term of employment.

Review of applications will begin January 1, 2018, and will continue until a suitable individual is hired. Applicants should submit curriculum vitae, a description of research interests, a statement of teaching philosophy and experience, and the names and contact information of three professional references. Applicants must submit their materials online at:

http://aufacultypositions.peopleadmin.com/postings/2596 More information about the department and its programs can be found at the following web site:

http://www.auburn.edu/cosam/departments/biology/index.htm Auburn maintains high levels of research activity and high standards for teaching excellence. Its 2017 enrollment of 29,776 students includes 23,964 undergraduates and 5,812 graduate and professional students. Organized into twelve academic colleges and schools, Auburn's 1,450 faculty members offer more than 200 educational programs.

Auburn residents enjoy a thriving community, recognized as one of the "best small towns in America," with moderate climate and easy access to major cities or to beach and mountain recreational facilities. Situated along the rapidly developing 1-85 corridor between Atlanta, Georgia, and Montgomery, Alabama, the combined Auburn-Opelika-Columbus statistical area has a population of over 500,000, with excellent public school systems and regional medical centers.

Auburn University is an EEONet/Disability Employer

Paula Norrell <pkn0001@auburn.edu>

BrooklynC CUNY CompBiol

Brooklyn College of the City University of New York (CUNY) invites applications for a full-time tenure-track Assistant Professor position in the Department of Biology with a starting date in August 2018.

Brooklyn College is a microcosm of the ethnically rich borough of Brooklyn it serves as well as a mirror of the wide diversity in New York City itself. A vibrant, intellectually engaged community, our student body comprises individuals from 150 countries, speaking 105 different languages. The College and the Department of Biology are committed to enhancing and supporting a diverse and inclusive community of students, faculty, and staff. Candidates with demonstrated commitment to diversity and inclusiveness through their research, teaching and/or service are encouraged to apply.

The selected candidate is expected to develop a strong independent research program that is competitive for external grants, promotes collaborations, mentors and trains Ph.D. students in the CUNY doctoral program. Desired areas of focus include: Systems approaches with applications to neuroscience, developmental biology, immunology, cancer research, environmental biology, evolution, ecology, genetics, cell biology, metabolism, and genomics.

The successful candidate will join a vibrant community of researchers in the Department of Biology, with areas of focus including Neuroscience, Ecology Evolution and Behavior, and Molecular, Cellular and Developmental Biology.

Responsibilities include: Teach existing courses and developing new undergraduate and graduate courses in topic area such as bioinformatics, computational biology, systems biology, neuroscience, immunology, and genetics/genomics.

Mentor undergraduate, graduate and postdoctoral Scholars in research and work with a diverse team of colleagues.

Develop a high-impact, nationally recognized, extramurally funded research program and excel in teaching at the Undergraduate, Masters and PhD levels.

Share responsibility for committee and department assignments, performing administrative, supervisory, and other functions.

QUALIFICATIONS Ph.D. in Biology or related field from an accredited institution.

Post-doctoral fellowship training including actively applying for extra-mural funding.

Preference will be given to candidates whose research includes a significant computational component.

Please see application instructions at: https://cuny.jobs/brooklyn-ny/assistant-professor-biology/40180f4bc4b34 98db03e9d8d3404045b/job/ CUNY encourages people with disabilities, minorities, veterans and women to apply. At CUNY, Italian Americans are also included among our protected groups. Applicants and employees will not be discriminated against on the basis of any legally protected category, including sexual orientation or gender identity. EEO/AA/Vet/Disability Employer.

Jeremy Draghi <jdraghi@gmail.com>

BrownU ComputationalBiology

Brown University

Center for Computational Molecular Biology and Department of Computer Science

TENURE-TRACK FACULTY MEMBER IN COMPUTATIONAL BIOLOGY

The Center for Computational Molecular Biology at Brown University (CCMB; https://www.brown.edu/-academics/computational-molecular-biology/) invites applications for a tenure-track or tenured faculty member in Computer Science who develops and applies analytical and computational approaches to important biological questions. We seek an innovative and accomplished scientist whose research program is motivated by understanding biological systems (for example, genomics, gene expression and regulatory genomics, gene genealogies and macroevolutionary relationships).

The successful candidate will be appointed in the Department of Computer Science, will be a core faculty member of CCMB, and will have opportunities to conduct undergraduate and graduate teaching in the Computational Biology degree programs. The prime intellectual mission of CCMB is to promote the development, implementation and application of quantitative methods to foundational questions in the biological and medical sciences. The research programs of the core faculty in CCMB lie fundamentally at the intersection of computer science, evolutionary biology, mathematics, and molecular and cellular biology. The research challenges at the heart of CCMB are a rich source of mathematical problems motivated by the complex nature of genomes, disease processes, and evolutionary relationships. These challenges are both multi-scale (with units of interest ranging from molecules to communities of organisms) and large-scale (data-intensive, in part due to advances in sequencing technologies). Along with the Department of Computer Science, CCMB is one of five intellectual units at Brown University that together round out the broader landscape of research in methodological development under Brown's Data Science Initiative (https://www.brown.edu/ initiatives/data-science/).

Brown University is located in Providence, RI, close to Narragansett Bay, an hour from Boston and about three hours from New York City. Providence has been consistently rated as among the Northeast's most livable cities and is home to diverse intellectual, artistic, and business communities.

We will consider applicants from all ranks with a preference for an appointment at the assistant professor level. Qualifications for Assistant Professors include a PhD degree in a related field (e.g., computational biology, computer science, mathematics, statistics) and strong research, mentoring, and teaching credentials. Senior candidates should be acknowledged international leaders in computational biology, with a distinctive record in scholarship and teaching.

Applicants should submit the following materials via Interfolio (https://apply.interfolio.com/44956): cover letter; current curriculum vitae; separate statements of research and teaching interests; and three letters of reference. Senior candidates should submit five names of references whom the search committee may contact. Applications will be considered until the position is filled but we strongly encourage the candidates to submit complete applications (including reference letters) by December 1, 2017.

Inquiries may be addressed to Sohini Ramachandran, chair of the search committee, at compbiosearch@brown.edu.

Brown University is committed to fostering a diverse and inclusive academic global community; as an EEO/AA employer, Brown considers applicants for employment without regard to, and does not discriminate on the basis of, gender, race, protected veteran status, disability, or any other legally protected status. We encourage applications from women, underrepresented minorities and those who can contribute, through their research, teaching or service, to the excellence, diversity and inclusivity of our academic community. We also encourage the candidates to report any relevant experience and plans in their teaching statements.

"Ramachandran, Sohini" <sramachandran@brown.edu>

CaliforniaStateU Pomona HostPathogenEvolution

Tenure-track Faculty Position Host-Pathogen Interactions

The Biological Sciences Department at California State Polytechnic University, Pomona (Cal Poly Pomona) invites applications for a tenure-track position in Host-Pathogen Interactions at the rank of Assistant Professor to begin Fall 2018. The Position: The successful candidate will have a strong commitment to excellence in teaching and research. Teaching responsibilities could include basic microbiology, immunology, cell biology, mycology, parasitology and specialty courses in the candidate's area of expertise, such as host-pathogen interactions, cellular microbiology, or medical microbiology as well as participation in introductory biology and other courses in microbiology. The candidate must conduct research in host-pathogen interactions at the cellular or organismal levels. The area of specialization is open, but candidates who study host responses to bacteria, fungi, or parasites are encouraged to apply. Post-doctoral experience and previous teaching experience are preferred. The successful candidate is expected to develop an extramurally funded research program involving undergraduate and Master's level students. The applicant will also be expected to assist in curriculum development, advise students, and serve on department, college, and/or university committees, and engage in professional activities. Applicants whose work incorporates a global perspective and a demonstrated commitment to diversity in higher education are particularly encouraged to apply.

Minimum Qualifications: - The successful candidate will have a PhD from an accredited university in Microbiology, Immunology, or related field by December 2017. - Demonstrated ability to be responsive to the educational equity goals of the university and its increasing ethnic diversity and international character.

Preferred Qualifications: - Previous teaching experience. - Post-doctoral research experience.

Application Procedure: An application consisting of a single PDF file application submitted electronically with "Host-Pathogen position" in Subject line to host_pathogen@cpp.edu that consists of:

- cover letter that describes how the candidate's teaching and research experience have prepared her/him to meet the duties and qualifications articulated in the position description (2 pages max); - curriculum vitae; - completed University application form which can be downloaded from our website at http://www.cpp.edu/~faculty-affairs/documents/acadapplication.pdf - statement of teaching philosophy (2 pages max); - a student success statement about the candidate's teaching or other experiences, successes, and challenges in working with a diverse student population (approximately one page, single-spaced); - proposed plan of research (2 pages max); - three representative publication reprints; - names, titles, addresses, emails and telephone numbers of three (minimum) to five (preferred) individuals who can speak to the candidate's potential for success in this position

Semi-Finalists for the position will be required to provide three letters of reference (PDF format by email) submitted by the reference on official letterhead and an official transcript showing highest degree earned.

The position will remain open until filled. First consideration will be given to completed applications received no later than November 15th, 2017. Electronic submission of application materials as a single PDF file is required. Please address application materials to:

Chair, Host-Pathogen Interactions Search Committee Biological Sciences Department California State Polytechnic University, Pomona Pomona, CA 91768 Phone: 909.869.4048 Fax: 909.869.4078 Email: host_pathogen@cpp.edu

Andrea Bonisoli Alquati, Ph.D.

Assistant Professor Department of Biological Sciences California State Polytechnic University, Pomona Pomona, CA 91768

Andrea Bonisoli-Alquati <aalquati@cpp.edu>

CCharleston MarineEnvironmentalGenomics

College of Charleston, Department of Biology

SmartState Endowed Professorship in Marine Environmental Biology

Applications are invited for an endowed professorship in Marine Environmental Biology at the College of Charleston. We seek an environmental biologist who studies the impacts of environmental variation or change on marine organisms with a research program that involves omics and/or bioinformatics. Rank for this position is open, but it is anticipated that the appointment will be made at the level of Associate Professor in the Department of Biology (see biology.cofc.edu). The appointee will maintain a modest teaching load (2 to 3 courses per year) that includes undergraduate and graduate courses in an area of expertise and service courses such as introductory biology.

This position is one of two endowed appointments that are part of the SmartState South Carolina Centers of Economic Excellence (smartstatesc.org/) in the Marine Genomics program and will include a joint appointment with the Medical University of South Carolina

(MUSC). The other endowed appointment will be at MUSC. Ideally, we seek a colleague who could potentially collaborate with their MUSC counterpart (whose research will focus on the linkage between marine and human health). The appointee will be expected to mentor graduate students, teach courses in an area of expertise, and interact with students and staff from the College of Charleston, MUSC, and their three other partners at the Fort Johnson marine campus (the SC Department of Natural Resources, the National Oceanic and Atmospheric Administration, and the National Institute of Standards and Technology).

The successful applicant will have a demonstrated track record as a scholar and a strong commitment to teaching at all levels and to mentoring both graduate and undergraduate students. Historic Charleston, SC provides a beautiful and culturally rich setting for developing a global perspective on marine environmental problems and solutions.

Applications should be submitted via http://jobs.cofc.edu/postings/6721 Additional information about this position can be obtained from Seth Pritchard, chair of the Biology Department (pritchards@cofc.edu) or Matt Rutter, chair of the search committee (rutterm@cofc.edu). Review of applications will begin December 7, 2017 and will continue until the position is filled.

The College of Charleston is an Affirmative Action/Equal Opportunity employer and does not discriminate against any individual or group on the basis of gender, sexual orientation, gender identity or expression, age, race, color, religion, national origin, veteran status, genetic information, or disability.

"Rutter, Matt" <RutterM@cofc.edu>

ColoradoStateU PlantGenetics

Tenure-track faculty position in plant breeding and genetics at Colorado State University

The Department of Soil and Crop Sciences at Colorado State University invites applications for a tenure-track faculty position in plant breeding and genetics. We seek dynamic and motivated scientists who have expertise in plant germplasm evaluation, enhancement, and utilization. Candidates are sought with demonstrated capacity to integrate next-generation technologies and large datasets with classical field- and laboratory-based plant improvement approaches in their research program. Commitment to teaching excellence and stakeholder engagement is an important part of this position.

Minimum requirements: - PhD in a related field by application date - Experience in plant germplasm enhancement or genetic resource evaluation - Experience with genomic technologies relevant to crop breeding and genetics - Effective communication skills - A strong record of scholarly achievement

Complete applications due by 01/01/18 for full consideration.

Full job description and application procedures at http://jobs.colostate.edu/postings/50923 . CSU is an EO/EA/AA employer and conducts background checks on all final candidates.

"McKay,John" <John.McKay@ColoState.EDU>

CornellU PlantMicrobeCoevolution

§Job Title: Assistant/Associate Professor; Plant-Microbe Biology

§Company Name: Cornell University

§Location: Ithaca, New York, United States, 14850

ASSISTANT/ASSOCIATE PROFESSOR; PLANT-MICROBE BIOLOGY

SCHOOL OF INTEGRATIVE PLANT SCIENCE

PLANT PATHOLOGY AND PLANT-MICROBE BIOLOGY SECTION

COLLEGE OF AGRICULTURE AND LIFE SCIENCES

CORNELL UNIVERSITY

POSITION: Assistant/Associate Professor; Plant-Microbe Biology; tenure-track, academic year appointment (9-month)

START DATE: September 1, 2018 or as negotiated

LOCATION: School of Integrative Plant Science, Plant Pathology and Plant-Microbe Biology Section, College of Agriculture and Life Sciences, Cornell University, Ithaca, NY

POSITION DESCRIPTION

The School of Integrative Plant Science at Cornell University (https://sips.cals.cornell.edu) invites applications for a tenure track position at the Assistant or

Associate Professor level in Plant-Microbe Biology. The coevolution of plants with their microbial partners and pathogens has produced a panoply of interaction systems that both benefit and threaten plants and global food security. The new faculty member will be expected to develop a strong, internationally recognized program in plant-microbe interaction biology. Examples of relevant research topics include, but are not limited to, mechanisms of plant immunity and pathogen virulence or symbiotic cooperation, host-microbe evolutionary genomics, systems biology, and biology of plants or plant-associated microbes with a focus on their adaptations for biotic interactions. Ideal projects will address fundamental questions in interorganismal biology and have a potential for translational benefit. The ideal candidate will thrive in the highly collaborative environment of Cornell University, which includes diverse faculty affiliated with the School of Integrative Plant Science (SIPS) in the College of Agriculture and Life Sciences, the University-wide Cornell Institute of Host-Microbe Interactions and Disease, Boyce Thompson Institute for Plant Research, and the USDA Agricultural Research Service. The expected affiliation for the position will be the SIPS Section of Plant Pathology and Plant-Microbe Biology on the Ithaca campus. The position will have a 60% research and 40% teaching responsibility, and the successful candidate will teach in the broad area of plant-microbe interactions and plant pathology.

QUALIFICATIONS

Ph.D. in Plant-Microbe Biology, Plant Pathology, Plant Biology or related disciplines. The candidate must be able to work in a multidisciplinary and multicultural setting and create a collegial professional environment. Well-qualified applicants are expected to have a demonstrated record of publication excellence, and preferred qualifications include postdoctoral experience, ability to work with a team, and ability to communicate effectively with students, colleagues, and external stakeholders.

SALARY AND BENEFITS: Salary is competitive and commensurate with background and experience. An attractive fringe benefits package is provided.

Cornell University seeks to meet the needs of dual career couples, has a Dual Career Program, and is a member of the Upstate New York Higher Education Recruitment Consortium to assist with dual career searches. Visit http://www.unyherc.org [1] to see positions available in higher education in the upstate New York area.

APPLICATION PROCEDURE

Submit as a single PDF file to Academic Jobs Online at https://academicjobsonline.org/ajo/jobs/10253 [2] a letter summarizing your background and qualifications, a statement of research accomplishments and interests (3 pages maximum), a statement describing your teaching experiences, philosophy and interests (2 pages maximum), a detailed curriculum vitae, and the names and contact information of three or four references (letters will be requested after the applications are reviewed). Inquiries may be sent to Prof.

Greg Martin, Search Chair (gbm7@cornell.edu). Initial screening of applications will begin on January 5, 2018 and continue until the position is filled.

OPPORTUNITY

The College of Agriculture and Life Sciences is a pioneer of purpose-driven science and Cornell University's second largest college. We work across disciplines to tackle the challenges of our time through world-renowned research, education and outreach. The questions we probe and the answers we seek focus on three overlapping concerns: natural and human systems; food, energy and environmental resources; and social, physical and economic well-being.

Cornell University is an innovative Ivy League university and a great place to work. Our inclusive community of scholars, students and staff impart an uncommon sense of larger purpose and contribute creative ideas to further the university's mission of teaching, discovery and

— / —

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

Hawaii Tech PopulationGeneticsGenomics

Extended Closing Date, November 14th, 2017.

The Laboratory of Dr. Scott Geib has a position opening for laboratory technician (hired through the University of Hawaii, Manoa) to work on USDA Farm Bill funded projects to develop genomic resources in pest Tephritid fruit flies. This position is currently posted at the University of Hawaii, 0078996T and closes on November 14th, 2017 (http://workatuh.hawaii.edu/Jobs/NAdvert/27762/4598809/1/postdate/desc). This research project is focused on analyzing populations of tephritid fruit fly species using genome-wide analysis techniques towards marker discovery and developing assays for determination of source populations.

For this position, salary starts at ~$42,000/yr, hired through the University of Hawaii at Manoa, and the job will be stationed at the USDA-ARS Pacific Basin Agricultural Research Center in Hilo, Hawaii (on the Big Island of Hawaii). Appointment is for 1 year, with extension annually, based on performance and funding. Currently, at least 2 years of funding is available. For details on the exact duties associated with this job, in addition to minimum qualifications, please refer to the online job ad http://workatuh.hawaii.edu/Jobs/NAdvert/27762/4598809/1/postdate/desc . The laboratory in general performs research that involves high throughput extraction of DNA/RNA; generation of NGS libraries (DNA, RNAseq, ddRAD, etc) for Illumina, single molecule (e.g. PacBio/Nanopore), and linked-read (e.g. 10x Genomics) sequencing; and traditional genotyping (e.g. TaqMan assays) etc. Additionally the lab performs functional genomic studies (CRISPR/RNAi), and maintains fruit fly strains and colonies utilizing for experimental crosses. We have in-house automated laboratory equipment for nucleic acid extraction and library prep as well as HPC computing resources for data analysis and software development

To learn more about our research program, you can view: https://youtu.be/dU2kFhI6bYI . If you have any questions, please contact Dr. Scott Geib at scott.geib@ars.usda.gov . To apply, complete and submit an application package (including UH Form 64 B) following instructions at http://workatuh.hawaii.edu/Jobs/NAdvert/27762/4598809/1/postdate/desc before the November 14th closing date

“Geib, Scott” <Scott.Geib@ARS.USDA.GOV>

INHS UIllinois BiodiversityGenomics

The Illinois Natural History Survey (INHS) is seeking a Visiting Assistant Research Scientist, Biodiversity Genomics to develop, plan, conduct, and direct an independent research program of significance on any of a broad range of topics using genome scale data to address questions in the biodiversity sciences. Scientist is expected to apply techniques in next-generation sequencing, genomics, transcriptomics, metagenomics, and bioinformatics to topics in biodiversity and systematics to understand mechanisms of diversification, including phylogenomics, speciation, adaptation, and population-level processes. Requires a Ph.D. in a scientific discipline relevant to the mission and goals of INHS and the ability to establish an independent research program that incorporates analyses of Big Data. Position may become a regular, non-visiting position at a later date. Applications must be received by December 11, 2017. For additional information, including instructions on how to apply, please visit https://jobs.illinois.edu/academic-job-board or contact Lori Walston-Vonderharr, Human Resources, Prairie Research Institute at lwalston@illinois.edu. The University of Illinois conducts criminal background checks on all job candidates upon acceptance of a contingent offer. The U of I is an EEO Employer/Vet/Disabled http://www.inclusiveillinois.illinois.edu . “Johnson, Kevin P” <kpjohnso@illinois.edu>

InstitutPasteur PathologyEmergence

Institut Pasteur has launched an international call for junior candidates wishing to establish new independent research groups in the cutting edge interdisciplinary environment of its campus in Paris, France. This year the call will be focused on the topics associated with the Institut Convergence entitled “Emergence of Pathologies Through Individuals and populatiONs” (INCEPTION program).

Institut Pasteur is a non-profit private foundation dedicated to fundamental, interdisciplinary research and to the translation of knowledge to medicine and public health. Topics of interest include microbiology and infectious diseases, immunology, cell biology, developmental biology and stem cells, neuroscience, genomics, structural biology, genetics and cancer. In 2014, a new center (the C3BI), fostering research in Bioinformatics, Biostatistics and Integrative Biology was established. Substantial resources were allocated for the creation and development of the C3BI, with the recruitment of 40 permanent research engineers in bioinformatics and biostatistics and several new research units. A dedicated building is being renovated on the Paris campus to house the C3BI. The aim is to facilitate collaborations in bioinformatics and biostatistics, to support and develop training in these fields, to encourage interactions between all Institut Pasteur research teams, and to stimulate the development of new computational and statistical approaches for biological data analysis and modeling.

Institut Pasteur was recently awarded a grant within the framework of the French National Agency for Research “Instituts Convergences” call (“Investing in the Future” French program PIA2) to strengthen Integrative Biology, Bioinformatics and Biostatistics. Today, the C3BI center is at the core of the new INCEPTION program, which includes grants for the launch of several 5-year junior groups (called G5).

The INCEPTION program would particularly welcome projects in the following fields: * Sequence analysis * Machine learning * Data management and analysis * Systems biology * Phylodynamics * Metagenomics * Precision medicine

The primary focus of the call is on computational and statistical analysis of biological “big data”, typically produced by New Generation Sequencing (NGS) and -omics technologies. Nevertheless, all modeling and computational approaches addressing biological questions closely related to the INCEPTION program areas are eligible.

Successful candidates will possess the following qualifications: * Significant achievements in bioinformatics/biostatistics/biomathematics, * Broad experience in methodological development and data analysis, * Relevant publication record of cutting-edge research as senior/first author, * Demonstrated ability to collaborate with experimental and computational biologists.

The successful junior candidate* will be appointed with a permanent position, heading a group of six persons at the Institut Pasteur of Paris. This group will be created for a period of five years. Thereafter, the group may compete for full research group status.

A highly attractive package matching the experience of the successful candidate will be provided, including salaries (principal investigator, permanent bioinformatician/biostatistician, post-doctoral fellowships), a substantial contribution to equipment and computing facilities and annual running costs.Support for relocation expenses will also be provided.

Applications must be submitted online at: https://c3bi.pasteur.fr/inceptioncallg5/ and should include: 1. A web form summarizing the application. 2. A complete application file uploaded as a single PDF file comprising: 1. An introductory letter of motivation (1-2 pages), including the name of the proposed group. 2. A Curriculum Vitae and a full publication list. 3. A description of past and present research activities (up to 6 pages with 1.5 spacing, Times 11 font size). 4. The proposed research project (up to 6 pages with 1.5 spacing, Times 11 font size) highlighting how it would fit into the defined themes of the Inception program, and how it would respond to interdisciplinary challenges of that program. 5. The names of 3 scientists from whom letters of recommendation can be sought, together with the names of scientists with a potential conflict of interest from whom evaluations should not be requested.

The deadline for application submission is January 14, 2018, 12:00 pm CET.

Shortlisted applicants will be notified by the end of March 2018 and will be invited for interviews to take place in May 2018 (please set aside 2-4 May). The final ranking will be established by the Pasteur Scientific Council during its June 2018 session (please set aside 05-06 May, when applicants will be interviewed).

— / —

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

---

JohnMooresU Liverpool 4 EvolutionaryBiology

Lecturer or Senior Lecturer in Wildlife Conservation (Genetics) Liverpool John Moores University

The School of Natural Sciences and Psychology is seeking to appoint a full-time Lecturer or Senior Lecturer in Conservation Genetics with demonstrated research experience. This post represents additional investment in the School in support of our ambition to become a leader in the sector, building on our delivery of excellent teaching and research. The School has thriving research programmes and outstanding facilities.

You will contribute to a range of undergraduate and postgraduate programmes, potentially including BSc Wildlife Conservation, BSc Animal Behaviour, BSc Zoology, MSc Wildlife Conservation and UAV Technology, and develop an independent programme of high quality research. Applications are particularly welcome from candidates with experience in population and conservation genetics of wild and captive populations.

https://www.ljmu.ac.uk/about-us/faculties/faculty-of-science/school-of-natural-sciences-and-psychology Informal enquiries may be made to one of the Subject

Leaders - Dr Alan Gunn (Biology & Zoology) on 0151 231 2209, email a.gunn@ljmu.ac.uk or Dr Jason Kirby (Geography and Environmental Sciences) on 0151 231 2410, email j.r.kirby@ljmu.ac.uk.

Or alternatively please contact the People and Organisational Development Department on 0151 904 6130 or email: recruitmentcampaign@ljmu.ac.uk

LJMU is committed to achieving equality of opportunity.

For further information about this vacancy, please see here: http://www.jobs.ac.uk/job/BFT328/lecturer-or-senior-lecturer-in-wildlife-conservation-genetics/ —–

Lecturer or Senior Lecturer in Wildlife Conservation ('ex-situ' conservation) Liverpool John Moores University

The School of Natural Sciences and Psychology is seeking to appoint a full-time Lecturer or Senior Lecturer in Wildlife Conservation with demonstrated research experience. This post represents additional investment in the School in support of our ambition to become a leader in the sector, building on our delivery of excellent teaching and research. The School has thriving research programmes and outstanding facilities.

You will contribute to a range of undergraduate and postgraduate programmes, potentially including BSc Wildlife Conservation, BSc Animal Behaviour, BSc Zoology, MSc Wildlife Conservation and UAV Technology, and develop an independent programme of high quality research. Applications are particularly welcome from candidates with experience in the maintenance and breeding of captive populations, and the management of reintroduction programmes.

https://www.ljmu.ac.uk/about-us/faculties/faculty-of-science/school-of-natural-sciences-and-psychology Informal enquiries may be made to one of the Subject Leaders - Dr Alan Gunn (Biology & Zoology) on 0151 231 2209, email a.gunn@ljmu.ac.uk or Dr Jason Kirby (Geography and Environmental Sciences) on 0151 231 2410, email j.r.kirby@ljmu.ac.uk.

Or alternatively please contact the People and Organisational Development Department on 0151 904 6130 or email: recruitmentcampaign@ljmu.ac.uk

LJMU is committed to achieving equality of opportunity.

For further information about this vacancy, please see here: http://www.jobs.ac.uk/job/BFT269/lecturer-or-senior-lecturer-in-wildlife-conservation-ex-situ-conservation/ —–

Lecturer or Senior Lecturer in Evolutionary Anthropology Liverpool John Moores University

The School of Natural Sciences and Psychology seeks to appoint a Lecturer or Senior Lecturer with an established or growing reputation for conducting research of leading international quality in Evolutionary Anthropology.

You will be expected to contribute to a range of undergraduate and postgraduate programmes, potentially including BSc Forensic Anthropology, MSc Bioarchaeology, and MSc Forensic Anthropology, and develop an independent programme of high quality research. Applications are particularly welcomed from candidates with a specialism in hominin functional morphology and physiology from an evolutionary perspective. This appointment is part of a strategic investment in the research and teaching of Anthropology in the School.

Informal enquiries may be made to Professor Joel Irish (Subject Leader for Anthropology and Archaeology) on 0151 231 2387 or email (j.d.irish@ljmu.ac.uk).

Or alternatively please contact the People and Organisational Development Department on 0151 904 6130 or email: recruitmentcampaign@ljmu.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

LockHavenU Pennsylvania EvolutionaryInvertebrateBiol

We are hiring in the specialty of invertebrate biologist (broadly speaking) to teach a survey type course in Zoology and develop a student focused research program in our area. We hope to attract candidates that approach invertebrate zoology from an evolutionary point of view => Folks with a strong evolutionary basis for their research/teaching will be viewed very favorably.

Thank you,

-Steve

Simple message directing to our HR site:

Lock Haven University of Pennsylvania invites applications for a tenure-track position in Invertebrate Biology beginning August 18, 2018. More information is available at https://jobs.lhup.edu/postings/3819 “Seiler, Steven M.” <sseiler@lockhaven.edu>

MaxPlanckInst Cologne ResAssist EvolVertAgeing

Dario Riccardo Valenzano group (valenzano-lab.age.mpg.de) Max-Planck-Institute for the Biology of Ageing - Cologne, Germany

The Max Planck Institute for Biology of Ageing (MPI-AGE) was founded in 2008 with the aim to understand fundamental mechanisms of healthy ageing. The institute is part of a broad network of research institutions in the Cologne-Bonn area dedicated to research on ageing and age-related disease, constituting a vibrant and collaborative environment for research. Equipped with state-of-the-art technology and excellent core facilities, to which the successful candidate will have access, the institute provides outstanding research opportunities for its scientists. At the moment, we host about 240 employees from 34 different nations.

The Valenzano Lab investigates the evolutionary genetic basis of vertebrate lifespan and ageing. Our main model system is the African turquoise killifish (Nothobranchius furzeri), which is the shortest lived vertebrate species bred in captivity. To identify the genomic regions associated with survival and ageing, and to study their evolution, we use a combination of approaches, including linkage mapping, transgenesis, population genetics on wild killifish populations, and computer simulations.

We are seeking full-time (39 hours/week). The position is available immediatley and will be initially time limited to 2 years.

Your tasks: - Experimental assistance on various molecular biology-related research projects - Possibility of managing your own projects - Molecular biology experiments on different organisms - General lab work - Lab organization and support in daily lab duties - Documentation of experimental results in English - Attending meetings and technical training of personnel

Your qualification - Professional training as technical assistant (BTA, BioTA, CTA, MTA), laboratory assistant or equivalent qualification - Ideally you have several years of experience working with molecular biology & biochemistry techniques (molecular cloning, protein and antibody purification, protein analysis, microbiology, etc.) - Experience in DNA library preparation for high-throughput sequencing is an advantage but not absolutely necessary - Experience in working with fish models is an advantage but not absolutely necessary - Excellent written and oral skills in English (the working language of the lab is English) - Excellent written and oral skills in German is highly favoured

We offer an exciting and multifaceted position in an enthusiastic and collaborative team, located in an outstanding, international scientific environment and the possibility of regular training. The employment contract is based on contracts for the civil service (TVöD-Bund, Tarifvertrag für den öffentlichen Dienst). The Max Planck Society is committed to employ more disabled individuals and especially encourages them to apply. We also seek to increase the number of women in those areas where they are underrepresented and especially encourage them to apply.

Your application should contain a one-page letter with a personal statement describing your relevant work experience, skills and accomplishments, your CV (including list of publications if applicable), and contact information for 2 references.

Informal inquiries are welcome and should be sent to valenzano@age.mpg.de. For further information about the Institute and the Valenzano lab see www.age.mpg.de and valenzano-lab.age.mpg.de

The ad is open until end of November

“dvalenzano@age.mpg.de” <dvalenzano@age.mpg.de>

NanyangTechU PopulationGenetics

Research Fellow ’V Population Genetics

Asian School of the Environment

Nanyang Technological University

Young and research-intensive, Nanyang Technological University (NTU Singapore) is ranked 11th globally. It is also placed 1st among the world’Âs best young universities.

Asian School of the Environment is currently looking for a candidate to join them as a Research Fellow. We seek to recruit a recent PhD graduate or experienced researcher in Population Genetics or Human Genetics, or related fields. The work involves mainly performing population genetic, bioinformatics, and statistical analyses using whole genome data sequenced by next generation sequencing technology. The research will use human population genome data to understand the genome diversity and genetic variation related to infectious diseases; therefore candidates need to handle big data on high performance computing system with excellent coding/scripting skills. Candidates will analyse the genome sequencing data and identify genetic variants to apply to population genetic analyses. Importantly, candidates should understand the principles of evolutionary biology to interpret to the data and results of analyses. In addition, candidates must have strong interests and knowledge on Population Genetics, Genomics, Human Genetics, or Bioinformatics, and it would be most helpful if the candidates have a great knowledge on infectious diseases especially for Malaria.

Requirements:

'P PhD degree received or expected in Population Genetics, Human Genetics, Bioinformatics

'P Experience on population genome data, coding skills in Python, Perl, and R or comparable data focused languages

'P Excellent communication skills to work with a team and ability to write an article paper

Application Procedure:

To apply, please submit an updated CV and cover letter, including academic qualifications, research records/ work samples and names and contact details of two referees to ase_humanresources@ntu.edu.sg indicating Research Fellow 'V Population Genetics.

We regret that only successful candidates will be informed.

Regards,

Revathy

HR Executive, ASE

69081146

Revathy D/O N Bamma <revathy@ntu.edu.sg>

NHM Bergen FishSystematics

https://www.jobbnorge.no/en/available-jobs/job/-144750/associate-profess or-in-fish-systematics

Associate professor in fish systematics

The Department of Natural History has the scientific and curatorial responsibility for botany, geology and zoology at the museum. There are currently 13 permanent scientific and 30 technical and administrative employees in this unit, in addition to temporary project staff.

Work tasks/research field:

We are seeking a productive and innovative academic who will be a dedicated researcher in fish systematics and a responsible curator for our scientific collection of fishes. The successful applicant has an excellent track record in systematics and taxonomy of fishes and is conducting research on phylogenetic relationships, taxonomy, species diversity, biogeography, and evolutionary processes underlying past and present diversity patterns.

We emphasize competence in both molecular and morphological methods of phylogenetics and taxonomy. The research should have a global perspective on fish groups that are common also in the Nordic / Atlantic waters, and must not be restricted by interest in commercial fish species.

The position also includes curatorial responsibility for our fish collections. The museum'swet and dry collections of vertebrates currently comprise 37,400 lots (c. 200,000 specimens), of which fish make up 22,300 lots (60%).

We hope to recruit an ichthyologist with a broader interest in vertebrates generally and a sincere dedication to collection development. The selected candidate will also take part in the production of exhibitions and other outreach activities at the museum. It is also expected that the employee will teach inhisorher area of expertise and contribute towards a successful development ofthe research school in biosystematics (ForBio).

The new employee will be an active partner in the systematics research group and is expected to submit extramural grant applications. There is currently a strong focus on lesser known species in Norway and the Arctic and the department continues to provide data for the Norwegian Biodiversity information Centre (Artsdatabanken), BoLD and GBiF.

Bjarte Jordal, PhD

Associate Professor in Systematic Entomology

The Natural History Museum

University Museum of Bergen

P.B. 7800, NO-5020 Bergen

Webpage: Bjarte Jordal

Research Group: "Phylogenetic Systematics and Evolution"

Associate Editor, BMC Evolutionary Biology

Subject Editor, Insect Systematics and Diversity

Bjarte Henry Jordal <Bjarte.Jordal@uib.no>

NHM Bergen PlantSystematics

Please post the following announcement for a vascular plant systematics position at the Natural History Museum, Bergen, Norway:

https://www.jobbnorge.no/en/available-jobs/job/144755/associate-profess or-in-botany

Associate Professor in Botany

The University Museum conducts research, collection management and dissemination within the fields of both natural and cultural history. The Arboretum and Botanic Gardens are organized as a section under the Department of Natural History. The section has a staff of ~20 technical and administrative positions. In addition to the Museum Gardens on the University Campus in central Bergen, it includes the Botanical Gardens and the Norwegian Arboretum at Milde ca. 22 km south of the city center.

We are seeking an active researcher within the fields of vascular plant systematics and evolution, phylogenetics, evolutionary relationships, taxonomy, plant biodiversity and underlying evolutionary processes, or related fields. The research should be relevant to the collections in the Arboretum.

Applicants must be able to document research activity and production on an international level within one or more of these fields. The successful candidate must also document the ability to attract external funding. It is also expected that the successful candidate will take part in the teaching of botany at UiB and contribute to the internordic research school in biosystematics, ForBio.

The successful candidate will also be taking part in the development of new natural history exhibitions.

Bjarte Jordal, PhD

Associate Professor in Systematic Entomology

The Natural History Museum

University Museum of Bergen

P.B. 7800, NO-5020 Bergen

Webpage: Bjarte Jordal

Research Group: "Phylogenetic Systematics and Evolution"

Associate Editor, BMC Evolutionary Biology

Subject Editor, Insect Systematics and Diversity

Bjarte Henry Jordal <Bjarte.Jordal@uib.no>

NorthwesternU EvolutionaryBiol

See the ad below and more information here http://www.envsci.northwestern.edu/visiting-assistant-professor.html We are open to a wide range of interest areas, and would love to have someone with expertise in evolution, phylogenetics, evolutionary ecology, or someone who applies GIS-based environmental data to evolutionary questions.

The successful candidate will be expected to teach six courses per year (two per quarter), including one introductory course focused on human-environment interactions broadly defined, a sequence of courses focused on the theory and application of geographic information systems (GIS), and additional advanced courses in their area of expertise. The appointment will begin September 1, 2018. The initial term is two years, with the possibility of renewal for one additional year. The candidate should have a Ph.D. in environmental science or a closely related field at the time of appointment.

Applicants should submit a cover letter, curriculum vitae, contact information for three references, and statement of teaching interests, experience, and philosophy. Review of applications will begin February 1, 2018 and continue until the position is filled.

< https://facultysearch.weinberg.northwestern.edu/apply/index/MjY3 >

Application Instructions Applications will only be accepted online. Please prepare all documents in advance as Adobe PDF files. All required fields are marked with an asterisk and must be filled in before clicking on the "Submit" button. Incomplete applications cannot be saved.

Prior to beginning the application:

1. Prepare a separate PDF (3MB max file size) for each of your documents. 2. Prepare a list of names and email addresses for your external academic references.

Three references are required. Please note that your references will not be automatically contacted upon completion of your application. You will be notified if and when your references are contacted to upload letters.

Once you have prepared the information above you may click on the link below to begin the application. Questions may be addressed to: search.environment@northwestern.edu.

Nyree J C Zerega <n-zerega@northwestern.edu>

NRM Stockholm InsectBiomics

The Department of Bioinformatics and Genetics (http://www.nrm.se/en/forskningochsamlingar/-bioinformatikochgenetik.9000580.html) at the Swedish Museum of Natural History (http://www.nrm.se) is looking to fill a position as RESEARCH LEADER IN COMPARATIVE INSECT BIOMICS Tasks The successful candidate will lead a large, five-year research project in comparative insect biomics funded by the Knut and Alice Wallenberg Foundation. The aim is to use metabarcoding of Malaise trap and soil samples to study the size, origins, structure and function of the insect biomes in Sweden and on Madagascar. The project is a collaboration between the Swedish Museum of Natural History (Fredrik Ronquist), the Swedish University of Agricultural Sciences (Tomas Roslin), Stockholm University (Ayco Tack) and SciLifeLab / KTH Royal Institute of Technology (Anders Andersson). The field campaign in Madagascar will be organized in collaboration with the Madagascar Biodiversity Centre (Brian Fisher, California Academy of Sciences).

Together with the PIs, the successful candidate will be expected to coordinate and lead all activities in the project including field work in Sweden and Madagascar, high-throughput sequencing of the samples, bioinformatics processing, research output, and public outreach. The project staff will include field assistants, lab technicians, a full-time bioinformatician, and four postdocs. We also expect the project to attract additional guest researchers and postdocs with external funding.

The research leader will be involved in the hiring of all project staff. She or he will have a decisive influence on the detailed planning of the project, and will have a large degree of freedom in leading the project. The position will be placed in the Ronquist lab. Contact Fredrik Ronquist (contact details below) for more information about the project and the lab.

Qualifications We expect the successful candidate to have a strong research background with a PhD degree and at least some postdoc experience within a field that is relevant for the project. Ideally, the candidate would have significant experience of research in: (1) insect ecology or systematics; (2) metabarcoding; and (3) computational biology. The candidate should at least be proficient in one of these areas, and minimally have an interest in and some previous exposure to the others. Previous experience of project management or of the design of field campaigns is desirable.

The position can serve as a good platform for a future research career in comparative insect biomics, in which case we expect the candidate to take a leading role in some of the research studies that will result from the project. The position could also be appropriate for someone aiming at a future career in a research support role. In either case, we expect a candidate with exceptional organizational and communication skills, and with solid leadership qualities. Expect that the coordination and logistic challenges will take up a large part of the working time throughout the project but especially during the first years.

Fluency in spoken and written English is essential. Ideally, the candidate would also have a working knowledge of Swedish and French (for the Madagascar part).

Starting date. The starting date is July 1, 2018, and the position is for 4.5 years with a possibility of prolongation if additional funds for the project become available.

For more information about the position, contact Professor Fredrik Ronquist, Head of the Department of Bioinformatics and Genetics (fredrik.ronquist@nrm.se; +46-8 519 540 94). Trade union representatives are Emily Dock-Ãkerman (emily.dock@nrm.se; +46-8 519 542 18) for SACO and Anna Sandberg (anna.sandberg@nrm.se; +46-8 519 542 17) for ST.

The application should consist of a personal letter, a description of the candidate's vision of her or his role in the project (max 5 pages), and a CV. Mark your application with dnr 2.3.1-574-2017 and send it to rekrytering@nrm.se no later than December 18, 2017

Fredrik.Ronquist@nrm.se

NTNU Taiwan SummerJob InsectSpeciation

The Systematics & Evolutionary Biology Lab in the National Taiwan Normal University (NTNU) is seeking 3-4 summer interns to study the speciation in damselflies in 2018.

We focus on a damselfly species, *Psolodesmus mandarinus*, with two subspecies differ in their distribution and wing pigmentations in Taiwan main island, providing a great opportunity to evaluate the relative importance of natural and sexual selection in damselfly divergence. We incorporate a wide range of techniques, including a whole-island field survey, behavioural observation, morphological manipulation experiments, population genetics and genomic analysis to investigate the divergence in damselflies. A description of research projects:

https://sites.google.com/site/yuhsunhsu/research?pli=3D1 Research training Morphological measurements and behavioural observation will be conducted in a damselfly population within a research station in northern Taiwan (Fusan Botanical Garden: http://fushan.tfri.gov.tw/en/index.php). This is a good opportunity for undergraduate students to be involved in a research project of the Asian tropics. The field survey will be conducted from 1st July to 31st August continuously, with the possibility to extend for another two to four weeks. The training will include individual marking, morphological measurements and behavioural observation. Basic statistical analysis can also be taught if perspective interns are highly interested in.

Funding Each intern will receive a total of NT$30,000/month (~$1,000 USD) for two months together from TIGP and Chung-Ping Lin's laboratory (the hosting PI). In addition, half of the cheapest round-way airfare at economy class of the batch will be provided upon completion of the training program by TIGP.

Accommodation and meals Accommodation will be arranged in a research center next to the field site. Accommodation fee varies for each year but generally ranges between 0 and 150 NTD/night. Meals and lodging will be covered by the research projects.

Eligibility - The position is open to all applicants that meet TIGP Internship admission criteria, but preference will be given to undergraduate students with prior experiences in field survey, animal behaviour, and/or insect biology. Interns with scooter/car driving license will be preferred. Criteria/material used to evaluate the applicant's qualifications for the admission: https://db1x.sinica.edu.tw/tigpSummer/pageEligibility.php How to apply perspective students should prepare (1) a CV, (2) a list of prior experience, and (3) a one-page statement of research interests in one PDF file and email it to Yu-Hsun Hsu (yuhsunhsu@gmail.com) with the subject line "TIGP Internship application Speciation in damselflies". Additionally, perspective interns should submit a formal online application for admission in TIGP International Internship (https://db1x.sinica.edu.tw/tigpSummer/index.php). The online application will be open between 1st January and 31st March 2018.

The Systematics & Evolutionary Biology Lab

(http://web.ntnu.edu.tw/~treehopper/index.php?page=3Dhome&lang=3Den)

The Department of Life Sciences

(http://www.biol.ntnu.edu.tw)

National Taiwan Normal University

(http://en.ntnu.edu.tw)

TIGP Biodiversity Program Website

(http://biodiv.sinica.edu.tw/TIGP-BP/)

TIGP International Internship

(https://db1x.sinica.edu.tw/tigpSummer/index.php)

Biodiversity Research Center, Academia Sinica

(http://biodiv.sinica.edu.tw/en/)

Fusan Botanical Garden

(http://fushan.tfri.gov.tw/en/index.php)

–

Dr Yu-Hsun Hsu (Post-doc research fellow) Department of Life Science National Taiwan Normal University, Taiwan Website: https://sites.google.com/site/yuhsunhsu/ yuhsunhsu@gmail.com

QuinnipiacU Connecticut EvolutionaryGenetics

Link to Apply: https://faculty-careers-quinnipiac.icims.com/jobs/2318/biological-sciences%3a-tenure-track-faculty/job

Biological Sciences: Tenure Track Faculty

The Department of Biological Sciences at Quinnipiac University invites applications for a tenure-track Assistant Professor in Genetics to start August 2018.

Applicants whose research focuses on bioinformatics, or Drosophila or similar non-mammalian model systems are especially encouraged to apply.

About the College of Arts and Sciences:

The breadth of programs offered in the College of Arts and Sciences provides the traditional strengths of a liberal arts education, with a focus on cultivating the intellectual and practical skills that students need for their personal and professional lives. The College of Arts and Sciences offers undergraduate majors in behavioral neuroscience, biochemistry, biology, chemistry, criminal justice, economics, English, game design and development, gerontology, history, independent majors, interdisciplinary studies, law in society, mathematics, philosophy, political science, psychology, sociology, Spanish language and literature, and theater.

In addition, the College of Arts and Sciences has 31 undergraduate minors, a combined 4 + 1 BS in Biology/MS in molecular and cell biology program, and a master of science in molecular and cell biology program.

About Quinnipiac University:

Quinnipiac is a private, coeducational, nonsectarian institution located 90 minutes north of New York City and two hours from Boston. The university enrolls 7,000 full-time undergraduate and 3,000 graduate and part-time students in 100 degree programs through its Schools of Business, Communications, Education, Engineering, Health Sciences, Law, Medicine, Nursing and College of Arts and Sciences. Quinnipiac consistently ranks among the top regional universities in the North in U.S. News & World Report's America's "Best Colleges" issue. Quinnipiac also is recognized in Princeton Review's "The Best 380 Colleges." The Chronicle of Higher Education has named Quinnipiac among the "Great Colleges to Work For." For more information, please visit www.qu.edu . Responsibilities

* Teaching of introductory and advanced courses in genetics, as well as some combination of core courses (introductory biology, non-majors, research methods, etc) * Develop and maintain an active research program involving undergraduates * Engage in academic advising and university service appropriate to interests * Apply for outside research funding * Publish in appropriate peer-reviewed journals * Committed to excellence in teaching

Qualifications & Special Instructions to Applicants

* PhD at the time of the appointment (August 2018) is required * Proven ability to effectively teach university-level lectures and laboratories * Experience with the use of instructional technologies highly desired * Excellent communication and interpersonal skills

Quinnipiac University is considering only those applicants who have valid authorization to work in the United States. Quinnipiac University does not sponsor employment based visas for this position.

TO APPLY:

Applications must be submitted electronically and include a cover letter which addresses the candidate's qualifications, curriculum vitae, statement of teaching philosophy, a research plan for the next 5 years, and the names and contact information for three references on the application form. Review of applications will continue until the position is filled. Review of applications will begin on December 1st and will continue until the position is filled.

Quinnipiac University has a strong commitment to the principles and practices of diversity throughout the University community and welcomes candidates who would enhance that diversity.

Quinnipiac University is an Equal Opportunity Employer.

Job Code: 2017-2318

Joanna Wayton, JD

HR Specialist

Quinnipiac University

Phone: 203-582-7738

joanna.wayton@qu.edu

"Wayton, Joanna" <Joanna.Wayton@quinnipiac.edu>

SGN Frankfurt ResAssoc NicheEvolution

Job offer ref. #11-17023

Senckenberg Gesellschaft fÂÂ^{1}r Naturforschung (SGN) is a member of the Leibniz Association and has an international reputation in all fields of Natural History research. It runs six research institutes and two museums in Germany and is also custodian of the UNESCO World Heritage Site at Messel. At our research institute and natural history museum in Frankfurt am Main, Germany we invite applications for a

Research Associate (65%)

within the context of the Research project "Niche evolution of Tibetan-Himalayan Rhyacophilidae (Trichoptera) II: Comparative Phylogeography and Niche Differentiation of alpine/subalpine Himalopsyche of the Himalayan/QTP Region"

Your tasks: The candidate will comparatively study the phylogeography of subalpine and alpine caddisfly species from genus Himalopsyche in the Tibetan-Himalayan region. The project will focus on using anchored hybrid enrichment methodologies and massive parallel sequencing data to address questions on the evolutionary history and population genetics of the target species. Additional research aspects will involve niche modelling and niche differentiation studies that will be performed in collaboration with working groups at the IGB Berlin. The successful candidate will join a highly motivated team of 8 scientists and research support staff working in the group of Dr. Steffen Pauls on a variety of topics in molecular systematics, population genetics and biodiversity of insects. The workplace is Frankfurt, Germany, but the project will also entail a significant of stream ecological field work in challenging environments (e.g. high elevation), and extended stays in central Asia.

Your profile: 'ñ Master Degree in Biology or related disciplines 'ñ background in evolutionary biology or molecular systematics and phylogenetics 'ñ strong interest in working with aquatic insects using molecular & morphological data 'ñ very good organization skills, and the ability and motivation to perform field work in remote mountain areas 'ñ experience with data handling and statistical analyses using programming language(s) (e.g. R, bash) is beneficial 'ñ excellent verbal and written communication skills 'ñ willingness to co-operate with other research groups at Senckenberg, associated projects on the evolution of Himalayan plants and animals, and our international collaborators in the Europe, North America and Asia

What is awaiting you? It is possible to work towards a PhD degree in the context of this position. Salary and benefits are according to a full time public service position in Germany (TV-H E13, 65%). The contract should start on February 1st, 2018 or as soon as possible thereafter and is limited for three years. The Senckenberg Gesellschaft fÂÂ^{1}r 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 fÂÂ^{1}r Naturforschung.

Please send your application, mentioning the reference of this job offer (ref. #11-17023) before December 15th, 2017 by e-mail (attachment in a single pdf document) and including a letter outlining your motivation and suitability for the position, a detailed CV including a list of publications and solicited funding (if available), contact details of 2 referees, and copies of educational transcripts in a single PDF file to:

Senckenberg Gesellschaft fÂÂ^{1}r Naturforschung Senckenberganlage 25 60325 Frankfurt am Main E-Mail: recruiting@senckenberg.de

recruiting <recruiting@senckenberg.de>

SonomaStateU EvolutionaryEcol

we are searching for a community ecologist at Sonoma State. I certainly hope that our candidates include an evolutionary component to their work.

Sonoma State University 'V Community Ecology Review of Applications begins Dec 3 2017

The Department of Biology at Sonoma State University seeks to hire a highly motivated and productive scientist for a tenure-track Assistant Professor position in Community Ecology. The candidate must have a proven track record of publication in peer-reviewed journals and will be expected to develop and maintain an externally funded research program. We are interested in candidates that work in terrestrial (above ground and/or below ground) or marine systems. We are especially interested in candidates whose research program uses a range of techniques that include field approaches to examine community processes. We seek a dynamic teacher-scholar with a strong commitment to undergraduate and graduate education and the ability to attract and mentor students in our graduate program. Teaching responsibilities include introductory, upper-division, and graduate classes, and for this position may include ecology or marine ecology. The candidate will also have the opportunity to contribute to other courses, which could include an offering in their area of specialty. See full job announcement at our web site: http://web.sonoma.edu/-aa/docs/poas/tt/poa_104478.pdf . Sonoma State University is located in Sonoma County, which offers access to a wide range of environments for research, and is home to the Center for Environmental Inquiry, which manages Galbreath Wildlands Preserve (3,670 acres) and Fairfield Osborn Preserve (450 acres). In addition, the Department of Biology has greenhouse facilities that are used for both teaching and research.

Nathan Rank <rank@sonoma.edu>

TexasTechU EvolutionaryTheory

ASSISTANT PROFESSOR IN QUANTITATIVE BIOLOGY: DEPARTMENT OF BIOLOGICAL SCIENCES, TEXAS TECH UNIVERSITY The Department of Biological Sciences at Texas Tech University invites applicants for a 9 month tenure track Assistant Professor position in Quantitative Biology to begin in Fall 2018. We seek an innovative scientist who develops novel mathematical or statistical methods to investigate fundamental questions in biology; especially those related to ecology, evolution, genomics, or systems biology. Research in the department spans fields ranging from molecules to ecosystems, and we are particularly interested in candidates who can interact productively with colleagues in different fields. The successful candidate will establish an innovative, externally funded research program, direct M.S. and Ph.D. student research, and teach courses on the analysis of biological data, as well as in their area of specialty. Service duties include program-building, as well as commitment to extra-curricular activities. Service to the department, college, and university is expected.

A Ph.D. in Biology or a related field is required and postdoctoral experience is preferred. Candidates with strong records of scholarship supported by extramural funding and the proven capacity or clear potential to bring externally sponsored research to Texas Tech University are encouraged to apply. Experience working with diverse student populations and first-generation students is highly desirable.

Applicants should submit: a cover letter, curriculum vita, three representative publications, and statements of research and teaching interests. Applicants should also arrange for three letters of recommendation to be sent, by the application deadline, to hrs.recruiting@ttu.edu with the subject $B!H(BQuantitative Biology Recommendation Letter.$B!I(B To submit all other materials, please go to http://www.texastech.edu/careers/-faculty-positions.php, click on Search Openings, and enter 12027BR as the Requisition ID.

To insure full consideration, all materials must be submitted by 12 Jan., 2018. Questions can be addressed to the search committee chair Dr. Sean Rice (sean.h.rice@ttu.edu). For further information on the department and graduate and undergraduate programs, see http://www.biol.ttu.edu . As an Equal Employment Opportunity/Affirmative Action employer, Texas Tech University is dedicated to the goal of building a culturally diverse faculty committed to teaching and working in a multicultural environment. We actively encourage applications from all those who can contribute, through their research, teaching, and/or service, to the diversity and excellence of the academic community at Texas Tech University. The university welcomes applications from minorities, women, veterans, persons with disabilities, and dual-career couples.

"Rice, Sean H" <sean.h.rice@ttu.edu>

UArizona EvolutionaryBiol

University of Arizona – Integrative Evolutionary Biologist ASSISTANT/ASSOCIATE PROFESSOR (TENURE TRACK)

The Department of Ecology and Evolutionary Biology at the University of Arizona seeks applicants with an excellent track record and promising trajectory of research integrating evolutionary biology with other disciplines utilizing transformative, innovative, and empirically driven approaches. The ideal candidate will have deep expertise in evolutionary genetics/genomics and related areas and will be expected to continue or build a successful record of extramural funding and to teach at both the undergraduate and graduate levels.

We are looking for an early to mid-career scientist, to be appointed as an Assistant or Associate Professor, who is using the power of cutting-edge evolutionary biology and new data streams to break new ground and address real-world biological or biomedical issues. Potential research areas could include, but are not limited to: evolutionary genetics and genomics, population genetics, phylodynamics, epidemiology, disease evolution/ecology, and human health/genetics. A focus on any organism or system is welcome.

At the University of Arizona, we value our inclusive climate, because we know that diversity in experiences and perspectives is vital to advancing innovation, critical thinking, solving complex problems, and creating an inclusive academic community. We translate these values into action by seeking individuals who have experience and expertise working with diverse students, colleagues and constituencies. Because we seek a workforce with diverse perspectives and experiences, we encourage minorities, women, veterans, and individuals with disabilities to apply. As an Employer of National Service, we also welcome alumni of AmeriCorps, Peace Corps, and other national service programs.

Further information about the position and instructions for applying are online at https://uacareers.com/postings/22451 . Mike Sanderson <sanderm00@gmail.com>

UArkansas DiseaseEvolution

TENURE-TRACK ASSISTANT PROFESSOR in DISEASE ECOLOGY The Department of Biological Sciences at the University of Arkansas invites applications for a tenure-track Assistant Professor faculty position in Disease Ecology (Posting # 23744). We specifically seek candidates that address the ecology of infectious disease, or host-pathogen interactions in non-domesticated animals or plants. Research areas may include, but are not limited to: Population and community-level dynamics of disease-causing agents and their hosts or vectors; Co-evolutionary interactions; The ecology of emerging infectious diseases; The synergy between anthropogenic impacts (climate change, habitat loss, urbanization) and disease ecology. The research emphases of our preferred candidates will also: (1) Bridge the interface between ecology and evolution; (2) Combine theoretical and empirical approaches; and (3) Complement existing departmental strengths in ecology and evolutionary biology. Candidates from historically underrepresented STEM groups are particularly encouraged to apply.

Requirements include: Ph.D. in biological sciences or related field, post-doctoral experience in ecology, evolutionary biology, or related field, and demonstrated research accomplishments. Expectations: establish externally funded research program, publish original research in peer-reviewed scientific journals, contribute to undergraduate/graduate education, and service. All applicants must submit cover letter/letter of application, curriculum vitae, teaching statement, research statement, and contact information for three references.

Visit https://jobs.uark.edu/postings/23744 for full position announcement and application instructions. See: http:/biology.uark.edu for departmental information.

Submit complete applications by December 17, 2017 for full consideration. Late applications will be reviewed as necessary to fill the position.

Search committee chair: Dr. J.D. Willson (jwillson@uark.edu).

The University of Arkansas is an equal opportunity institution committed to achieving diversity in its faculty. Therefore, the university is especially interested in applications from qualified candidates who would contribute to the diversity of our academic departments. The university welcomes applications without regard to race/color, sex, gender, pregnancy, age, national origin, disability, religion, marital or parental status, protected veteran or military status, genetic information, sexual orientation, gender identity or any other characteristic protected under applicable federal or state law. 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.

Adam Michael Siepielski <amsiepie@uark.edu>

UCalifornia Irvine Evolution

The Department of Ecology and Evolutionary Biology in the Ayala School of Biological Sciences at the University of California, Irvine invites applications for a tenure-track faculty position in Evolutionary Biology, broadly interpreted. Relevant topics include, but are not limited to: evolution of development, complex traits, population genetics, ecological genetics, evolutionary theory, systematics, phylogenetics, and comparative genomics. We are interested in applications from scientists applying both empirical approaches (including genetics, high-throughput genomics, and development) as well as computational/theoretical approaches (including statistics, theory, simulation, and bioinformatics). We encourage candidates studying any organism(s) to apply.

The successful candidate is expected to build an independent, externally funded research program leading to innovations in the understanding of evolutionary biology. The candidate will also contribute to teaching and mentoring at the graduate and undergraduate levels.

Biological Sciences at UC Irvine is a vibrant community of scholars comprised of over 100 faculty members, including six Fellows of the National Academy of Sciences, seven of the American Academy of Arts and Sciences, and two of the Royal Society. UCI is a Minority Serving Institution (MSI), designated as a Hispanic-Serving Institution (HSI) and as an Asian American and Native American Pacific Islander-Serving Institution (AANAPISI). These federal designations align with UCI's aspiration to be a national leader and global model of inclusive excellence. Biological Sciences at UCI is highly interdisciplinary with many connections to the Schools of Medicine, Physical Sciences, Information and Computer Sciences, and Engineering through its Center for Complex Biological Systems. The Department of Ecology and Evolutionary Biology is home to 38 faculty and about 55 graduate students. Research in Ecology and Evolutionary Biology, http://ecoevo.bio.uci.edu/, uses a range of methodologies spanning field studies, experimental approaches, and theoretical and computer modeling. Students and faculty have easy access to field sites that include marine, desert, and California chaparral communities. UCI is a top ten public research university that excels at improving outcomes for students from economically disadvantaged backgrounds and as a consequence has consistently been ranked as the best university in the nation in promoting upward mobility of its graduates.

Salary is commensurate with qualifications and based on University of California pay scales.

Review of applications will begin December 20, 2017.

REQUIREMENTS Curriculum Vitae - Your most recently updated C.V. Cover Letter (Optional) Statement of Research Statement of Teaching - See our guidance for writing a reflective teaching statement. Statement of Contributions to Diversity - Statement addressing how past and/or potential contributions to diversity will advance UCI's Commitment to Inclusive Excellence. 3-5 letters of reference required

For full instructions and application form, please go to https://recruit.ap.uci.edu/apply/JPF04381 . "J.J. Emerson" <jje@uci.edu>

UCollegeLondon PlantOrFungalEvolution

Dear Colleagues,

We would be very grateful if you could bring the following position at University College London to the attention of suitable candidates.

Quain Professor or Associate Professor of Plant or Fungal Evolutionary Biology University College London http://bit.ly/UCL-Quain We seek to appoint a scientist as Quain Professor or Associate Professor of Plant or Fungal Evolutionary Biology. The successful candidate will have an international reputation in the field of Plant or Fungal Evolutionary Biology and will provide leadership in expanding the study and teaching in this area across UCL.

The Research Department of Genetics, Evolution and Environment (GEE) is one of four Research Departments in the Division of Biosciences at UCL, one of the world's leading centres for basic biological sciences and part of the UCL Faculty of Life Sciences. The post will be held in the Centre for Life's Origins and Evolution (http://bit.ly/UCL-CLOE), a cross-departmental institute within GEE. The candidate's research will fit into one of the three themes of CLOE: origins of life and of major innovations; pattern of evolution at all time scales, across the tree of life; and the processes underpinning the emergence of biological complexity/diversity. Areas of interest include, but are not restricted to: comparative genomics; diversification of major groups; evolution of plant/fungal interactions; the genetic basis of key transitions; plastid origins; evodevo. We welcome applicants working on any taxa from unicells to angiosperms. The research may be computational, experimental or both.

Many thanks

Max Telford

To apply follow: http://bit.ly/UCL-Quain-apply Max Telford Professor of Zoology Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 (Internal: 32554) Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/academic-staff/telford/telford.html Open access journal EvoDevo: http://www.evodevojournal.com/ "Telford, Max" <m.telford@ucl.ac.uk>

UColorado Denver EvoDevo

Note: This is a broad search, encompassing evolution of development, among other sub disciplines. Full details are available through the website listed below.

University of Colorado Denver The Department of Integrative Biology (http://www.ucdenver.edu/-academics/colleges/CLAS/Departments/biology/-Pages/Biology.aspx) on the University of Colorado Denver downtown campus seeks to fill a new tenure-track faculty position: Assistant Professor in Developmental Biology (Job #11590 at www.jobsatcu.com).

Review of applications will begin as they are received, and will continue until the position is filled.

UCD is dedicated to ensuring a safe and secure environment for our faculty, staff, students and visitors. To achieve this goal, we conduct background investigations for all prospective employees. The University of Colorado is committed to diversity and equality in education and employment.

GREGORY.RAGLAND@ucdenver.edu

UColorado Denver QuantitativeComputationalBiol

Quantitative/Computational Biology Faculty Position University of Colorado Denver

The Department of Integrative Biology at the University of Colorado Denver seeks to hire a tenure-track faculty member in quantitative/computational biology at the rank of Assistant Professor. The successful candidate will demonstrate a strong record of research accomplishments centering on the use or development of modern computational, statistical, or theoretical methods to answer fundamental questions at any scale from molecular to macrosystems. Preference will be given to candidates who would complement and build on existing departmental strengths in comparative genomics, development, behavior, and physiological or population ecology. The successful candidate is expected to establish a vigorous, externally funded research program that will support PhD and Masters programs in Integrative Biology, as well as contribute to graduate and undergraduate teaching in modeling and quantitative analysis, advising, and mentoring that support diversity and inclusion.

Application packets should include contact information for 3 references, CV, cover letter, summary of research accomplishments and goals, and a statement of teaching experience and interests. Within their materials, applicants should specifically address past contributions and future commitments to promoting diversity, equity and inclusion. Review of applications will begin on November 24, 2017, and will continue until the position is filled. Please refer to the full job announcement for additional details and instructions: https://cu.taleo.net/-careersection/2/jobdetail.ftl?job=11665&lang=en CU Denver is dedicated to ensuring a safe and secure environment for our faculty, staff, students and visitors. To achieve this goal, we conduct background investigations for all prospective employees. The University of Colorado is committed to diversity and equality in education and employment.

GREGORY.RAGLAND@ucdenver.edu

UDallas ComputationalBiology

The Biology Department at the University of Dallas seeks applicants for a tenure-track position starting in Fall 2018. Candidates must have a Ph.D. by time of employment with a strong commitment to undergraduate research and a record of past work in the area of computational biology/bioinformatics as part of a human genetics, biomedical sciences, biochemistry, systems biology or equivalent. Postdoctoral experience is preferred. The successful candidate will regularly teach upper-division courses that cover fundamental biological principles, an upper-division course in the candidate's area of specialization (computational biology/bioinformatics/biophysics/biomedical/biostatistics) with the potential to occasionally teach interdisciplinary courses in collaboration with other university programs. The candidate will aid in advising majors, including students interested in graduate careers.

Candidates should submit a letter of application explaining their suitability for the position, C.V., undergraduate and graduate transcripts, the names and contact information for three references, a research plan, a statement on teaching philosophy, and evidence of teaching effectiveness to https://hr.udallas.edu/apply/.

Any questions about the position should be directed to Dr. William Cody, Department of Biology, University of Dallas, 1845 E. Northgate Dr., Irving, TX 75062; wcody@udallas.edu. Review of applications will begin as soon as received and continue until January 15, 2018 or the position is filled.

The University of Dallas is a Catholic university which seeks to educate the whole person, encouraging its students to pursue wisdom, truth, and virtue as the primary ends of education, and we invite you to review our Mission (http://www.udallas.edu/about/mission.php). The University of Dallas is an Equal Opportunity/Affirmative Action employer. The university does not discriminate against individuals on the basis of race, color, religion, sex, national origin, genetic information, protected veteran status, age or disability in the administration of its employment practices.

Link: https://chroniclevitae.com/jobs/0000399757-01 – Deanna Soper, PhD Assistant Professor of Biology University of Dallas

Deanna Soper <dsoper@udallas.edu>

UFlorida EvoDevo

Animal Developmental Biology ASSISTANT PROFESSOR, TENURE-TRACK Department of Biology University of Florida

The Department of Biology at the University of Florida seeks a tenure-track Assistant Professor in the area of developmental biology to begin August 16, 2018. This position is intended to expand and strengthen cross-college collaborations in the area of reproductive and developmental biology, which is currently an area of significant research strength at UF. We target researchers who are working to understand development and/or reproduction in non-mammalian animals, including evolution of development.The successful candidate will be expected to establish an extramurally-funded, internationally recognized research program. The candidate will also be expected to develop and teach courses at the undergraduate and graduate levels.

The University of Florida is among the top ten public universities in the United States. The Department of Biology provides an integrative and collegial environment in which faculty engage in teaching, research and service across evolutionary, ecological, physiological and molecular disciplines. Research in the biological sciences at the University of Florida is conducted by faculty in many departments and across several Colleges and Institutes, providing a rich intellectual environment and extensive opportunities for collaboration. The University of Florida provides state of the art infrastructure and core facilities for molecular biology, and possesses a world-class supercomputing facility.

The University of Florida counts among its greatest strengths ’V and a major component of its excellence ’V that it values broad diversity in its faculty, students and staff and creates a robust, inclusive and welcoming climate for learning, research and other work. UF is committed to equal educational and employment opportunity and access, and seeks individuals of all races, ethnicities, genders and other attributes who, among their many exceptional qualifications, have a record of including a broad diversity of individuals in work and learning activities.

The University of Florida is an Equal Opportunity Institution dedicated to building a broadly diverse and inclusive faculty and staff. The selection process will be conducted in accord with the provisions of Florida's 'Government in the Sunshine' and Public Records Laws. Persons with disabilities have the right to request and receive reasonable accommodation.

ADVERTISED SALARY: The salary is competitive and commensurate with qualifications and experience and includes a full benefits package.

MINIMUM REQUIREMENTS: Successful candidates must have obtained a Ph.D. or equivalent degree in biological sciences or another relevant discipline.

PREFERRED QUALIFICATIONS: Strong preference will be given to applicants with at least one year of postdoctoral experience, but exceptional applicants at the Ph.D. level may be considered.

SPECIAL INSTRUCTIONS TO APPLICANTS: Applications must be submitted through Careers at UF http://explore.jobs.ufl.edu/cw/en-us/listing/ [http://explore.jobs.ufl.edu/cw/en-us/listing/] (search job 505276) and must include: 1) a cover letter summarizing the applicant's qualifications and interests in the Department, (2) a complete curriculum vitae, (3) a statement of research interest, (4) a statement of teaching philosophy, and (5) names and contact information of three references. Applications will be reviewed beginning December 1, 2017 as received and the position will remain open until filled.The final candidate will be required to provide an official transcript prior to hiring. A transcript will not be considered “official” if a designation of “Issued to Student” is visible. Degrees earned from an educational institution outside of the

United States must be evaluated by a professional credentialing service provider approved by the National Association of Credential Evaluation Services (NACES), which can be found at http://www.naces.org/ [http://-www.naces.org/] .

OFFICIAL ADVERTISEMENT: http://-explore.jobs.ufl.edu/cw/en-us/job/505276/biology-assistant-professor-animal-developmental-biology
Joseph Ryan <joseph.ryan@whitney.ufl.edu>

UFlorida ResTech SpatialDataPostGIS

The MabLab at the University of Florida's Fort Lauderdale Research and Education Center (Davie, FL) is looking to fill an immediate opening for the position of a Biological Scientist. We are looking for an enthusiastic, highly motivated and responsible individual to join an exciting research team focused on spatial ecology, from fine-scale movement and habitat selection to range dynamics. Candidate will be responsible of the data system of the Lab (database, GIS and documents), and will assist research and extension projects within the Lab's themes.

The primary missions of the Biological Scientist will be:

1. Manage the Lab data system: the Lab relies on a data server using Linux (Debian). Most notably, the server runs a PostGIS database system, which hosts data from research projects of the Lab (notably wood stork, sea turtle and raccoon telemetry data and associated GIS layers), as well as Rstudio Server, Shiny, and GitLab, among others. The candidate will entirely manage the server (keep the data base and the associated metadata clean and up-to-date, set permissions for users and groups, develop Shiny apps to access and display data, etc.). 2. Assist and train other Lab members for data processing and analysis: candidate will assist Lab members (notably students) to process the data stored in the Lab database system, in order to prepare them for statistical analysis. He/she will also assist the next step of statistical analysis when relevant. 3. Maintain and develop the Lab R packages (basr, hab, rpostgis, rpostgisLT,), and publish them on CRAN when appropriate. Maintaining packages means keeping them up-to-date with changes in R and package dependencies, while developing involves the integration of new functions or the improvement of existing ones. 4. Contribute to the Labs extension program, through extensive communication with the Lab's partners (USGS, USFWS,), the preparation of brochures or posters, or the participation in outreach events. 5. Participate in field work: The Lab and its partners periodically needs help in various field work projects in the area, in the Everglades or beyond. The candidate will contribute to the field work effort whenever necessary. 6. Finally, significant time will be reserved for the candidate to conduct personal projects, which can include side projects or overarching issues within the Lab themes, and eventually lead to peer-reviewed publications.

Details of the position and application can be found here:

http://explore.jobs.ufl.edu/cw/en-us/job/505347/-landscape-ecology-biological-scientist-ii Start Date: Flexible, as early as January 2018. This is a permanent position from the University of Florida.

Closing Date: 07 January 2018.

Contact: For more information, please contact:

Mathieu Basille Assistant Professor in Landscape Ecology University of Florida basille@ufl.edu

–

Mathieu Basille

basille@ufl.edu | +1 954-577-6314 | University of Florida FLREC

≪ Le tout est de tout dire, et je manque de mots Et je manque de temps, et je manque d'audace. ≫ Paul Ãluard

basille@ufl.edu

UGeorgia EvolutionaryHumanGenetics

ASSISTANT PROFESSOR IN HUMAN GENETICS

The Department of Genetics at the University of Georgia invites applications for a tenure-track assistant professor faculty position in the area of human genetics. The ideal candidate will establish an active and independent research program grounded in the genetic analysis of human populations related to human biology, development, evolution, and/or disease, and may also use computational and/or model experimental systems to address mechanistic questions. UGA Genetics is strong in evolution, molecular genetics, and genomics, and we are looking for a colleague who will both strengthen and diversify our core areas.

Candidates must hold a Ph.D. or equivalent in a biological science or a relevant field; a strong record of scientific productivity and at least 1 year of postdoctoral experience is preferred. The candidate will be expected to maintain a rigorous, externally funded research program. Teaching will be at both the undergraduate and graduate level, with an expectation of participation in graduate training. For information about the department, see http://www.genetics.uga.edu. Please submit applications online at https://facultyjobs.uga.edu/postings/3011 . Applications should include a cover letter, CV, and no more than 2 page (each) statements of research and teaching interests, and copies of up to three publications. Applicants will be asked to provide names and e-mail addresses of three letter-writers who will receive an online link for submitting letters of reference. Review of applications will begin on November 20, 2017 and continue until the position is filled. Informal enquiries and questions may be addressed to one of the co-chairs of the search committee, Drs. Kelly Dyer (kdyer@uga.edu) and Doug Menke (dmenke@uga.edu).

The University of Georgia 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, gender identity, sexual orientation or protected veteran status. Persons needing accommodations or assistance with the accessibility of materials related to this search are encouraged to contact Central HR (facultyjobs@uga.edu). Please do not contact the department or search committee with such requests. The Franklin College of Arts and Sciences, its many units, and the University of Georgia are committed to increasing the diversity of its faculty and students, and sustaining a work and learning environment that is inclusive. Women, minorities and people with disabilities are encouraged to apply. Faculty members are expected to support the college's goals of creating and sustaining a diverse and inclusive learning environment. Georgia is well known for its quality of life in regard to both outdoor and urban activities (http://exploregeorgia.org). UGA is a land- and sea-grant institution located in Athens, 70 miles northeast of Atlanta, the state capital (www.visitathensga.com; www.uga.edu).

Kelly Dyer Associate Professor Department of Genetics University of Georgia Athens, GA 30602-7223 email: kdyer@uga.edu phone: 706 542 3154

Kelly A Dyer <kdyer@uga.edu>

UHohenheim Bioinformatics

The Faculty of Agricultural Sciences invites applications for the position of a

Full Professor (W3) of Bioinformatics

at the Institute of Animal Science to be filled as soon as possible.

The successful candidate will teach management and analysis of omics-data in agriculture in the Faculty of Agricultural Sciences' degree programs. Participation in teaching in the Faculty of Natural Sciences and the Faculty of Business, Economics and Social Sciences is also required. The candidate should be able to teach both in German and in English.

The research focus of the Professorship should be on the development of bioinformatic methods and algorithms and the analysis of massive DNA and RNA data sets from livestock and associated microorganisms. This includes assembling and functional annotation of sequenced genes and transcripts as well as taxonomic and functional classification of data from microbiological multi-omics projects. Interdisciplinary collaboration with associated research groups of the University of Hohenheim is expected.

The position offers attractive conditions for first-time full professor appointees. Scientists with interest in the research focus and excellent methodological skills in Bioinformatics are encouraged to apply. Prerequisites for applicants are habilitation or an equivalent research and teaching record which may have been established during a Junior or Assistant Professorship.

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

The University of Hohenheim seeks to increase the proportion of women in research and teaching, and strongly encourages female scientists to apply.

Please attach the following documents to your application: a statement of your future research interests, a curriculum vitae, a documentation of academic achievements (copies), a list of publications, a list of third-party funded projects, a teaching record, information on teaching evaluations, and three key publications.

Please apply online at www.uni-hohenheim.de/prof-appt-portal before the 31 st of January 2018.

Questions regarding the position may be directed to Prof. Dr. Reiner Doluschitz (Reiner.Doluschitz@uni-hohenheim.de). University of Hohenheim Faculty of Agricultural Sciences 70593 Stuttgart | Germany

– Dr. Karl Schmid Professor of Crop Biodiversity and Breeding Informatics Institute of Plant Breeding, Seed Science and Population Genetics (350) University of Hohenheim Fruwirthstrasse 21, D-70599 Stuttgart Tel: +49 711 459-23487 Email: karl.schmid@uni-hohenheim.de Web: evoplant.uni-hohenheim.de

Karl Schmid <karl@minzer-schmid.de>

ULiverpool ChairEvolBiology

Head of Department of Evolution, Ecology and Behaviour Competitive salary Deadline: 12-Jan-2018 23:30

http://tinyurl.com/yby2yzt9 The University of Liverpool, which is ranked in the top 1% of higher education institutions in the world, is an institution with global reach whose activities are rooted in world-leading research excellence and reflect the dynamics of the knowledge economy.

The Institute of Integrative Biology (IIB) is one of the 5 research-focused Institutes within the Faculty of Health and Life Sciences and lies at the heart of a thriving biomedical science campus in Liverpool. The Institute currently consists of 64 academic staff including 25 Professors. A number of independent research fellows, ˜100 staff on permanent and fixed-term research contracts, ˜100 postgraduate students and 28 technical staff. It is administered by 18 professional services staff providing management, financial, research and clerical support to the institute. With a research income of approximately 9.2m annually, the Institute's scientists deliver groundbreaking research which spans the complete range of biological scales from genes and genetic regulation through proteins, post-translational modification and cellular function to whole organisms, populations and ecosystems. The Institute has a strong profile in organismal biology – broadly defined to include evolution, ecology and behaviour – with an expanding portfolio of research funding and the appointment of several new members of staff in this area. IIB benefits from state-of-the-art facilities in genomics, proteomics, metabolomics and computational biology and expertise in applying these techniques to answer questions in evolution, ecology and behaviour. Particular emphasis is placed on breaking down disciplinary barriers and on encouraging the development of thematic networks of active research groups, both within IIB, but also extending externally into environmental science, mathematics and veterinary and clinical medicine. The Institute has Athena SWAN Gold status in recognition of its activities and policies promoting gender equality, placing it in the 1.6% of university departments holding such an award (see ECU website). IIB is committed to supporting its staff in reaching their full potential, providing a fair and supportive working environment and organisational structure.

The IIB now seek to appoint a new Head of the Department of Evolution, Ecology and Behaviour. As a full Professor, the appointee will be expected to conduct his/her own programme of internationally-leading research, including the regular production of high calibre research outputs; the provision of academic leadership, supervision and mentorship; the ability to secure a high volume of research grants from a range of sources; and the identification and energising of collaborative research activity within the Department, across the University, and externally.

Further, as Head of the Department of Evolution, Ecology and Behaviour, the appointee will act as a proactive and engaged academic and administrative leader for the Department. You will be responsible for driving forward the development of the Department through direct and collegial engagement with faculty members; through forging connections within the Department and across the University; and through the management of departmental-level administrations and through leadership of the peer-review process for grant applications and outputs.

Informal questions regarding the post should be directed to Professor Steve Paterson (s.paterson@liverpool.ac.uk)

The salary will be competitive and will be made on an appropriate point on the professorial academic pay scale, commensurate with experience. The position will be based at the University of Liverpool, UK.

Applications will be considered by the Selection Committee and provisionally shortlisted candidates will be invited to have informal conversations with relevant colleagues at the University (either by visiting in person or by skype or phone, depending on which is most convenient).

Following these conversations, shortlisted candidates will be invited to give a presentation, meet with a range of Department, Institute and Faculty members and observe relevant facilities on Tuesday 20 February 2018;

they will be formally interviewed with the appointing panel on Wednesday 21 February 2018, at which point selection of the preferred candidates will take place.

– Steve Paterson Professor of Genetics Institute of Integrative Biology University of Liverpool Liverpool, L69 7ZB, UK Tel +44 151 795 4521 Fax +44 151 795 4408 Mob +44 797 024 7668 s.paterson@liv.ac.uk http://www.liv.ac.uk/genomic-research/ Twitter: @scottishwormboy

"Paterson, Steve" <S.Paterson@liverpool.ac.uk>

ULiverpool DepartmentHead EvolutionaryBiol

Appointment of Head of Department of Evolution, Ecology and Behaviour, Institute of Integrative Biology

The University of Liverpool, which is ranked in the top 1% of higher education institutions in the world, is an institution with global reach whose activities are rooted in world-leading research excellence and reflect the dynamics of the knowledge economy.

The Institute of Integrative Biology (IIB) is one of the 5 research-focused Institutes within the Faculty of Health and Life Sciences and lies at the heart of a thriving biomedical science campus in Liverpool. The Institute currently consists of 64 academic staff including 25 Professors. A number of independent research fellows, ˜100 staff on permanent and fixed-term research contracts, ˜100 postgraduate students and 28 technical staff. It is administered by 18 professional services staff providing management, financial, research and clerical support to the institute. With a research income of approximately 9.2m annually, the Institute's scientists deliver groundbreaking research which spans the complete range of biological scales from genes and genetic regulation through proteins, post-translational modification and cellular function to whole organisms, populations and ecosystems. The Institute has a strong profile in organismal biology broadly defined to include evolution, ecology and behaviour with an expanding portfolio of research funding and the appointment of several new members of staff in this area. IIB benefits from state-of-the-art facilities in genomics, proteomics, metabolomics and computational biology and expertise in applying these techniques to answer questions in evolution, ecology and behaviour. Particular emphasis is placed on breaking down disciplinary barriers and on encouraging the development of thematic networks of active research groups, both within IIB, but also extending externally into environmental science, mathematics and veterinary and clinical medicine. The Institute has Athena SWAN Gold status in recognition of its activities and policies promoting gender equality, placing it in the 1.6% of university departments holding such an award (see ECU website). IIB is committed to supporting its staff in reaching their full potential, providing a fair and supportive working environment and organisational structure.

The IIB now seek to appoint a new Head of the Department of Evolution, Ecology and Behaviour. As a full Professor, the appointee will be expected to conduct his/her own programme of internationally-leading research, including the regular production of high calibre research outputs; the provision of academic leadership, supervision and mentorship; the ability to secure a high volume of research grants from a range of sources; and the identification and energising of collaborative research activity within the Department, across the University, and externally.

Further, as Head of the Department of Evolution, Ecology and Behaviour, the appointee will act as a proactive and engaged academic and administrative leader for the Department. S/he will be responsible for driving forward the development of the Department through direct and collegial engagement with faculty members; through forging connections within the Department and across the University; and through the management of departmental-level administrations and through leadership of the peer-review process for grant applications and outputs.

Informal questions regarding the post should be directed to Professor Christiane Hertz-Fowler (inbiohoi@liv.ac.uk)

The salary will be competitive and will be made on an appropriate point on the professorial academic pay scale, commensurate with experience. The position will be based at the University of Liverpool, UK.

The deadline for applications for this position is Friday 12th January 2018 and applications will be considered by the Selection Committee and provisionally shortlisted candidates will be invited to have informal conversations with relevant colleagues at the University (either by visiting in person or by skype or phone, depending on which is most convenient). Following these conversations, shortlisted candidates will be invited to give a presentation, meet with a range of Department, Institute and Faculty members and observe relevant facilities on Tuesday 20th February 2018; they will be formally interviewed with the appointing panel on Wednesday 21st February, at which point selection of the preferred candidates will take place.

Best wishes,

Bernie

Bernie King On behalf of

IIB Staffing Administration Account Institute of Integrative Biology University of Liverpool Biosciences Building Liverpool L69 7ZB iib@liv.ac.uk http://www.liverpool.ac.uk//integrative-biology "King, Bernadette" <B.King@liverpool.ac.uk>

UMassachusetts Boston EvolutionaryGenomics

The position is intended for evolutionary biologists and population geneticists - someone working at the interface of ecology-evolution.

ASSISTANT PROFESSOR IN ECOLOGICAL GENOMICS

UNIVERSITY OF MASSACHUSETTS BOSTON

The Biology Department at the University of Massachusetts, Boston seeks applicants for a full-time tenure track Assistant Professor in Ecological Genomics starting in September 2018. We seek candidates who use genomic approaches to address fundamental questions in ecology, population genetics, and evolution. Applications are particularly welcome from candidates who use creative molecular, experimental, comparative, or theoretical approaches to study genomic responses to global changes, but candidates working in any area at the interface of ecology and evolution using genomic approaches are welcome to apply. The successful applicant is expected to establish an externally funded research program, direct the research of students at the undergraduate, masters and doctoral levels, and interact with a dynamic group of ecologists and environmental biologists. Excellence in teaching at the undergraduate and graduate levels is expected. A Ph.D. and postdoctoral training (or equivalent professional experience) in evolution, ecology, or population genetics is required.

The University has a strong faculty with substantial research programs in environmental areas, and doctoral programs in Environmental Biology; Molecular, Cellular and Organismal Biology; and Environmental Sciences. Excellent opportunities exist to collaborate and engage in multidisciplinary research on campus, across the five UMass campuses and at UMass Boston's Nantucket Field Station.

Application materials must be submitted online:

http://umb.interviewexchange.com/-candapply.jsp?JOBID=91792 Applications should include a cover letter addressed to the search committee, a current curriculum vitae, 3-5 representative publications, a statement describing research interests and goals, and a teaching statement documenting teaching experience and philosophy. Applicants should also arrange for three letters of reference to be sent electronically to biology@umb.edu, or to Ecological Genomics Search, Biology Department, University of Massachusetts, 100 Morrissey Blvd., Boston, MA 02125. For further information, visit the Biology Department website at www.umb.edu/academics/csm/biology, or contact Ron Etter (ron.etter@umb.edu or 617-287-6613), search committee chair. Target date for receipt of applications is December 30, 2017, but applications will be reviewed until the position is filled.

UMass Boston is an Affirmative Action, Equal Opportunity, Title IX employer. Women and minorities are encouraged to apply.

Ron J. Etter Professor Biology Department University of Massachusetts 100 Morrissey Blvd. Boston, MA 02125 Voice 617-287-6613 FAX 617-287-6650 email ron.etter@umb.edu

Ron Etter <ron.etter@umb.edu>

UOklahoma ComputationalBiology

The University of Oklahoma College of Arts and Sciences and Gallogly College of Engineering seek creative and dynamic applicants for an open-rank tenured or tenure-track faculty position in Computational Biology. The position will start in August 2018 and is part of a cluster hire in data scholarship across the university. This initiative connects researchers from diverse scholarly domains for collaboration via common approaches and for improvement of educational opportunities and research opportunities.

Possible departmental home(s) for the candidate include the School of Computer Science, the Department of Microbiology and Plant Biology, and the Department of Biology, among others. A joint appointment is likely depending on the interests of the applicant. The successful candidate will conduct research and be teaching in Computational Biology and/or Bioinformatics, such as in algorithm development (sequential, parallel, and/or distributed), systems analysis and modeling, genomic or ecological data mining and/or visualization. We particularly seek applicants with research directed to big data, including large-scale microbial, plant, or animal -omics, multi-scale biological modeling, or machine learning/artificial intelligence. If desired, support for laboratory work is available. In-line with the norms of the affiliate department(s), the incumbent will contribute to teaching and training of undergraduate and graduate students, including in the Data Science and Analytics M.S. program (datascience.ou.edu). The incumbent will have a leadership role in the development of the cross-disciplinary data scholarship initiative.

More info here:

https://apply.interfolio.com/46604 Katharine Marske

Assistant Professor

Department of Biology

University of Oklahoma

kamarske.org

“kamarske@ou.edu” <kamarske@ou.edu>

Uppsala 2 PlantEcolEvolution

Department of Ecology and Genetics, Division of Plant Ecology and Evolution, Evolutionary Biology Centre, Uppsala University seeks to appoint two positions in Plant Ecology and Evolution:

Associate Professor/Senior Lecturer in Plant Ecology

(with the possibility of being employed as Professor)

The position includes research, teaching at graduate and undergraduate level, outreach activities and some administration. The holder of the position is expected to contribute actively to applications for external research grants and to the development of the research and teaching of the department.

In ranking eligible candidates, equal importance will be given to scientific and teaching skills. When judging scientific proficiency special importance will be given to research qualifications within plant population and community ecology.

More detailed information about the position and information about how to apply can be found

http://www.uu.se/en/about-uu/join-us/details/-?positionId=174434 Closing date for application is 8 December, 2017

Postdoctoral Research Fellow in Plant Ecology and Evolution

This four-year position is intended for a promising researcher at an early career stage.

The position includes research, teaching, and administration. Teaching duties include course responsibility, course administration and supervision of second- and third-cycle students. A position as postdoctoral research fellow is intended to qualify the holder for a teaching position with higher qualification requirements, and can be held for a maximum of four years.

Applicants who have obtained a doctoral degree or achieved the equivalent competence in seven years or less prior to the end of the application period will be given priority. The ranking of eligible applicants will be based primarily on research expertise. In assessing research expertise special weight will be attached to research merits in Plant Ecology and Evolution.

More detailed information about the position and information about how to apply can be found

http://www.uu.se/en/about-uu/join-us/details/-?positionId=171843 Closing date for application is 8 December, 2017

For further information about these positions, please contact Professor Jon Agren telephone +46-(0)18-471 2860 or email Jon.Agren@ebc.uu.se

The Evolutionary Biology Centre of Uppsala University offers a vibrant research environment and bridges a broad range of disciplines in the biological sciences. Information about the Evolutionary Biology Centre and the Department of Ecology and Genetics can be found at http://www.ebc.uu.se/ and http://www.ieg.uu.se/?languageId=1

Jon Ãgren <jon.agren@ebc.uu.se>

UVirginia LabSpecialist EvolutionaryGenetics

The Department of Biology is looking to hire a Laboratory Specialist in the Bergland lab (http://bergland-lab.org) at the University of Virginia. The Bergland lab uses Drosophila and Daphnia to study ecological and evolutionary genetics. Current projects in the lab include the genetics and physiology of rapid adaptation over seasonal time scales in Drosophila and adaptive evolution of predator induced phenotypic plasticity through time and space in Daphnia.

The main objective of this position to develop computational algorithms and experimental tools to aid in ongoing research in the Bergland lab. Responsibilities of the position include, but are not limited to, development of automated image classification tools and experimental apparatus for high-throughput phenotyping. Knowledge of scripting and programming languages as well as microelectronic design and manufacture are required.

For a complete announcement and to apply online, go to search for posting number 0622026 at https://jobs.virginia.edu. Initial review of applications begins 11/09/17 and will continue as long as required to identify a qualified pool.

The University of Virginia is an equal opportunity and affirmative action employer. Women, minorities, veterans and persons with disabilities are encouraged to apply.

For inquiries, contact Alan Bergland: aob2x@virginia.edu

“Bergland, Alan (aob2x)” <aob2x@virginia.edu>

UWisconsin-Milwaukee Genetics

The Department of Biological Sciences at the University of Wisconsin-Milwaukee (UWM) invites applications for a full-time tenure-track ASSISTANT PROFESSOR position in genetics beginning in Fall 2018. We seek an outstanding candidate with a strong record of research in any area of eukaryotic genetics using a plant or animal model organism or other species to address fundamental biological questions. This position requires a Ph.D. degree and postdoctoral experience in genetics or in a related area with expertise in genetics. The successful candidate is expected to establish a vigorous, extramurally funded research program involving students (undergraduate, M.S., and Ph.D.) and postdoctoral associates. Responsibilities also include teaching a general genetics course and an advanced course in his or her area of expertise.

To apply, please go to http://jobs.uwm.edu/postings/26864. A completed application should include a cover letter, curriculum vitae, statement of research interests (4 page maximum), teaching philosophy (1 page maximum). Additionally, as part of our application process, we are requesting a minimum of 3 letters of reference. Please provide the names and email addresses for your references in the Reference Letter section of the employment application. Upon submission of your application, an automated email will be generated and sent to your references with instructions on how to attach the reference letter to your application through a confidential on-line portal. Review of applications will start on January 15, 2018 and will continue until the position is filled.

UWM is a public urban R1 research university with a commitment to academic excellence. UWM is an Equal Opportunity/Affirmative Action Employer. More detailed information about UWM and the department may be found at: https://uwm.edu/biology/ . Emily Latch <latch@uwm.edu>

Vienna PopulationGenetics EvolutionaryGenomics

In a joint hire, the University of Vienna (Max F. Perutz Laboratories) and the Gregor-Mendel Institute of the Austrian Academy of Sciences offer a position that combines the best of both worlds: Substantial start-up and funding for a high-profile research group via the Academy of Sciences and University tenure-track.

Tenure-track position in Population Genetics and Evolutionary Genomics

A tenure-track junior position (equivalent to Assistant Professor) in population genetics and evolutionary genomics is available at the Vienna BioCenter. The position is a joint hire between the Gregor Mendel Institute (GMI) of the Austrian Academy of Sciences, and the Max F. Perutz Laboratories at the University of Vienna. We are primarily targeting junior scientists (i.e., Junior Group Leader or Assistant Professor), but exceptional applications at a more senior level will be considered. Although we are particularly interested in building strength in computational and genome-enabled biology, we welcome all applications focusing on basic research with relevance to evolutionary biology. Our main criterion is scientific excellence and we favor research with potential for high impact. Candidates are expected to develop an independent research program at the highest level. The position comes with an internationally competitive start-up package, including a substantial research budget and access to state-of-the-art facilities.

We are part of the Vienna BioCenter, a research cluster with 1,700 researchers from over 60 countries, located near the center of Vienna, one of the world's most livable cities. In recent years, Vienna has developed into one of the leading centers in evolutionary biology (www.evolvienna.at, www.popgen-vienna.at). The working language on campus is English, and the environment is family-friendly, with subsidized on-campus child-care facilities.

Please send your application, including a curriculum vitae, a brief description of your proposed research (no more than four pages), and contact details for at least three referees to Ms. Mariola Glawischnig (joint_recruitment@gmi.oeaw.ac.at).

Informal inquiries can be directed to Dr. Magnus Nordborg (magnus.nordborg@gmi.oeaw.ac.at), Scientific Director of the GMI, or Dr. Joachim Hermisson (joachim.hermisson@univie.ac.at), Professor of Mathematics and Biosciences at the University of Vienna.

Review of applications for the present search will begin Dec 31st, 2017 and will continue until the position is filled.

– Joachim Hermisson Professor for Mathematics and Biosciences University of Vienna Department for Mathematics Nordbergstr. 15, 1090 Vienna, Austria and Max F.Perutz Laboratories Dr.-Bohrgasse 9, 1030 Vienna, Austria phone: +43 (0) 1 4277 50648 email: joachim.hermisson@univie.ac.at www.mabs.at joachim.hermisson@univie.ac.at

---

WilliamJewellC Missouri PlantEvolution

William Jewell College Department of Biology seeks applicants for a full-time, tenure-track faculty position with teaching and research interests in plant evolutionary ecology to begin August 2018. The department seeks an individual who enjoys and is committed to excellence in undergraduate instruction, and is passionate about mentoring undergraduate students in the execution of authentic, quality, biological research. The research equipment and facilities at William Jewell College exceed that typically found at small, liberal arts colleges, and support exceptional opportunities for faculty and student research.

Qualifications - Ph.D. in Biology/Ecology/Evolution - Experience teaching inquiry-Â'based biology courses - A high aptitude for and interest in undergraduate teaching, including a desire to develop and engage in innovative pedagogical approaches - A passion for authentic, peer-Â'reviewed, biological research, and for mentorship of undergraduates in that research - A willingness to contribute to the college mission as described in the mission statement (see below).

Duties and Responsibilities

The faculty member will be expected to contribute to individually and team-Â'taught, introductory and upper-Â' division courses in ecological, evolutionary, and organismal biology. Teaching duties in the Department of Biology and in contribution to the core program in Critical Thought and Inquiry will include the following, spread across a two-Â'year teaching cycle:

Introductory Evolution and Ecology Lecture and Labs Upper division Ecology Lecture and Lab Plant Biology Lecture and Lab Introductory Biological Diversity Lecture and Labs Ethnobotany

The faculty member will also be expected to establish an active, undergraduate-Â'driven research program involving (but not necessarily limited to) investigation of questions at the level of plant population ecology.

Application Procedure

Candidates must submit the following documents in PDF or MS Word format via email to jobs@william.jewell.edu :

- Letter of application and curriculum vitae - William Jewell College application - Response to the College mission and philosophy, including statement of how the candidate will foster diversity and inclusion on our campus - Statement of teaching philosophy - Evidence of teaching effectiveness and promise of future excellence - Research statement detailing plans for future research and describing effective use of undergraduate researchers. Though plans for research at remote field sites are acceptable, the successful candidate must demonstrate a willingness and an ability to mentor students in local field or greenhouse research. - Undergraduate and graduate transcripts (copies are acceptable until finalists are selected) - Three confidential letters of recommendation will be requested for finalists, and sent via email to jobs@william.jewell.edu - Applicants who need accommodation for the application or interview process, please make such accommodation request in advance to the Office of Human Resources.

William Jewell College 500 College Hill Box 1017 Liberty, MO 64068 (816) 415-Â'6904

Availability Review of applications will begin November 3, 2017 and continue until the position is filled. All final candidates will be required to successfully pass a criminal background check prior to beginning employment.

Our Mission: William Jewell College promises students an outstanding liberal arts education that cultivates leadership, service, and spiritual growth within a community committed to open, rigorous intellectual pursuits.

Our Philosophy: We are critical thinkers in community pursuing meaningful lives.

William Jewell College is committed to achieving the goal of a diverse and inclusive academic community of faculty, staff and students. We seek individuals who are committed to this goal.

William Jewell College is an equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, age, sex, sexual orientation, gender identity or expression, national origin, genetic information, disability, or veteran status.

Rose M. Reynolds, Ph.D. Chair, Department of Biology Make an appointment: rosemreynolds.youcanbook.me Office: 816.415.7894 Fax: 816.415.5027 William Jewell College | www.jewell.edu "Reynolds, Rose" <reynoldsr@william.jewell.edu>

Other

Call proposals SMBE 2021

Want to meet like-minded colleagues from all over the world?

Wish you could have an international conference in your field closer to home?

SMBE is looking for a local host for its 2021 international meeting. Informal expressions of interest should be from a prospective local organizing committee of scientists headed by an SMBE member, and should reach SMBE President-Elect Bill Martin (smbe.contact@gmail.com) by 15 December 2017. Full proposals will need to be submitted using the SMBE template by April 30, 2018.

For details of meeting organization, please see the SMBE Conference Guidelines (http://www.smbe.org/smbe/-MEETINGS/ConferenceGuidelines.aspx).

The primary role of the local organizing committee will be to plan the scientific programme. All other aspects of the organization will be done in association with SMBE representatives and a professional conference organizer appointed by SMBE.

SMBE rotates its meetings geographically to encourage international participation. For 2021, we are particularly requesting proposals from outside North America and Europe. The next three years' meetings will be in Yokohama, Japan (2018), Manchester, UK (2019), and Quebec, Canada (2020).

Please note that SMBE is not interested in proposals from professional conference organizers. Looking forward to hearing from you.

Sincerely,

Bill Martin President-elect, SMBE

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

ESEB AttendanceAidGrant Call2018

*** Equal Opportunities Congress Attendance Aid Grants ***

The European Society for Evolutionary Biology is pleased to announce the call for applications for the ESEB Equal Opportunities Congress Attendance Aid Grants 2018.

The grant aims to ensure equal opportunities at the Joint Evolution conference in Montpellier, France in 2018, e.g. by facilitating the attendance of women with caring responsibilities, who would not otherwise be able to attend. The grant provides stipends of financial aid for scientists to help with the additional costs borne privately due to responsibilities for dependents when attending the ESEB congress. The stipend will contribute to covering expenses for care of dependents, but also for travel.

DEADLINE: FRIDAY, 16 FEBRUARY 2018

ELIGIBILITY

- Applicants must be ESEB members (for becoming a member of ESEB please visit http://eseb.org/society/-membership/). - Applications can be submitted by scientists at any stages of their professional career (e.g., undergraduate, Masters and PhD students, postdocs, and lecturers). - Applicants must explain explicitly how their attendance will increase equal opportunities at the society - Applicants must present either an oral communication or a poster at the respective meeting to be eligible for the award. This will be verified before the reimbursement, but no proof that a poster or talk is accepted is necessary at the application stage. - Applicants must detail how they intend to use the grant. Eligible costs include, but are not limited to: childcare on site, childcare at home, extra care at home for dependents, extra travel costs for babysitter (grandparents) etc. - The stipend will be paid out as a flat rate of 250, - EUR (in certain cases up to 500, - EUR) after the congress when confirmation of attendance is provided.

HOW TO APPLY

The application should be no more than 2 pages long and include:

- Name of the applicant - An explanation of how attendance at the meeting improves equal opportunities at ESEB - An explanation of how attendance at the meeting will further the attendant's professional goals - Budget - CV

Please submit the application as a single PDF-file by email to Ute Moniatte <office@eseb.org, subject: EO conference grant at the ESEB Office and take care to limit the size of attachments (total < 10 MB) in any one email.

Kind regards, Ute Moniatte

Dr. Ute Moniatte | ESEB Office Manager| office@eseb.org European Society for Evolutionary Biology | www.eseb.org ESEB <office@eseb.org>

ESEB ConferenceTravelAwards Call2018

**ESEB CONFERENCE TRAVEL AWARDS 2018*

The European Society of Evolutionary Biology (ESEB) is pleased to announce the call for applications for conference travel awards 2018.*

These stipends are for students and young scientists to attend the joint Evolution congress in Montpellier, France (http://evolutionmontpellier2018.org/). The stipend will consist of a waiver of the conference registration fee (early bird rate at registration and a contribution towards travel and living expenses (to be paid out as a reimbursement after the congress, based on specification of the expenses).

ELIGIBILITY: - Applicants must be ESEB members (for becoming an ESEB member, please visit www.eseb.org). - Applications can be submitted by scientists at various stages of their professional career (e.g., Masters and PhD students, postdocs, and lecturers). - Scientists working in a country with high GDP are not eligible (for the list of excluded countries see below). - People who received an ESEB travel stipend in the last five years are not eligible. - Applicants must submit to present either an oral communication or a poster to be eligible for the stipend. This will be verified before the reimbursement, but no proof that a poster or talk is accepted is necessary at the application stage.

PLEASE NOTE THAT THESE STIPENDS ARE GIVEN IN CONJUNCTION WITH ANALOGOUS STIPENDS OFFERED BY THE SSE (separate call), SO THERE IS NO NEED TO APPLY TO BOTH

HOW TO APPLY: Send your application by email to the ESEB Travel Bursary Committee, c/o Dr. Martijn Egas, Email: egas@uva.nl

The application should be no more than 2 pages long and include:

- Name of the applicant; - Budget, including sources of additional support; - An explanation of how attendance to the meeting will support the attendant's professional goals; - and a CV.

Please submit the application as a single PDF-file. A support letter from the applicant advisor/mentor/senior colleague is also required. Support letters should be sent to the same email address (egas@uva.nl) by the applicant's mentor.

Deadline: 28 February 2018

Members professionally based in the following countries are not eligible for the travel stipend: Australia, Austria, Belgium, Canada, China, Croatia, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Israel, Italy, Japan, Luxembourg, Malta, Netherlands, New Zealand, Norway, Poland, Portugal, Singapore, Slovakia, Slovenia, South Korea, Spain, Sweden, Switzerland, United Kingdom, United States of America.

Dr. Ute Friedrich | ESEB Office Manager Postfach 910225 | 90260 Nuernberg | Germany | office@eseb.org

European Society for Evolutionary Biology | www.eseb.org office@eseb.org

---

ESEB Hewitt MobilityAward

REMINDER! DEADLINE: Monday 15 January 2018, 12.00 GMT.

Godfrey Hewitt Mobility Award 2018 'V Call for Applications

Godfrey Hewitt (1940-2013) was President of the European Society for Evolutionary Biology (ESEB) from 1999-2001. He was exceptionally influential in evolutionary biology both through his research and through his mentoring of young scientists. He was also a great believer in seeing organisms in their environment firsthand and in exchanges of ideas between labs. Therefore, ESEB has decided to offer, annually, mobility grants for young scientists in his name.

Closing date: Monday 15 January 2018, 12.00 GMT.

*Eligibility: *

The award is open to PhD students or postdoctoral scientists who are, at the closing date for applications, both within 6 years of the start date of their PhD and ESEB members. In addition, applicants will be considered who are more than 6 years from the start of their PhD if they have had career breaks, worked part-time, or for other reasons have not worked continuously. The maximum single award will be 2000 Euros. It must be used to support fieldwork or a period of research at a lab that you have not previously visited. There is no restriction on the country of residence or nationality of the applicant. A report will be required by 30 April 2019, by which time the funds must have been used.

*Application procedure: *

Your application should be sent as a single PDF file to Ute Friedrich at the ESEB office, office@eseb.org. It should include your name, current status and institution, your PhD start date, your ESEB membership number, a description of the work to be carried out (maximum 500 words), an outline budget with brief justification (maximum 100 words) and a signed statement from your PhD supervisor or postdoctoral adviser (maximum 100 words) explaining why the work cannot be funded from your home institution or your proposed host institution.

Applications will be considered by a committee chaired by Roger Butlin. The aim will be to announce decisions before the end of March 2018. In previous rounds, success rates have been between 20 and 40%.

The committee will consider the following key criteria:

1.The value of the proposed mobility in terms of its expected output and impact on the applicant'Âs career. The committee prefers projects that are: a. Not a core component of the applicant'Âs existing PhD or postdoctoral project, but a new venture. b. Clearly based on the applicant'Âs own initiative c. Likely to be completed and have definable output within the award period d. Have the potential to lead to larger future projects or to enhance the applicant'Âs career in evolutionary biology

2. The need for the GHM award, i.e. the potential for the funding provided by ESEB to make a difference, in relation to resources already available through the home or host institution.

Please endeavour to address these points in your application.

Sincerely, Ute Friedrich ESEB Office Manager

– European Society for Evolutionary Biology Email: office@eseb.org Homepage:www.eseb.org ESEB <office@eseb.org>

ESEB JohnMaynardSmith Prize

****John Maynard Smith Prize 2018: Call for Nominations**

Every year the European Society for Evolutionary Biology (ESEB) distinguishes an outstanding young evolutionary biologist with a prize named after John Maynard Smith (1920 - 2004), eminent scientist, great mentor, author of many books on evolution, and a former President of ESEB.

NOMINATION:

The prize is open to any field of evolutionary biology. The candidates for the 2018 prize must have begun their PhD study after January 1, 2011. In addition, nomineeswill be considered who are more than 7 years from the start of their PhD if they have had career breakstaken 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 Ute Friedrich at the ESEB office <office@eseb.org>. 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 Ute Friedrich.

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

The nomination committee, chaired by the ESEB Vice President Anna-Liisa Laine, will evaluate the nominations and inform the winner approximately by the end of February 2018.

The prize winner is expected to attend the Joint Evolution congress in August 2018 in Montpellier, France, where he or she will deliver the 2018 John Maynard Smith Lecture. The Society will cover registration, accommodation, and travel expenses (economy fare). The JMS Prize comes with a monetary prize of 2500 Euro and the possibility of a Junior Fellowship of generally 3 months at the Institute of Advanced Study (Wissenschaftskolleg) in Berlin, Germany. For more information on the Wissenschaftskolleg see www.wiko-berlin.de/en/ . Previous winners of the JMS Prize are listed on the ESEB web site: www.eseb.org Sincerely, Ute Friedrich ESEB Office Manager – Email: office@eseb.org European Society of Evolutionary Biology - eseb.org

ESEB <office@eseb.org>

ESEB Progress Meetings CallForProposals DeadlineDec12

****Progress meetings in evolutionary biology****

We are excited to announce a new initiative by the European Society of Evolutionary Biology (ESEB), in partnership with the Journal of Evolutionary Biology (JEB).

We invite applications for funding to support focussed conference or workshops on a topical issue where rapid progress is currently being made in understanding Evolutionary Biology. ESEB will supply funds up to 'Â15,000 to assist with workshop planning (venue, travel or attendance support). We encourage proposals on any topic.

We expect these meetings to bring together a range of researchers focussed around a topic for a "state of the art" conference, ideally proposing a new synthesis, view-point or technical or analytical breakthrough facilitating new avenues of research. Attendees would represent researchers from all career stages and must accord with our Equal Opportunities guidelines. Attendance should be open to all, but ESEB members should be prioritised. Typically, meetings would last 2-3 days.

A condition of the funding is that the meeting has a clear objective to produce either a Special Issue or Target Review for JEB. Within 4 months of the meeting manuscripts arising from the meeting should be submitted to the journal, to be handled by the organisers as guest editors or the editorial board of JEB, as appropriate.

This is a new opportunity for a one-off topical meeting for ESEB members and the evolutionary community. There will be one round per year, with a deadline of *Dec 12h 2017*. Applicants should be members of ESEB or our sister society, the Society for the Study of Evolution.

There is no official application form. The application document should include

- The title of the conference and why this is suitable for a Progress Meeting.

-Names and addresses of the organisers, with short (1 page each) CVs

- List of keynote speakers, with justification (potentially key recent references). They should have agreed in principle to participate

- A 2-page description of the aims and potential scope of the conference

- Conference venue details

- Methods of selecting participants

- Publication plans

Applications should be submitted to office@eseb.org <mailto:office@eseb.org> by the deadline. The successful application will be chosen by an ESEB committee.

Mike Ritchie, former Editor in Chief, JEB Wolf Blanckenhorn, Editor in Chief, JEB Luke Holman, Reviews Editor, JEB Tanja Schwander, Deciding Editor and former Special Issue Editor, JEB

Ute Moniatte| ESEB Office Manager| office@eseb.org European Society for Evolutionary Biology | www.eseb.org
ESEB <office@eseb.org>

FrontiersGenetics GenomicFootprintsRecombination

The open access journal, Frontiers in Genetics is pleased to invite submissions to the research topic, “Genomic Footprints of Meiotic Recombination” (https://www.frontiersin.org/research-topics/7027/-genomic-footprints-of-meiotic-recombination). The aim of this research topic is to promote the awareness of the diverse impacts of meiotic recombination on genome evolution. Detailed description of the research topic can be found in the above link.

This topic issue will accept various types of articles, including original research (both empirical and theoretical), methods, opinions and review manuscript submissions on meiotic recombination in the following fields:

Population genomics, Speciation, Molecular evolution, Genome evolution, Natural selection, Adaptation, Systematics, Comparative genomics.

The topic editors (guest editors) are Carina Farah Mugal (Uppsala University, Sweden), Takeshi Kawakami (Uppsala University, Sweden), Sylvain Glémin (ISEM, France) and Benoit Nabholz (University of Montpellier, France). Abstract submission deadline is January 31st 2018, and manuscript submission deadline is May 31st 2018.

To submit your abstract or manuscript, please use the online submission system (https://www.frontiersin.org/-research-topics/7027/genomic-footprints-of-meiotic-recombination).

Best wishes,

Carina Farah Mugal Takeshi Kawakami Sylvain Glémin Benoit Nabholz Research Topic Editors

David B Allison Chief Editor

kawakami.t@gmail.com

HarvardU PlantResearchFunding

Research Funding opportunities at the Arnold Arboretum of Harvard University

The Arnold Arboretum of Harvard University promotes and supports research consistent with its mission to discover and disseminate knowledge of the plant kingdom. To foster both independent and collaborative work, the Arboretum offers fellowships and awards to students, post-doctoral researchers, and professionals of the biological sciences including evolution, ecology, development, and genetics. Applicants are encouraged to define and develop paths of inquiry using the Arboretum's resources, including its world-renowned living collection, herbarium, plant records, library and archives, greenhouse and laboratories, and the expertise of its staff.

There is currently one fellowship, eight awards, and an internship program. Applicants must submit a research proposal online by Feb 1. The deadline for the Undergraduate Research Internship Program is March 15.

Please see the website for the specific requirements of each award.

http://www.arboretum.harvard.edu/research/-fellowships/ Available Opportunities:

DaRin Butz Research Internship Program of the Arnold Arboretum of Harvard University

Ashton Award for Student Research

Cunin / Sigal Research Award

Deland Award for Student Research

Shiu-Ying Hu Student/Postdoctoral Exchange Award

Putnam Fellowship in Plant Science

Arnold Arboretum Genomics Initiative and Sequencing Award

Jewett Prize

Sargent Award for Visiting Scholars Sinnott Award

– Faye Rosin, PhD Director of Research Facilitation Arnold Arboretum of Harvard University 1300 Centre St Roslindale, MA 02131

phone: (617) 384-5095 fax: (617) 384-6596

frosin@oeb.harvard.edu http://arboretum.harvard.edu/ frosin@oeb.harvard.edu

LifeHistory Database

Dear Colleagues,

I thought you may be interested in our AnAge database of ageing and longevity in animals. We have recently released build 14 with over 4,200 species and over 3,500 longevity records.

In addition to longevity records, which continue to be our main focus and we make a great effort to verify their authenticity, AnAge features one of the most comprehensive collections of quantitative life history data (age at sexual maturity, litter (or clutch) size, adult body weight, etc.) in vertebrates. Metabolism data is also available for hundreds of species of birds and mammals.

AnAge is freely available online at: http://-genomics.senescence.info/species/ We hope you will continue to find this resource useful for your research. Comments, suggestions and contributions are always appreciated.

With the very best wishes, Joao Pedro

–

Joao Pedro de Magalhaes, PhD

Institute of Ageing and Chronic Disease University of Liverpool William Henry Duncan Building, Room 281 6 West Derby Street, Liverpool L7 8TX United Kingdom

Phone: +44 151 7954517; Follow me @jpsenescence Integrative Genomics of Ageing Group: http:/-/pcwww.liv.ac.uk/ ˜ aging/ J Pedro Magalhaes <aging@liverpool.ac.uk>

Negotiating webinar

Negotiating an Academic Position Presented by: The University of Florida/American Association of Anthropological Genetics Hosted by Professor Connie Mulligan, UF Department of Anthropology and AAAG President

Tuesday, November 14, 4-5pm ET Turlington 1208

Securing a teaching position is one of the most important steps in an academic career, yet most PhD students graduate with little knowledge of how to negotiate a salary, laboratory start-up funds, office and lab space, and teaching responsibilities. These are critical components to a successful academic position and valid points of negotiation once you have been offered a position. The webinar will focus on how to apply, interview, and negotiate a position in order to ultimately build a successful and mutually beneficial partnership with your institution. Participants are encouraged to come with questions about getting an academic position, as well as questions about non-academic positions.

The webinar will be held at the University of Florida and will be attended by in-person and online students.

Please register for the event and submit questions to cleclere@ufl.edu with the subject line “Webinar”.

The webinar will be live and archived for later viewing at: https://www.youtube.com/watch?v=Kz2IoKRSvGo Joanna Malukiewicz <jmalukie@gmail.com> Joanna Malukiewicz <jmalukie@gmail.com>

Phylogeography ConcatenatedSequences

Dear folks, I am studing phylogeography of a Neotropical lizard by Cytb and an intron sequences.

Is correct to concatenate the sequences from those two dna markers to obtain a large dataset to each specimen?

All the best. Rodrigo

rodrigotorres@ufpe.br

Phyloseminar CelineScornavacca Nov22

Next on http://phyloseminar.org: Occam’s razor in phylogenetic network reconstruction Celine Scornavacca University of Montpellier Wednesday, November 22, 2017, 9:00 AM PST

Several parsimony-based methods aiming at reconstructing explicit phylogenetic networks have been developed in the last two decades. In the first part of this talk I will review several of these methods that share the same underlying approach: First, combinatorial objects such as phylogenetic trees, hierarchical clusters or trinets are constructed from the data of the species under study; Second, these combinatorial objects are combined into an explicit phylogenetic network. The way they are combined and the parameters to optimise (e.g. minimising the hybridisation number, i.e. the number of reticulations of the network, or the level, i.e. the maximum number of reticulations in each biconnected component) give a large range of different problems, each of biological interest. In the second part of the talk I will discuss different definitions of maximum parsimony for phylogenetic networks, as well as the pros and cons of each of them. Then I will introduce several algorithmic results to lay the foundations for new parsimony-based methods for phylogenetic network reconstruction.

Frederick “Erick” Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ Erick Matsen <ematsen@gmail.com>

Software PGT

Dear All,

I am releasing a new software PGT for plotting geophylogenies (i.e., mapping a phylogenetic tree onto a map):

http://dambe.bio.uottawa.ca/PGT/PGT.aspx It is available for Windows, Macintosh and Linux (with Mono installed/enabled). Here is the link for a screenshot of PGT on Ubuntu:

http://dambe.bio.uottawa.ca/PGT/Ubuntu.png PGT is extremely easy to use. It takes just a few clicks to install. Start PGT, click ’File|Open’ to open a sample file Banza.pgt which is in plain text. The first part of input file is a phylogenetic tree in Newick (or PHYLIP) format and the second is a list of OTUs with associated latitude and longitude. The last column is optional. If used, it specifies which map symbol to use for which OTU. The sample file Banza.pgt uses the same symbol for the same species (i.e., different specimens from the same species will have the symbol).

You can switch between regular and satellite maps, and zoom in/out to any resolution. I bet that you will be impressed by its user-friendliness and its quality. Enjoy!

Best Xuhua http://dambe.bio.uottawa.ca http://science.uottawa.ca/biology/people/xia-xuhua “Xuhua.Xia@uottawa.ca” <Xuhua.Xia@uottawa.ca>

SSB StudentCoucil Nominations

Call for SSB Student Council Member Nominations

The Society of Systematic Biologists Council is inviting nominations for one new graduate student representative for 2018-2019. As a member of the SSB Council, you will have the opportunity to participate in the workings of a society and interact with many of the great researchers in the society. Student council members will aid the society in developing initiatives to better serve our student members, participate in council meetings to provide input, and engage with student representatives from other societies (e.g., the American Society of Naturalists and the Society for the Study of Evolution) to support joint activities, such as student-oriented events at the Evolution meetings.

We are electing one representative for a 2-year term beginning February 1, 2018. Student representatives are expected to be active members of SSB (student membership is $25), to attend the annual Evolution meeting (travel costs and one night of accommodation are covered by the society), and to serve on the council for their full term (extension into postdoctoral work is fine).

To Apply

If you would like to join us, please email ssbstudentcouncilreps@gmail.com by January 1, 2018 with the subject $B!H(BSSB Student Rep$B!I(B and attach a single PDF document (SSBStudentRep_LastName.pdf) containing your CV and a short paragraph (less than 1 page; about 120 words) about your research interests and why you want to be a part of the council. You can visit our website, www.systbio.org, to learn more about the society and its activities.

Any student member of SSB is allowed to nominate themselves or other students, and faculty are also strongly encouraged to nominate students.

Voting

Ballots to vote for the graduate student representative will be sent out to student members of SSB in January 2018.

Sincerely,

Anne Chambers and Genevieve Mount

SSB graduate student representatives

Genevieve Mount <ggmountt@gmail.com>

Systematics ResearchFund

The Councils of the Linnean Society (https://www.linnean.org/) and the Systematics Association (http://www.systass.org/) jointly administer the Systematics Research Fund (SRF) that provides grants annually for small-scale research projects in the field of systematics.

Typical activities supported include contributions to fieldwork expenditure, the purchase of scientific equipment or expertise (e.g. buying time on analytical equipment), specimen preparation (including the cost of temporary technical assistance), and contributions to publication costs. However, please note that it is unable to fund the cost of article publication charges. Projects of a more general or educational nature will also be considered, provided that they include a strong systematics component. Typical activities not supported include attendance at scientific meetings and contributions to student maintenance or tuition fees. The fund does not provide payments for Bench Fees. Projects already substantially funded by other bodies may be disadvantaged.Applications of all nationalities are welcome but applicants must be a current member of the Systematics Association or Linnean Society of London.

Successful projects are selected by a panel of systematists who represent a wide range of conceptual interests and taxonomic groups. Generally, applications in the range of 500-1,000 are preferred, the value of any single award will not exceed 1500.

Deadline 15 February 2018

More information on SRF on the Systematics Association webpage: http://www.systass.org/awards/srf.shtml Questions about the application procedure can also be sent to the SRF Administrator (srf@systass.org)

Dr. Anne D. Jungblut Grants & Awards Secretary for SRF The Systematics Association

Anne Jungblut <a.jungblut@nhm.ac.uk>

Taxing Students

Evolution 2018 and Grad Student Taxation

Two pieces of information from SSB: One relates to the upcoming Evolution 2018 meeting in Montpellier, France [see separate posting in the EvolDir]: all talks and posters must be accepted into a symposium, and abstracts for these are due Jan. 15. This includes student talks in the Mayr symposium. This policy is common for ESEB meetings but unusual for SSB/ASN/SSE meetings, so we are trying to call attention to it (please tell your colleagues). Actual registration for the meeting happens later (once decisions about talks and posters have been announced). If you do not submit an abstract by Jan. 15, 2018, you will not be giving a poster or talk at Evolution 2018. The other is a letter by the SSE, ASN, and SSB presidents about the effect of a proposed US tax plan on students studying in the United States. SSB has released other statements informing the public about areas relating to our expertise, often in conjunction with other scientific societies. See them all at http://www.systbio.org/letters.html . Negative Impacts of the Proposed Tax Cuts and Jobs Act

We are writing as the presidents of the Society for the Study of Evolution (2,674 members), the American Society of Naturalists (1,323 members), and the Society of Systematic Biologists (700 members) to express significant concerns regarding the proposed Tax Cuts and Jobs Act. If the deduction for qualified tuition and related expenses is repealed, taxes will greatly increase for many graduate students, such that such that pursuing a doctoral degree in the United States may no longer be financially feasible. As you may know, most PhD students in the United States receive a small stipend, which is taxed as income, to cover living expenses while conducting research. Many also receive a tuition waiver in exchange for working as a teaching assistant or research assistant. If the Tax Cuts and Jobs Act is passed, and students' tuition is taxed, graduate students' tax burden will increase by roughly 30 to 60 percent for students at public universities, and 200 to 400 percent for students at private universities, where tuition is typically much higher [1]. This tax burden would be more than a third of a student's salary at a private university. Such a change would make pursuing a doctoral degree prohibitively expensive for many students. Graduate students are invaluable players in the field of scientific research. Taxing tuition will prevent many from finishing their work, leaving their programs without a degree. Many more will be prevented from entering into a doctoral program. These changes would decimate advanced education in the United States. To ensure the continuation of valuable research by graduate students across the country, please preserve the deduction for qualified tuition and related expenses. Sincerely, Sally Otto Society for the Study of Evolution Kathleen Donohue American Society of Naturalists Luke Harmon Society of Systematic Biologists [1]. "How Does the "Tax Cuts and Jobs Act" Affect Ph.D. Students?" by Vetri Velan, Ph.D. student in Physics at UC Berkeley: https://drive.google.com/file/-d/1e3oIk8AO9F_UL98z5cieKha1V5e9azzB/view Copyright Â© 2017 Society of Systematic Biologists, All rights reserved. Thank you for being a member of the Society of Systematic Biologists. Our mailing address is: Society of Systematic Biologists 446 Hesler Biology University of Tennessee, Knoxville Knoxville, Tn 37996 Add us to your address book Want to change how you receive these emails? You can update your preferences or unsubscribe from this list. Email Marketing Powered by MailChimp

Society of Systematic Biologists <bomeara@utk.edu>

TeachingEvolution VisuallyImpaired

I teach General Biology II (covering pop gen, evolution, and ecology) and would appreciate supplemental teaching material suggestions for blind students. Really anything, but especially tactile options for in-person instruction and home review.

Many thanks, James

James Beck Department of Biological Sciences Wichita State University 1845 Fairmount 537 Hubbard Hall Wichita, KS 67260-0026 (316) 978-6063

james.beck@wichita.edu www.becklaboratory.com/-James http://webs.wichita.edu/?u=bioscience&p=/-people/faculty/beck/index/ "James.Beck@wichita.edu" <James.Beck@wichita.edu>

PostDocs

AuburnU ConservationGenomics

Postdoctoral position in Conservation Genomics of Freshwater Mollusks

The College of Agriculture's School of Fisheries, Aquaculture, and Aquatic Sciences at Auburn University is seeking candidates for the position of Postdoctoral Fellow in the area of conservation genomics. Potential start date is January 15, 2018, but this is very flexible.

RESPONSIBILITIES: This is a benefit eligible, non-tenure track position. The appointment is for an initial period of one year, with a possibility of renewal up to a maximum of a three year period depending on performance and funding availability. The successful candidate will be expected to design and conduct population genomic studies using RAD-seq based approaches for sequencing single nucleotide polymorphisms (SNPs). Focal species include five mussel species. The primary objective of this research is to better understand genetic diversity, population connectivity, and broad biogeographic patterns of threatened and endangered mussels species. We are also interested in understanding genetic diversity of captively reared mussels and snails compared to natural broodstock populations. One goal of this project is to use population genomic data to design mollusk propagation protocols that ensure a reasonable amount of genetic diversity in reintroduced populations. Ultimately, the results of the study will be used to inform management and captive propagation protocols for freshwater mollusks across the U.S.

The successful candidate will also be expected to generate peer-reviewed publications and contribute to the writing of U.S. Fish and Wildlife Service genetics management plans for study species. Depending on the candidate's interests, opportunities may exist for pursing population genetic studies on other aquatic taxa (e.g., freshwater snails, fish, and crayfish). This is a unique opportunity to combine basic population genomics research with applied management efforts of U.S. Fish and Wildlife Service.

QUALIFICATIONS: An earned Ph.D. from an accredited institution in Biology, Genetics, or a related field by the position start date. Applicants should also have experience generating SNP data, preferably for population genetics studies, and bioinformatics experience for analyzing such data. The successful candidate should be able to work independently, possess excellent problem solving skills, organizational abilities, be willing and able to travel (including overnight trips), work outside during summer months, possess excellent interpersonal and written communication skills, and enjoy working in diverse teams. Experience with freshwater mollusks is preferred, but not required. However, the candidate should have an interest in fieldwork. Experience with SNP data and bioinformatics will weigh heavier in the hiring decision than experience with specific taxa. The selected candidate must meet eligibility requirements to work in the United States by the start date and continue working legally for the proposed term of employment.

APPLICATION: Applicants must apply for the position electronically through: http://aufacultypositions.peopleadmin.com/postings/2590 and submit the following: 1) cover letter addressing the candidate's experience pertinent to the responsibilities of the position, 2) current curriculum vita, and 3) copies of all graduate level academic transcripts. When prompted during the on-line application process, please provide names, phone numbers and email addresses of three professional references. Only complete application materials will be considered. Active review of applications will begin December 1, 2017, but the search will continue until the position is filled. Salary will be commensurate with education and experience.

Questions about the position should be directed to the following:

Dr. Jim Stoeckel School of Fisheries, Aquaculture, and Aquatic Sciences jas0018@auburn.edu

Dr. Nathan Whelan U.S. Fish and Wildlife Service, Southeast Conservation Genetics Lab nathan_whelan@fws.gov

THE UNIVERSITY: Auburn University is one of the nation's premier public land-grant institutions. In 2018, it was ranked 46th among public universities by U.S. News and World Report. Auburn maintains high levels of research activity and high standards for teaching excellence, offering Bachelor's, Master's, Educational Specialist, and Doctor's degrees in agriculture and engineering, the professions, and the arts and sciences. Its 2017 enrollment of 29,776 students includes 23,964 undergraduates and 5,812 graduate and professional students. Organized into twelve academic colleges and schools, Auburn's 1,450 faculty members offer more than 200 educational programs. The University is nationally recognized for its commitment to academic excellence, its positive work environment, its student engagement, and its beautiful campus. The University is located in

— / —

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

---

AWI Germnay SticklebackEvolution

The Alfred-Wegener-Institute Helmholtz Centre for Polar and Marine Research (AWI) is a member of the Helmholtz Association (HGF) and funded by federal and state governments. AWI focuses on polar and marine research in a variety of disciplines such as biology, oceanography, geology, geochemistry and geophysics.

Researchers at the AWI Wadden Sea Station Sylt investigate changes to biological processes and coastal areas due to anthropogenic climate change. Ecological and evolutionary effects in conjunction with ecosystem consequences are the main research foci of the working group 'Community and evolutionary ecology?.

The section ?Coastal Ecology? at the Wadden Sea Station Sylt invites applications for a Postdoctoral Researcher (Post Doc): (100% position).

Theme: Epigenetics underlying transgenerational plasticity in stickleback

Background: Transgenerational plasticity (TGP) generated by epigenetic mechanisms such as DNA methylation can provide a temporal buffer for genetic adaptation of populations facing rapid climate change. We will use populations of a marine model species (threespine stickleback) to identify epigenetic signatures potentially underlying TGP seen at the phenotypic level (physiology and growth) in response to ocean warming, and to disentangle the relative contributions of genetic and epigenetic change to adaptive potential along a latitudinal gradient from the North Sea to the Arctic.

Tasks: We are looking for an enthusiastic, self-motivated and well-organised person to participate in ongoing and new projects where strong bioinformatics expertise is needed. The main project will investigate DNA methylation underlying TGP, but also includes analyses of transcriptome data as well as neutral genetic/genomic diversity of populations across large-scale environmental gradients. Participation in experiments and field sampling to obtain the genetic material is encouraged.

Requirements: - PhD in biology, bioinformatics or related field - practical experience with standard molecular genetic techniques and large scale NGS data analyses tools (R, bioinformatics programs) - competence in computational biology, population genetics and/or genome assembly is an asset - excellent skills in English (spoken and written) - willingness to participate in laboratory and mesocosm experiments as well as field sampling campaigns in Norway - works well in a team - drivers licence (B)

The position starts early 2018. German funding is available for 2 years, but a third year funded from Norwegian partners may be possible. For further information, please contact Dr. Lisa Shama, Coastal Ecology, Wadden Sea Station Sylt (lisa.shama@awi.de).

Dr. Lisa N.S. Shama Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research Wadden Sea Station Sylt D - 25992 List phone: +49 (0)4651 956 4204 fax: +49 (0)4651 956 200 email: lisa.shama@awi.de homepage: www.awi.de/ueber-uns/-organisation/mitarbeiter/lisa-shama.html Lisa Shama <Lisa.Shama@awi.de>

ColumbiaU BehavioralGeneticsGenomics

I am looking for a postdoctoral fellow to join my group at Columbia University. I am part of the Department of Ecology, Evolution and Environmental Biology and of the Zuckerman Mind Brain Behavior Institute (https:/-/zuckermaninstitute.columbia.edu/). My lab is located in the brand new Jerome L. Greene Science Center (http://www.thirteen.org/programs/treasures-of-new-york/the-jerome-l-greene-science-center-dsaqxg/), a state-of-the art building host to 55 labs devoted to the study of the brain and behavior. We are also part of Evolution at Columbia (https://evolutionatcolumbia.org/), a group that meets regularly to discuss ongoing work.

My lab studies the genetic and neuronal mechanisms underlying variation in behavior and its evolution, with a particular interest on social behaviors of vertebrates. We take quantitative genetics, population genetics, transcriptomics, genomics and other approaches to find genetic hits, which we then characterize experimentally with the goal of finding detailed mechanisms. My lab is brand new and people in my group have close mentorship and freedom to develop their ideas.

The ideal candidate will have a strong background in genetics, computational biology, and statistics and be interested in applying these skills to the study of behavior. Knowledge of molecular biology and sequencing technology are great pluses.

If interested please contact me directly and include your CV, a description of your research interests and why you would like to join my group, as well as the contact info of two or three references.

Thanks,

Andres

â euro “ Andres Bendesky, MD, PhD Investigator, Zuckerman Mind Brain Behavior Institute Assistant Professor, Department of Ecology, Evolution and Environmental Biology Columbia University

Jerome L. Greene Science Center 3227 Broadway L3.051
New York, NY 10027

email: a.bendesky@columbia.edu web: https:/-/bendeskylab.com ”ab4463@columbia.edu“ <ab4463@columbia.edu>

CornellU KelpStatisticalGenetics

Postdoc: Statistical Genetics of Sugar Kelp 'V Cornell University

The position is in the lab of Jean-Luc Jannink, Section of Plant Breeding and Genetics at Cornell, and is part of a large ARPA-E grant to develop open-ocean grown sugar kelp (Saccharina latissima). S. latissima is a brown algae or kelp. It is phylogenetically distant from both plants and animals, having diverged from green algae early in the evolution of eukaryotes. The project will explore its genome, the population history of New England sugar kelp, and take advantage of its biphasic lifecycle to rapidly domesticate it using cutting edge genomic selection methods. The Jannink lab works with several crop species (wheat, oat, barley, cassava, and now kelp) to develop new genomic prediction methods and integrate them optimally within breeding schemes. These efforts source tools from genomics, quantitative, statistical, and population genetics, and from machine learning and operations research.

In research for this project the postdoc will collaborate with scientists at the Woods Hole Oceanographic Institute, the University of Connecticut, and the HudsonAlpha Institute for Biotechnology. Primary tasks include the bioinformatic analysis of a large panel of resequenced haploid kelp gametophytes to identify variants, use the panel as an imputation reference population, and estimate important population genetic parameters of New England sugar kelp. Individuals from this panel will be mated for evaluation by collaborators. The postdoc will prepare and communicate mating and field designs for estimation of inbreeding depression and various quantitative genetic parameters. The postdoc will analyze these experiments for genome wide association and for training genomic prediction models. Data generated from the project will also enable research on linear models to predict heterosis in breeding and the identification of evolutionary conservation and signatures of selection in the sugar kelp genome.

Term is one year renewable to three years contingent on performance.

Anticipated Division of Time Sequence and trait data analysis, experiment and breeding program design: 60% Communication, coordination, and training with collaborators: 30% Preparation of quarterly reports to ARPA-E: 10%

Position Requirements Ph.D. in statistical, population or quantitative genetics with experience or interest breeding applications, or Ph.D. in plant or animal breeding with emphasis on genomics, or population and quantitative genetics. Proven scientific writing ability and communication skills.

Preferred Specific Skills Sequence alignment and variant calling methods. Variant imputation methods. Genome-wide association studies and genomic prediction methods. High-dimensional data analysis. Basic notions of mating designs in breeding. Optimization and experimental design for field studies. Analysis of multi-generation breeding experiments. Quantitative genetic analysis of trials, estimation of inbreeding depression and variance components.

How to Apply A letter of interest in the position, CV, and contact information for three references should be emailed to Jean-Luc Jannink: jeanluc.work@gmail.com Review of applications will begin immediately and continue until the position is filled. Complete Information on the position can be found here: bit.ly/KelpStatGen

–

Jean-Luc Jannink USDA-ARS, Robert W. Holley Center for Agriculture and Health Phone: +1 607 255 5266 Fax: +1 607 255 6683

Cornell University Dept. of Plant Breeding and Genetics 258 Emerson Hall Ithaca, NY 14853 USA

Jean-Luc Jannink <jeanluc.work@gmail.com>

DalhousieU Canada ModellingMicrobialCommunities

Postdoctoral fellowship position in statistical modelling and analysis of microbial communities

A position is immediately available 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 Mathematics and Statistics Department of Biology Dalhousie University P.O. Box 15000 Halifax, NS, Canada B3H 4R2â euro Â (or) email to j.bielawski@dal.ca

Joseph Bielawski <J.Bielawski@Dal.Ca>

DukeU SocialMammalGenomics

Post-doctoral position in social mammal behavior and genetics

A postdoctoral position in social mammal behavior and genetics is available in the Tung lab < http://www.tung-lab.org/index.html > at Duke University. Our current research < http://www.tung-lab.org/research.html > focuses on the biological consequences of social relationships and social stressors in primates and other social mammals, using genomic and computational tools. Open project areas involve the functional genomic analysis of life history trade-offs in wild meerkats and gene regulatory signatures of social experience in wild baboons and captive rhesus macaques. Applicants are also encouraged to be creative in developing their own projects, as long as they fit within the lab's general interests.

Postdoctoral applicants should have a strong background in evolutionary biology, behavioral ecology, and/or functional/computational genomics. Strong data analysis skills, including programming and statistical modeling experience, are essential. Familiarity or experience with mammalian behavior or genetics is a plus.

The Tung lab offers a congenial research environment that fosters strong interdisciplinary training and collaborative exchange. The lab is based in Duke's Department of Evolutionary Anthropology < http://evolutionaryanthropology.duke.edu/ >, and is affiliated with the Duke Department of Biology < http://biology.duke.edu/ >, the Center for Genomic and Computational Biology < https://genome.duke.edu/ >, and the Duke Population Research Institute < https://dupri.duke.edu/ >. Depending on research project, the successful may work under the co-mentorship of Dr. Luis Barreiro < http://luis-barreirolab.org/ > at the University of Chicago.

To apply for the position please send an email to Jenny Tung (jt5@duke.edu) including a cover letter, current CV, and contact information for at least two references.

Duke University is an Equal Opportunity Employer dedicated to building a diverse academic community.

Jenny Tung Associate Professor Departments of Evolutionary Anthropology and Biology Duke Population Research Institute jt5@duke.edu 919-668-4912 www.tung-lab.org "Jenny Tung, Ph.D." <jenny.tung@duke.edu>

HarvardU EnvironmentalBioinformatics

Postdoctoral Opportunities in Environmental Epigenetics, Genomics, and Bioinformatics

A postdoctoral position is available in the Lemos lab (www.lemoslab.org) at Harvard University T. H. Chan School of Public Health. The ideal candidate would have a strong expertise in bioinformatics and keen interests in specific themes of genomics, epigenetics, repetitive DNA, genome and nuclear architecture, environmental impacts on the genome/epigenome, and complex trait architecture. The ideal candidate would be motivated to pursue computational/statistical analyses of genomic/epigenomic data as well as be inspired by molecular biology and molecular variation of genetic and environmental origin.

Our laboratory is housed at the Harvard Chan School of Public Health, located within a vibrant research community that also includes the Harvard Medical School and several affiliated hospitals. The school has significant strengths in biostatistics, computational biology, genomics, engineering, and experimental biology that will be within reach of the fellow. Candidates should be self-motivated and have the ability to work independently as well as collaborate and support other team members.

Requirements Proficiency in one or more statistical or scripting languages, such as R, Python, and/or Perl, appropriate for scalable data analysis. Experience with genomics and/or epigenomics, as indicated by a publication record. Ability to lead her/his own projects as well as collaborate well and contribute to the projects of others.

Informal enquires of interested candidates with this or other backgrounds and interests are also welcome.

Applications should be sent to Bernardo Lemos at blemos@hsph.harvard.edu. Please send a cover letter describing your interests, expertise, and research vision (˜ 1-2 pages) and a C.V. containing contact information for three references.

Bernardo Lemos www.lemoslab.org Harvard T. H. Chan School of Public Health https://www.hsph.harvard.edu/bernardo-lemos/

"Lemos, Bernardo" <blemos@hsph.harvard.edu>

HarvardU PlantEvolution

Katharine H. Putnam Fellowships in Plant Science

The Arnold Arboretum of Harvard University invites applicants for research fellowships in any field of plant science including evolution, ecology, and development. Putnam Fellowships offer excellent opportunities for advanced research and study using the Arboretum's living collections of woody plants. Scientists with a PhD and who have identified an independent research project that would utilize the Arboretum's living collections are encouraged to apply. The living collection, numbering some 15,000 plants, in over 2,200 species, is distinguished as one of the most thoroughly documented collections of temperate woody plants in the world. Taxonomic diversity and breadth within the collection are noteworthy, and the floras of China, Japan, and Korea are particularly well represented.

Proposals are sought from early-career individuals with a PhD in plant biology, evolution, plant genetics, plant ecology, horticulture, or related discipline. Applicants should be well positioned to conduct original, independent research and to publish their findings in peer-reviewed publications.

Fellowship Details

Putnam Fellows are full-time employees of Harvard University during their tenure, with stipends of up to $48,000 per year depending on the duration of the fellowship, and are eligible for health insurance benefits. Modest support is available for research expenses and travel costs. The fellowship is typically awarded for 2 years, pending a satisfactory progress report at the end of the first year. Putnam Fellows are expected to be in full-time residence at the Arboretum and are provided office and research space.

The Putnam Fellowship is an independent post-doctoral position. As an independent scholar, Putnam Fellows have access to shared laboratories, resources, and interactions with fellow scientists, students and staff. It is not necessary to have a specific faculty host. More information is available via our website: http://arboretum.harvard.edu/ research/fellowships/.

– Faye Rosin, PhD Director of Research Facilitation Arnold Arboretum of Harvard University 1300 Centre St Roslindale, MA 02131

phone: (617) 384-5095 fax: (617) 384-6596

frosin@oeb.harvard.edu http://arboretum.harvard.edu/
frosin@oeb.harvard.edu

IBG-1 Julich MicrobialGenomeEvolution

Forschungszentrum Julich pursues cutting-edge interdisciplinary research on the pressing issues of our time. It helps to solve the grand challenges facing society in the fields of energy and environment as well as information and the brain. With around 5,900 employees, Julich - a member of the Helmholtz Association - is one of the large interdisciplinary research centres in Europe. The successful candidate will work in an ERC funded project (ERC starting grant "Pro_Phage") and will be part of a Helmholtz research group located at the Institute of Bio- and Geosciences - Biotechnology (IBG-1) of the Forschungszentrum Julich. Current projects of the group focus on phage-host regulatory interaction and the integration of prophage elements in host networks. Forschungszentrum Julich is a member of the Helmholtz association and is one of the largest research centres in Europe. The Institute of Bio- and Geosciences - Biotechnology (IBG-1) performs research in the field of molecular and applied microbiology. Major topic is the development of bacteria as biocatalysts for production of industrially or pharmaceutically relevant products from renewable carbon sources. We are looking to recruit as soon as possible a

Postdoc (f/m) (Bioinformatics / Microbial genome evolution)

Your Job: We are seeking a highly motivated postdoctoral researcher to perform comparative phage and prophage genomics to study genome evolution and (pro-)phage-host interaction. Furthermore, the candidate will be involved in the integrative analysis on large genomic datasets which are generated using state-of-the-art sequencing techniques. The applicant will have ample opportunities to work with experimentalists to validate and address resulting findings. Your Profile: * Master's degree and PhD (or equivalent) in bioinformatics, microbiology, genomics, computer science, Engineering or related fields * Good understanding of molecular and microbiology * Strong programming skills in at least one scripting language (Python, Perl, etc.) and R * Previous experience working with large-scale biological data sets, NGS data, etc. is a strong plus * Candidates should have a high motivation to succeed in science but it is also crucial that they are kind, efficient and reliable team players * Strong English writing and communication skills

Our Offer: * Working in an interdisciplinary environment as well as excellent facilities for biologic and biotechnological research * A comprehensive training and mentoring programme * Limited for 2,5 years * Salary and social benefits in conformity with the provisions of the Collective Agreement for the Civil Service (TVoD)

Forschungszentrum Julich aims to employ more women in this area and therefore particularly welcomes applications from women. We also welcome applications from disabled persons. We look forward to receiving your application, preferably via our online recruitment system on our career site until December 7, 2017 quoting the reference number 2017-270. Contact:

Henning Eggert Tel.:+49 2461 61-9700 www.fz-juelich.de
Kind regards Sven Sievers M.A., Mediaberatung & Lektorat

as mediendesign advanced services as mediendesign - Lanker StraÃŸe 28 b - 13125 Berlin Telefon +49 30 661 80 56 - Telefax +49 30 661 80 55 - info@as-mediendesign.com www.as-mediendesign.com Inhaberin: Andrea Sindermann Steuer-Nr: 35/535/61760

as mediendesign <info@as-mediendesign.com>

IndianaU GenomicBasisPhenotypicEvolution

Postdocs: Indiana_University.GenomicBasisPhenotypicEvolution POSTDOC POSITION IN THE GENOMIC BASIS OF PHENOTYPIC EVOLUTION One full-time postdoctoral position is available in Lynda Delph's lab, Department of Biology, Indiana University, Bloomington. Our lab takes a quantitative-genetic perspective of phenotypic evolution as a result of adaptive population differentiation, sexual antagonism, and genetic constraints.

The position will explore the genetic architecture of phenotypic traits in the herbaceous, flowering plant Silene latifolia, a model system for understanding sexual dimorphism and sex-chromosome evolution. This work will combine QTL, pool-seq, and other genomic approaches. Long-term objectives are to characterize how sex-specific selection, adaptive population differentiation, and sexual dimorphism impact sex-chromosome evolution. The successful candidate would have opportunities to develop additional independent lines of research in these and related areas.

We seek a collegial, self-motivated, independent, and intellectually curious individual. A PhD in evolutionary biology or related field is required. Applicants for this position must have strong bench skills and strong familiarity with bioinformatic analyses of next-gen sequencing data. In addition, candidates must have demonstrated written and oral communication skills. The position is available for 16 months, with the possibility of an extension. Salary will be 47,500, and full benefits are included.

To apply, please submit a letter of application, a CV, a statement of research interests, and the contact information for three references to http://-indiana.peopleadmin.com/postings/4953. For best consideration, please apply before Dec 11, 2018. Preferred start date is March-April 2018. Inquiries about this position can be directed to Lynda Delph at ldelph@indiana.edu. Additional information about research in the Delph lab can be found at http://www.indiana.edu/~delphlab/ . Indiana University has an interactive and highly ranked Evolution, Ecology, and Behavior program that is part of a large Department of Biology. Bloomington is situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater.

The College of Arts and Sciences is committed to building and supporting a diverse, inclusive, and equitable community of students and scholars.

Indiana University is an Equal Employment and Affirmative Action employer and a provider of ADA services. All qualified applicants will receive consideration for employment without regard to age, ethnicity, color, race, religion, sex, sexual orientation or identity, national origin, disability status, or protected veteran status.

“Delph, Lynda F.” <ldelph@indiana.edu>

IowaStateU SnakePopGenomics

Postdoc: Population and Physiological Genomics of Garter Snake Life-history Strategies

Postdoctoral Research Associate Department of Ecology, Evolution, and Organismal Biology Iowa State University

The Bronikowski lab is recruiting a Postdoctoral Research Associate to study the population genomics and molecular evolution of garter snakes (Thamnophis elegans) from the Eagle Lake basin in California. Populations of garter snakes in this vicinity are arrayed along a slow-to-fast continuum of life history strategies, with upper elevation populations comprised of individuals that grow slowly, mature late, reproduce infrequently, and live longer relative to lower-elevation populations. The successful applicant will collaborate with myself and colleagues on an NSF-supported project to analyze allelic-time series for signatures of population genomic response to recent extreme environmental change. We will also leverage the past 40 years of data on meta-population demography, life-history evolution, stress-response evolution, and behavior to test for population- or ecotype-specific characters that correlate with population persistence through extreme environmental events. We env ision the principal duties will be 80% computational and project management, plus some time for supervising basic molecular lab work and field work. Collaborators on the project include Drs. Anne Bronikowski and Nick Serao (Iowa State University), Dr. Stevan J. Arnold (Oregon State University), Dr. David Miller (Penn State University), and Dr. Amanda Sparkman (Westmont College). Required qualifications, terms of employment and application instructions follow below.

Required Qualifications

Education: A PhD degree in evolutionary genetics or bioinformatics, or acceptable equivalent combination of education and experience.

Experience/Skills: Experience with population genomic/transcriptomic data; demonstrated experience working in a Linux/Unix shell environment; competency with at least one scripting language (e.g., Perl, Python, R). Demonstrated experience with population genomic analyses for complex demography, admixture, and local adaptation. Preferred experience or willingness to help with annotation of the Thamnophis elegans genome. Well-developed organizational and time management skills, and leadership ability to direct (with the PIs) a large and productive project.

Terms of Appointment

Starting salary is dependent on previous post-doctoral experience, (https://www.grad-college.iastate.edu/post_doc/policies.php) plus benefits. Funds are available for one year and are renewable for up to two years, pending satisfactory progress. The optimal start date is Feb 1, 2018.

Application Instructions

For consideration, applicants must apply by Jan 1, 2018. Informal inquiries are encouraged prior to formal application. For formal application, please send 1) a cover letter, 2) a curriculum vitae, 3) a brief statement of research experiences/interests, and 4) names and contact information for three references to Dr. Anne Bronikowski at broniko-job@iastate.edu.

Iowa State University is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, age, religion, sex, sexual orientation, gender identity, genetic information, national origin, marital status, disability, or protected veteran status, and will not be discriminated against. Inquiries can be directed to the Director of Equal Opportunity, 3350 Beardshear Hall, (515) 294-7612.

Please contact Anne Bronikowski if you have any questions about this postdoctoral position.

Anne Bronikowski, Professor Email: bronikojob@iastate.edu https://www.eeob.iastate.edu/people/anne-bronikowski abroniko@iastate.edu

---

JagiellonianU EvolutionaryGenomics

The Institute of Environmental Sciences of the Jagiellonian University

is hiring a postdoctoral fellow in

evolutionary physiological genomics

Research tasks:

The post-doc will perform the “molecular” part of project entitled

Experimental evolution of physiological and behavioral adaptations in the bank vole: molecular background and alimentary system bacterial symbionts

The project is based on a long-term experimental evolution program, with lines of bank voles selected in three distinct directions. The specific objective is to investigate molecular basis of the evolution of increased aerobic exercise metabolism and propensity towards predatory behavior in the selected lines, through a) identification of genes with modified frequency of Single Nucleotide Polymorphism (SNP) alleles, and b) analyses of the correlation between SPN genotypes and phenotypic values of the selected traits. The specific tasks performed by the post-doc will include laboratory molecular analyzes, bioinformatic and statistical analyzes of high-throughput sequencing data, and participation in physiological measurements on laboratory rodents. This project is a continuation of the research presented in Konczal et al. 2015 (doi:10.1093/molbev/msv038) and 2016 (doi:10.1093/molbev/msw121). Additional information can be obtained from the principal investigator, Dr. PaweÃ Koteja (pawel.koteja@uj.edu.pl).

Key words: animal physiology, behavior, evolution, genomics, high-throughput sequencing, locomotor performance, metabolism, neurophysiology, predation, selection experiment, SNP

The main requirements:

- PhD degree in biology or related sciences obtained not earlier than 7 years prior to employment in the project (note: this period does not include periods of maternity or parental leave, or other circumstances described in the Polish National Science Centre OPUS project regulations),
- or a statement that the PhD dissertation has been submitted and the candidate is expected to obtain the degree before commencing the employment;
- Experience in analyzing data from high-throughput sequencing and working in a Unix/Linux environment.

Conditions of employment:

- full-time contract for 24 months, about 7000 PLN/month (gross; an equivalent to associate professor salary),
- benefits of a full-time employee according to the Polish law (health insurance, retirement benefits, etc.)
- all social benefits of the University staff (www.en.uj.edu.pl/en/staff/staff-benefits/office),
- beginning of the employment: between 1.12.2017 and 1.04.2018 (negotiable).

Deadline for applications: 30 November 2017 (automatically prolonged if needed)

If no candidate meets the requirements, the recruitment period will be extended. If you are interested in this position but cannot apply before the deadline, let us know and we will inform you about the extension.

For details of the requirements and the recruitment procedure see:

http://www.eko.uj.edu.pl/index.php/en/institute/announcements Contact person:

Dr. PaweÃ Koteja (pawel.koteja@uj.edu.pl)

Institute of Environmental Sciences

Jagiellonian University

7 Gronostajowa Street, 30-387 Krakow, Poland

office phone: +48 12 664 5209

mobile phone: +48 606 240 746

skype: pkoteja

fax: +48 12 664 6912

PaweÂ³ Koteja <pawel.koteja@uj.edu.pl>

LiverpoolSchMedicine VectorEvolution

Postdoc: Liverpool School of Tropical Medicine The Department of Vector Biology is seeking a Post-Doctoral Research Associate to work on genomic and transcriptomic analysis of mosquito insecticide resistance.

Full Time, Fixed Term for 2 years Based in Liverpool with overseas travel The Liverpool School of Tropical Medicine (LSTM) is an internationally recognised centre of excellence for research in tropical diseases. Through the creation of effective links with governments, organisations and institutions and by responding to the health needs of communities, LSTM aims to promote improved health, particularly for people of the less developed/resource poorest countries in the tropics and sub-tropics.

The Department of Vector Biology seeks to appoint a Post-Doctoral Research Associate to work with Dr David Weetman and Professor Martin Donnelly on genetic and transcriptomic variation underlying resistance to insecticides used for Anopheles malaria vector control in Africa, and to map the predictive value of diagnostic markers. The Post-Doctoral Research Associate will provide bioinformatics support for analysis of genomic and transcriptomic data from insect disease vectors, including whole genome sequencing results from the WellcomeTrust Sanger Institute Anopheles gambiae 1000 genome project, with whom the work will be interlinked. You will liaise with external partners, produce reports, prepare and present results at scientific meetings and consultations. You will deliver training to project partners from disease endemic countries as well as supervise postgraduate students and collaborate on their project analyses in addition to assisting in the development of training packages. You will also be involved in projects which will involve work on other disease vectors and will include analyses of reduced representation genomic data and SNP diagnostic panels. Development of other research projects to support fellowship applications will be encouraged in this position.

To be successful, you must hold a PhD in a relevant area like genetics, biology or biological computing. You must demonstrate experience in programming with strong bioinformatic skills, and experience of using PYTHON or R will be advantageous to your application. Your proven ability to communicate and collaborate with specialists from a variety of disciplines is as essential as your ability to work independently and within a team, with good organisational skills. Although based in Liverpool, you will be required to travel to African Partner institutes and there may be additional opportunities for fieldwork.

Closing Date: 23rd November 2017 This job is unlikely to attract a Tier 2 Certificate of Sponsorship (formerly a work permit). Applications from candidates who require Tier 2 immigration status to work in the UK may not be considered if there are a sufficient number of other suitable candidates. To apply for a Tier 2 Certificate of Sponsorship, employers need to demonstrate that they are unable to recruit a resident worker before recruiting an individual overseas.

We believe that this post will not be suitable for individuals on Tier 5 visas as these posts are not considered to be supernumerary to the organisation. For further details, please visit the UKVI website: https:/-/www.gov.uk/browse/visas-immigration (link is external) LSTM actively promotes an Equal Opportunities Policy To apply please visit https://www.lstmed.ac.uk/-post-doctoral-research-associate-7 David Weetman <David.Weetman@lstmed.ac.uk>

MaxPlanck Germany Aposematism

We invite applications for a postdoctoral position to join an exciting new research group studying the evolutionary ecology of chemical defences, based at the Max Planck Institute for Chemical Ecology in Jena, Germany. Funding is for 2.5 years, with a possible extension of 2 years contingent on progress.

Background: Chemically defended organisms communicate their unprofitability to potential predators with conspicuous warning signals - aposematism. A profitability spectrum among chemically defended organisms may be important in shaping ecological communities and interactions among species. For example, variability in chemical defences can switch the evolutionary dynamics of signalling systems from mutualistic to parasitic, from signal monomorphism to signal diversity. But what constitutes unprofitability, and how important is it in shaping interactions among species? We investigate these questions using a combination of laboratory experiments and field studies.

The postdoctoral researcher will be part of a team working in two systems: (i) laboratory experiments on the link between warning colours and chemical defences will investigate how organisms optimise their aposematic defences; the project includes aspects of insect culturing, characterization of aposematic traits, including their costs (using biochemical, metabolic, spectroscopy, machine learning and imaging techniques), and efficacy assays with predators; (ii) lab and field experiments on ecological pharmacodynamics will explore the mechanisms by which the chemical defences of prey have their effect. The project will utilise techniques such as working with specialist and generalist invertebrate or vertebrate predators/consumers, toxicokinetics, identification and cloning of genes, quantitative real-time RT-PCR, heterologous expression techniques, and bioinformatics procedures including comparative analyses.

Position details: Applicants should have a PhD in relevant biological subject (e.g., biology, ecology, zoology, biochemistry, or genetics) or related area, and a strong background in evolutionary biology/ecology, chemical ecology, or sensory biology (or any combination of those fields). They should provide clear evidence of research productivity, and of having been responsible for the direction of their research.

Proficiency in statistics and the use of R is particularly encouraged.

The starting dates is negotiable, starting from March 2018 (but no later than July 2018). The working language in the group is English (German skills are not essential). Candidates should have proficiency in both written and spoken English. We are an inclusive and diverse institute, and we encourage applications from women, people with disabilities, and all underrepresented minority groups.

Location: The lab is based at the Max Planck Institute for Chemical Ecology (MPI-CE), in Jena, Germany: https://www.ice.mpg.de/ext/index.php?id=travel#header_logo The MPI-CE is an internationally renowned research institution with more than 200 employees working in five departments and across more than 30 research groups.

Application process: Applicants should send a single pdf file comprising of a cover letter with a - statement of their research interests, a C.V. (including publication list), and the names and contact details of at least one referee. Please send this to Dr Hannah Rowland (hrowland@ice.mpg.de).

Applications will be accepted up to and including December 13th 2017, with interviews conducted in January 2018. For more information contact hrowland@ice.mpg.de https://www.ice.mpg.de/ext/index.php?id=predators_prey&L=0 Hannah Rowland <hrowland@ice.mpg.de>

MaxPlanck Jena Germany LanguageEvolutionPhylodynamics

The Transmission, Infection, Diversification & Evolution Group (TIDE) led by Denise Kühnert is offering one PhD and one Postdoctoral position to begin on 01.06.2018.

The project:

The “phylodynamics” of language evolution

There is evidence of infectious diseases having had major effects on the course of history, mostly by directly diminishing population sizes or by causing people to flee from disease. For example, the expansion of Austronesian languages into Remote Oceania has been theorized to have been pushed by one of the plasmodia causing malaria infection. Testing such theories requires both, an understanding of the past pathogen dynamics and the cultural and linguistic evolution. The field of phylolinguistics has so far mainly been using methods that were developed for viruses or other pathogens.

The initial aim of this project is to develop, test and employ mathematical concepts to describe the tree-generating processes appropriate for language evolution. They will be based on birth-death processes, which are suitable to model language evolution as they can incorporate periods of constant growth or decline, stagnation, but also bursts and extinction events.

This project will be performed in close collaboration with the Department of Linguistic and Cultural Evolution, led by Professor Dr. Russell Gray.

Your tasks:

- Development of birth-death process based methods for the reconstruction of language phylogenies in a Bayesian framework. - Analysis of language families, such as the Austronesian and Austroasiatic language families, to test hypotheses about their origins and historic development. - Test dependence of language diversification on demographic dynamics and potential links to ancient infectious disease outbreaks.

Your qualifications:

- PhD position: o Master or equivalent in a quantitative discipline such as Computational Biology, Mathematics, Statistics, Computer Science, Physics.

- Postdoc position: o Have or are about to obtain a PhD degree in a quantitative discipline such as Computational Biology, Mathematics, Statistics, Computer Science, Physics. o Experience with phylogenetic methods o Strong research record

- Both: o Strong interest in language evolution o Experience in programming o Proficient English skills

The overarching goal of the Max Planck Institute for the Science of Human History is to explore the history of humans using state-of-the-art analytical methods. Scientists from different disciplines, such as genetics, linguistics, archaeology, anthropology and history are working together to answer fundamental questions about the biological and cultural evolution of man from the paleolithic until today, and they jointly develop innovative methods, in particular in the areas of genome sequencing, language documentation, bioinformatics and phylogeography.

We offer an interesting and responsible job in a competitive, dynamic and stimulating international research environment. The Postdoc position is for 2 years with the possibility of extension. Remuneration will follow the public service pay scale (TVöD), according to qualification and experience. In addition, social benefits are paid according to the regulations of the Civil Service. The PhD position is for 3 years and paid with 50% of E13 TVöD under a Max Planck PhD contract.

The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. The Max Planck Society seeks to increase the number of women in areas where they are underrepresented and therefore explicitly encourages women to apply.

Your application: Please submit your application to kuehnert@shh.mpg.de. Candidates are requested to submit the application in English as a single pdf file including a Cover letter (explaining research experience and reason for interest in this project), curriculum vitae, a list of publications, copies of certificates, and names and contact information (email and phone) for up to three referees. Informal enquiries are welcome.

Information regarding the Max Planck Institute for the Science of Human History can be found at www.shh.mpg.de . Denise Kühnert <denise.kuehnert@gmail.com>

MaxPlanck Leipzig PrimateGenomics

*Postdoc Molecular Primatology *

The Department of Primatology of the Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, invites applications for a post-doctoral position using genetic analysis of noninvasive DNA samples. The focus of the research is the genetic analysis of wild ape populations and the integration of genomic data with observational, ecological or spatial information to address questions about social behavior, population history, and natural selection. The goal of the current project is to apply next generation sequencing for efficient, automated and cost-effective sequencing of hundreds of noninvasive DNAs, and apply the data to genetic capture mark recapture studies, determination of extended kin relationships among population members, and assessment of variation at genes relevant for immune response.

We seek candidates with laboratory experience (DNA extraction, PCR, sequencing) and bioinformatic expertise in analyzing high throughput sequencing data. A proven ability to put molecular genetic data into an evolutionary context is an asset as well as a publication record in well-regarded scientific journals. Employment is based on contracts for the German civil service (TVöD-Bund, Tarifvertrag für den öffentlichen Dienst) and will be for an initial period of 2 years. Applications will be considered immediately, and the expected starting date is no later than April 1, 2018.

Applications should be a single pdf comprising a cover letter, curriculum vitae, the names of three referees and a short statement of research interests. The Max Planck Society is committed to employing more people with impairments and to increasing the share of women in areas where they are underrepresented, and therefore expressly encourages applications from such qualified individuals. For more information on the lab please see (http://www.eva.mpg.de/primat/research-groups/molecular-genetics-laboratory/main-page.html?Fsize=0%2FBley) and address informal enquiries as well as applications to Dr. Linda Vigilant (vigilant@eva.mpg.de)

Linda Vigilant <vigilant@eva.mpg.de>

MBL WoodsHole EvolutionAging

Postdoctoral Scientist: Maternal effects on mitochondrial function and neurodegeneration

Marine Biological Laboratory, Woods Hole, MA

Position Summary: A postdoctoral position is available in the laboratory of Dr. Kristin Gribble at the Marine Biological Laboratory in Woods Hole, MA, to study the role of mitochondrial homeostasis in neurodegenerative disease. This project takes a multidisciplinary approach, using phenotypic, transcriptomic, genetic, genomic, epigenetic, biochemical, and imaging methods in a novel animal model system, the monogonont rotifer.

The Gribble lab focuses on understanding the cellular, epigenetic, and evolutionary mechanisms of aging. We are specifically investigating the genetic and epigenetic mechanisms of maternal effects in determining offspring health and lifespan. The successful applicant will have the opportunity for independent and novel research in an innovative new laboratory. For more information about the laboratory, please see our website, http://www.mbl.edu/jbpc/gribble/ or contact Dr. Gribble at kgribble@mbl.edu.

The position is available immediately, and is renewable annually depending upon progress.

Basic Qualifications: Applicants should posses a Ph.D. and/or M.D. in molecular biology, cell biology, biochemistry, genetics, or a related field. The ideal candidate will have a record of scientific rigor, productivity, and creativity; the ability to work both independently and as part of a team; and a strong publication record. Excellent oral and written communication skills are required. Highly motivated individuals with experience in other model systems are encouraged to apply.

Preferred Qualifications: The preferred applicant will have a background in mitochondrial biology, developmental biology, and/or neurobiology. Prior experience in confocal microscopy, RNAi, and/or bioinformatics is beneficial.

Physical Requirements: Minimal exposure to biohazardous chemicals. Occasional lifting of heavy objects (<30 lbs).

Special Instructions to Applicants: To apply, please submit:

(1) A cover letter describing your research goals and motivation for joining the lab;

(2) a CV;

(3) a 1-2 page research statement; and

(4) contact information for three references

To Apply: https://mbl.simplehire.com/postings/3834 Kristin Gribble, Ph.D. Assistant Scientist Marine Biological Laboratory Woods Hole, MA 02543 508-289-7194 kgribble@mbl.edu

Kristin Gribble <kgribble@mbl.edu>

McGillU EnvironmentalGenomics

Bioinformatics and Environmental Genomics Preferred Disciplines: Biology, Bioinformatics (Postdoc Position) Project length: 2 years, renewable for 3rd year Approx. start date: February 1st, 2018 Location: McGill University, Montreal, QC

Summary of Project: The Postdoctoral Fellow will be involved in long-term and highly replicated laboratory and field experiments on the effect of multiple stressors on the structure and function of aquatic communities. The research will involve developing and implementing bioinformatic tools for analysing metabarcoding and metagenomics data sets and assessing biodiversity trends for broad taxonomic groups (bacterial, phytoplankton, zooplankton). The fellow will compare biodiversity estimates obtained from traditional sampling techniques with estimates based on refined metabarcoding approaches to describe the biodiversity of contaminated aquatic habitats and will characterize genomic responses to selection. The project involves the biodiversity group at McGill University and collaborators from the Biodiversity Institute of Ontario (BIO), University of Guelph, University of Quebec at Montreal and University of Montreal.

Research Objectives/Sub-Objectives: 1) Develop sensitive metabarcoding bioinformatics protocols to describing aquatic communities; 2) Investigate the impact of multiple stressors on complex aquatic communities; 3) Characterize genomic responses to selection.

Methodology: 1) Use high-throughput sequencing to develop metabarcoding and metagenomics protocols for describing aquatic communities in complex environmental samples; 2) Validate protocols; 3) Apply protocols on highly replicated field experiments.

Expertise and Skills Needed: Experience with next generation sequencing or very-large sequence data and related bioinformatics / computational / programming skills is required. Familiarity with one or more of the following would be an advantage: genomics, phylogenetic analyses, genome evolution / programming language (R/Unix/Python or Perl). Experience working with aquatic organisms would be an asset. The candidate should have a PhD in evolution / genetics / computational biology, a good publication record and the ability to work well in a collaborative research environment.

Applicants should send a curriculum vitae, short statements of research interests, and 3 representative publications to melania.cristescu@mcgill.ca. The application deadline is December 30, 2017.

McGill University is strongly committed to diversity and equity within its community. McGill University is among Canada's leading research-intensive universities with students from over 140 countries. The university is located in Montreal, a cosmopolitan city with great cultural and linguistic diversity.

Melania E. Cristescu Canada Research Chair in Ecological Genomics Co-Editor, Genome (http://www.nrcresearchpress.com/journal/gen) Associate Professor Department of Biology (http://biology.mcgill.ca/faculty/cristescu) McGill University 1205 Docteur Penfield Stewart Biology Building N6/1 Montreal, QC, Canada H3A 1B1 Ph: 514.398.1053; Fax: 514.398.5069

Melania Cristescu <melania.cristescu@mcgill.ca>

Montpellier PLantQuantGenetics

Postdoc position (24 months)

Quantitative genomics of root traits in pearl millet

Studies of the genetic basis of adaptation have, for a long time, considered mainly above ground phenotype. Genetic basis of root traits and how plants shape their root microbial community only begin to be investigated as adaptive traits.

Pearl millet is an important crop for food security especially in the semi-arid areas of the Sahel where other crops tend to fail because of low rainfall and poor soil conditions. We recently characterized the variability of exudation (Ndour et al. 2017) and root growth (Passot et al. 2016) in pearl millet. These results led us to conduct a genetic association studies on a large panel of inbred lines to identify genome regions controlling root growth and exudation. We plan to expand this research in a recently funded ANR project "Root traits for adaptation of pearl millet to future climate in West Africa" that targets root traits in pearl millet to enhance water and nutrient acquisition, production stability in changing climates, and concomitantly to increase global food security.

The postdoctoral fellow will be in charge of the research to identify and characterize genes controlling QTLs for root growth and exudation in pearl millet.

Profile: * Ph.D. in biosciences, plant biology, bioinformatics or related fields * Experience in statistical methods for evaluating effects of various treatments and detection of QTL in mapping populations * Ability to work independently and in a research team * Knowledge of both written and spoken English

Location:

The postdoctoral fellow will be hosted at IRD Montpellier (France). The IRD is the French public research institute dedicated to research on international development issues. With a permanent staff of over 2000, many posted abroad, it develops interdisciplinary research in partnership with university and research institutes in developing countries to advance knowledge on sustainable development issues such as neglected tropical diseases, climate change, water resources or food security. The IRD research centre in Montpellier host 300 scientists, postdocs and students. It provides dedicated plant growth (greenhouses, growth chambers), imaging, molecular & cell biology and bioinformatics platforms with state-of-the-art equipment and experiences technical staff.

The position will be shared between the CERES and DYNADIV teams of UMR DIADE (IRD/U. Montpellier/Cirad). The CERES team brings together researchers in plant physiology, functional genomics and systems biology to study the genetic determinants of root architecture and root-microbe interactions in two cereals, pearl millet and rice (https://sites.google.com/site/cerealrootsystem/). The DYNADIV team has expertise in population genetics and genomics, as well as in association mapping using crossed or natural population.

Selected publications related the project (last 3 years):

Varshney R. et al. 2017. Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. Nature Biotech. 35:969-976.

Ndour PMS, Gueye M, Barakat M, Ortet P, Bertrand-Huleux M, Pablo AL, Dezette D, Chapuis Lardy L, Assigbetse K, Kane N, Vigouroux Y, Achouak W, Ndoye

I, Heulin T, Cournac L. 2017. Pearl millet genetic traits impact rhizobacterial diversity and rhizosphere soil aggregation. Front Plant Sci 8:1288

Ousseini IS, Bakasso Y, Kane NA, Couderc M, Zekraoui L, Mariac C, Manicacci D, Rhone B, Barnaud A, Berthouly-Salazar C, Assoumane A, Moussa D, Moussa T, Vigouroux Y. 2017. Myosin XI is associated with fitness and adaptation to aridity in wild pearl millet. Heredity in press. doi: 10.1038/hdy.2017.13.

Passot S, Gnacko F, Moukouanga D, Lucas M, Guyomarc'h M, Moreno Ortega B, Atkinson J, Niang M, Bennett M, Gantet P, Wells D.M., Guedon Y, Vigouroux Y, Verdeil J-L, Muller B and Laplaze L. 2016. Characterization of pearl millet root architecture and anatomy reveals three types of lateral roots. Front. Plant Sci., 7:829.

Berthouly-Salazar C, Thuillet AC, Rhone B, Mariac C, Ousseini IS, Couderc M, Tenaillon MI, Vigouroux Y. 2016. Genome scan reveals selection acting on genes linked to stress response in wild pearl millet. Mol Ecol. 25:5500-5512.

Contact: Yves VIGOUROUX, yves.vigouroux@ird.fr

Laurent LAPLAZE, laurent.laplaze@ird.fr

Yves VIGOUROUX <yves.vigouroux@ird.fr>

NIOO Wageningen Evolution Avian Morphology

The department of Animal Ecology at NIOO-KNAW offers a position for a

Post-doc on Predicting the evolution of beak size

Project description: In a recent study (Bosse et al., 2017, Science), we studied genetic differentiation and genomic signatures of selection by comparing the genomes of great tits (Parus major) from our Dutch long-term study populations with those from a UK population. Several genes that underlie beak size were found to have been under recent selection in the UK population but not in the Netherlands. This is concordant with an observed phenotypic change in beak size and more fledglings raised by the genotype for longer bills in the UK. We proposed human-induced natural selection as the cause of selection on beak size, as field data show that UK birds with large beaks make more use of artificial feeders. Garden feeding has more recently also become common in the Netherlands, therefore it is expected that there will be directional selection on beak size in Dutch great tits over the coming decades.

This project aims to predict the genetic and phenotypic changes of beak size in Dutch great tits. The candidate is expected: (1) to identify the network of genes shaping beak size and to understand how variation in this network affects beak size phenotypes, and (2) to measure and predict how selection favours certain beak phenotypes over others. The combination of the two may allow us to predict genetic and phenotypic changes in beak size in the great tit. This research will include bioinformatics (GWAS, RNA data, network analysis), data collection and analysis (phenotype-fitness associations) on our long-term field data, as well as behavioural observations on feeder use in our aviaries.

Requirements: We are looking for a candidate with a PhD degree in molecular or evolutionary genetics or related areas, who is highly motivated and committed to pursuing interdisciplinary research and with experience with genomics and bioinformatics tools. Good communication skills in English (written and spoken) and the ability to work in a team environment is essential as this project is in close collaboration with other Dutch and UK groups.

Appointment: This is a temporary appointment, initially for one year and upon satisfaction to be prolonged for a maximum of three years total at the NIOO-KNAW Animal Ecology Department (full time). Starting date is 1 March 2018.

Salary: Salary depends on training and work experience. The gross salary starts at Eur 3.111,- (scale 10.4) per month to the maximum gross monthly salary of a full-time appointment at Eur 4.048,- (scale 10.12) per month, Collective Agreement for Dutch Universities (CAO Nederlandse Universiteiten), excluding 8% holiday pay and a year-end bonus. We offer an extensive package of fringe benefits.

Information: Additional information is available upon request from Prof Dr Marcel E. Visser (m.visser@nioo.knaw.nl or +31 317-473439). Information on NIOO-KNAW can be found here: http://www.nioo.knaw.nl Applications: Please send your application letter including a complete curriculum vitae, names of three referees and vacancy number (AnE-017010) to vacature@nioo.knaw.nl

Closing date for application: 20 December 2017

Interviews will take place on: 10 January 2018

"phillip.gienapp@helsinki.fi"
<phillip.gienapp@helsinki.fi>

Norwich EvolutionaryGenomics

Applications are invited for a Postdoctoral Researcher to join the Laboratory of Dr Levi Yant at the John Innes Centre.

Background:

Our projects employ large scale population genomics, but at the same time have explicitly phenotype-first orientations. In each case we aim to determine the genetic basis and evolutionary repeatability of adaptation to intense, quantifiable selection pressures, both environmental and intracellular. We do this by applying population genomics to wild plant populations that have evolved to overcome demonstrable hazards.

We currently focus on adaptation to genome duplication as well as adaptation to highly challenging, quantifiable environmental stressors in species ranging from Arabidopsis arenosa, to Chamerion angustifolium, to Mimulus guttatus and back throughout the Brassicaceae to A. lyrata and A. thaliana.

See http://yant.jic.ac.uk/ for more.

The role:

Primary activities will include conducting large-scale population genomic projects. This includes exhaustive demographic and selection analyses of population genomic data. We require candidates who are not only motivated to run with these objectives, but who can also propose new creative project contributions. By the end of your postdoctoral term with us, we expect you to be able to, for example, begin your own group, bringing along your project from our work together. We also expect to engender the development of new directions as a result of discoveries in our group that can spur independent trajectories for your future research group.

The ideal candidate:

Applicants passionate about evolutionary genetics or population genomics are encouraged to apply. The successful candidate will possess a PhD and a strong relevant publication history. They will also have good knowledge of population genetics and demonstrable use of computational methods in an evolutionary context. The ideal candidate will have initiative, analytical skills, and a drive to push forward on new problems in evolutionary genomics as part of a highly collaborative team.

Additional information:

To apply for this role please include a covering letter with your application explaining your specific motivations to join the Yant Lab, as well as some specific description of your use of computational genomic or population genetic methods. This is a required element of the application process.

We welcome applications from candidates seeking part-time or other flexible working arrangements.

For further information and details of how to apply, please click here or contact the Human Resources team on 01603 450462 or nbi.recruitment@nbi.ac.uk quoting reference 1003326.

The John Innes Centre is also proud to hold a Gold Award from Athena SWAN and is a member of Stonewall's Diversity Champions programme.

Salary: pounds 31,250 to pounds 38,100 depending on qualifications and experience Applications Close: 10 December 2017

"Levi Yant (JIC)" <levi.yant@gmail.com>

OregonStateU EvolutionaryDiffMethylationBelugas

POSITION ANNOUNCEMENT: Postdoctoral Scholar

Epigenetic aging of beluga whales by next-generation sequencing

The Marine Mammal Institute of Oregon State University invites applications for a full-time (1.00 FTE), 12-month, fixed-term Postdoctoral Scholar position funded by a grant from the North Pacific Research Board (NPRB). Reappointment is conditional on funding and at the discretion of the Unit Head. This position will help validate methodology for epigenetic aging of cetaceans using next-generation sequencing to measure the levels of cytosine methylation in candidate genes. The assay will be calibrated using a large set of samples with estimated ages from growth-layer groups in teeth. The age assay will then be applied to biopsy samples from living beluga whales of unknown age to better understand the life history and age structure of the endangered Cook Inlet population of beluga whales. Depending on funding, the incumbent will extend the methods developed for the beluga to other species, subspecies or populations of cetaceans, including evolutionary differences in the patterns of methylation of candidate genes among taxa.

The position is located at the Hatfield Marine Science Center in Newport, Oregon where the Scholar will work with Scott Baker in the Cetacean Conservation and Genomic Laboratory and, remotely with collaborators Paul Wade (NOAA), Simon Jarman (Curtin University), and Steve Horvath (UCLA).

Required qualifications include a PhD in biological sciences (genetics, ecology or evolution), with an emphasis in molecular ecology, genomics, bioinformatics, statistics or population modeling, and demonstrated publication record. The PhD must have been awarded within the last five years. Preferred qualifications include experience with programming and management of large datasets typical of next-generation sequencing.

The minimum stipend for a candidate with no prior postdoctoral experience is $47,484/year with annual increments for experience following NIH guidelines.

Starting date is approximately January 15, 2018 (negotiable).

For the full announcement and instructions for application, see

http://gradschool.oregonstate.edu/postdocs/open-positions For further information, contact Scott Baker by email, using the subject 'NPRB beluga postdoc information'

email: scott.baker@oregonstate.edu

C. Scott Baker Associate Director, Marine Mammal Institute Professor, Department of Fisheries and Wildlife Hatfield Marine Science Center Oregon State University 2030 SE Marine Science Drive Newport OR 97365

Phone: 541-867-0255; Mobile 541-272-0560 Fax: 541-867-0345 email: scott.baker@oregonstate.edu http://mmi.oregonstate.edu/ Scott Baker <scott.baker@oregonstate.edu>

Oxford BioBankProject

Postdoctoral Research Scientist in Genetics Wellcome Centre for Human Genetics, Roosevelt Drive, Headington, Oxford.

Applications are invited for a Postdoctoral Research Scientist in Genetics to join Professor Adrian Hill's group at the Wellcome Centre for Human Genetics.

This work aims to understand how variation in human genetic architecture shapes the responses to vaccines and infectious agents across populations in order to facilitate discoveries that can be translated into effective preventative strategies such as improved vaccination.

You will be motivated scientist who strives to produce work of the highest quality and who is keen to support the international development of capacity for genetics and genomics. The research work will involve using bioinformatic tools including genome-wide association analyses in structured populations to identify genetic signals that impact on the host immune system and the ability to respond to infectious agents. It is likely that the post will involve periods of overseas travel to support ongoing initiatives developing capacity for genetics and genomics in low-to-middle income countries such as Mexico.

You will have a PhD/DPhil (or be in the process of completing) with appropriate research experience; strong publication record and familiarity with the existing literature and research in human genetics, immunology and infectious disease; significant experience in human bioinformatics and proficient in statistical programming using R or equivalent. You will work effectively within an international team of scientists, manage your worktime efficiently and deliver high quality results to a required standard schedule. Previous laboratory experience, computer skills, good communication skills and the ability to work as part of a team are essential.

This position is fixed-term until 13 April 2019 in the first instance and funded by the Research Councils UK.

Please quote ref. 131497 on all correspondence. You will be required to upload a CV and supporting statement as part of your online application.

Only applications received before 12.00 midday on Wednesday 22 November 2017 can be considered.

Please note that the University of Oxford's retirement policy has changed. With effect from 1 October 2017, all employees at Grade 8 and above have a retirement age of the 30 September before the 69th birthday. All employees at Grades 1-7 do not have a set retirement age. Further details are available here: www.ox.ac.uk/about/jobs/preemploymentscreening . Contact Person : Sarah Hickin

Contact Phone : 01865 287620

Contact Email : personnel@well.ox.ac.uk

More info in : goo.gl/LZYbL4

Consuelo DayzÃº Quinto Cortés <consuelo.quinto@cinvestav.mx>

QueensU EvolutionaryTheory

Dear Colleagues

I am recruiting a postdoc for a 2-year fellowship, to develop models and theory for life history evolution in size-structured populations. The position is joint with Dustin Marshall's group at Monash University and provides an excellent opportunity to develop theory jointly with empiricists working on the same questions. The successful applicant will be based at Queen's University in Kingston Canada but will also spend time at Monash University in Melbourne Australia. Salary for the position is very competitive and research funds will also be provided for the candidate to use at their discretion for conference attendance etc.

There is no formal application deadline or start date but we are hoping to find someone sooner rather than later.

Interested applicants should contact me via email. sincerely -Troy

Troy Day Department of Mathematics & Statistics Department of Biology Jeffery Hall, Queen's University Kingston, ON, K7L 3N6, Canada Phone: 613-533-2431 Mobile: 613-539-1540 Fax: 613-533-2964 day@queensu.ca http://www.mast.queensu.ca/~tday/ day@queensu.ca

SARS Bergen BioinformaticsNeuralDevelopment

A postdoctoral opportunity from our friends at the Sars International Centre for Marine Molecular Biology in Bergen, Norway. Please respond directly to Fabian Rensch with any questions.

Andy

UNIVERSITETET I BERGEN

Sars International Centre for Marine Molecular Biology Postdoctoral Position Bioinformatic Analysis of Neural Development in Nematostella

There is a vacancy for a two-year Postdoc position at the Sars International Centre for Marine Molecular Biology (www.sars.no/) in the research group headed by Dr. Fabian Rentzsch. The position is available from January 2018. Closing date for application: October 29, 2017

About the project/work tasks:

The research group studies neurogenesis in the cnidarian Nematostella vectensis with the aim to understand cellular, molecular and evolutionary aspects of nervous system development (see Richards and Rentzsch, Development, 2014 and 2015). The main task for this position is the computational analysis of single cell RNA sequencing data with the aim to understand the transcriptional changes that control the development of neural progenitor cells into differentiated neurons. If desired, contribution to the experimental validation of the computational analyses is possible in collaboration with a postdoc. The successful candidate is also expected to provide support for other projects (ATAC-seq, differential gene expression) and to contribute to the further development of the main project in line with his/her interests.

Qualifications and personal qualities:

- The applicant must hold a Norwegian PhD or an equivalent degree within informatics or molecular biology or must have submitted his/her doctoral thesis for assessment prior to the application deadline. It is a condition of employment that the PhD has been awarded. - Experience in the analysis of high-throughput sequencing data and a strong interest in gene regulatory networks, developmental biology or stem cell biology is required. - Ability to work both independently and in close collaboration with others in a structured manner. - Personal communication skills to interact with the scientific environment are required. - Proficiency in both written and oral English â€Applications in English must include:

- A cover letter that includes brief account of the applicant's research interests and motivation for applying for the position - CV - List of publications - The names and contact information for two reference persons. One of these must be the main â€advisor for the PhD programme. - Transcripts and diplomas and official confirmation that the doctoral thesis has been submitted - Relevant certificates/references

Please send your application with attachments electronically via JobbNorge by clicking on the button "Apply for this job" (choose English page) - https://www.jobbnorge.no/en/available-jobs/job/143047/postdoc-position-in-bioinformatic-analysis-of-neural-development-in-nematostella . If your diploma, grade transcripts and other documentation are in a language other than English, you must upload certified translations of these (diploma and grade transcripts in a Scandinavian language are acceptable). Please note that applications will be assessed only with the information available in JobbNorge when the deadline expires. It is the applicant's responsibility to ensure that all relevant attachments are submitted by the deadline. Further information about the position can be obtained from Group Leader Dr. Fabian Rentzsch, tlf +47 55 58 43 04, email fabian.rentzsch@uib.no. Applications by e-mail only will not be considered.

"Baxevanis, Andy (NIH/NHGRI) [E]" <andy@mail.nih.gov>

SeoulNatlU EvolutionDiseaseResistance

Post-Doctoral Fellow: Microbiome Dynamics and the Evolution of Resistance to Amphibian Chytridiomycosis

Seoul National University, Korea

We are seeking to appoint a Post-Doctoral Fellow to work on a continuing research project on the evolution of resistance to amphibian chytridiomycosis.

Recent results from our laboratory suggest that Asian amphibians have evolved resistance to chytrid fungal pathogens and thus populations persist without presenting clinical signs of chytridiomycosis. However, pathogen loads vary among populations depending on levels of immunogenetic variation, inbreeding, and climatic factors. Furthermore, individuals with resistance alleles may incur some life-history trade-offs.

Our current research program examines how immunogenes regulate microbiota that are important in immune defense and the maintenance of population structure of Asian amphibian populations.

The Post-Doctoral Fellow will conduct genetic analyses on major histocompatibility complex and neutral marker variation, together with microbiome analyses based on an extensive NGS dataset. She or he also will have the opportunity to develop their own research questions. The successful candidate will have ample opportunities to interact with Korean colleagues and with our international collaborators.

Experience in molecular biology with a strong interest in evolution is desirable. Research will be conducted in well-equipped, modern laboratory facilities.

Seoul National University is one of the leading universities in Asia and ranks 35th internationally (QS World University Rankings, 2017). The campus is set in a mountain reserve on the outskirts of Seoul and offers excellent opportunities for outdoor activities as well as the full range of cultural activities of one of the most modern, dynamic cities in the world. Subsidized housing and meals are available on campus.

Expressions of interest should include a curriculum vitae, names of three referees, and a brief statement of research interests and goals. Submissions by email are encouraged.

For more information, please contact Prof Bruce Waldman, email: waldman@snu.ac.kr; telephone +1 512 782 9905 (USA) or +82 10 8686 2121 (Korea). Or visit our lab group's web page: http://biosci.snu.ac.kr/behavior Bruce Waldman School of Biological Sciences Seoul National University 1 Gwanak-ro, Gwanak-gu Seoul 08826 South Korea

waldman@snu.ac.kr

SGN Frankfurt BiodiversityChange

Dear all, the Senckenberg Gesellschaft fuer Naturforschung invites applications for a postdoc position in Frankfurt/Main, Germany.

Many thanks for your consideration.

Job offer ref. #11-17019 The Senckenberg Gesellschaft fur Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. SGN conducts natural history research with almost 800 employees and research institutions in six federal states. Within SGN, the Senckenberg Biodiversity and Climate Research Centre (BiK-F) explores the interactions between biodiversity, climate, and society.

Senckenberg BiK-F invites applications for a Postdoctoral researcher (m/f) Causes and Consequences of Biodiversity Change (full time position) We are seeking a postdoctoral quantitative ecologist (m/f) to work within the Causes and Consequences of Biodiversity Change working group led by Prof. Markus Fischer and Dr. Peter Manning.

The research theme of the position is open although the work should complement that conducted within the group, and more broadly that of the SBiK-F institute, e.g. by contributing to the large-scale and long-term DFG funded Biodiversity Exploratories project.

We welcome innovative approaches which may address, but are not limited to the following areas: biodiversity-ecosystem function relationships, plant-soil interactions, ecosystem management, and conservation biology. We also welcome work that combines empirical data collection with the analysis and synthesis of large datasets.

Your profile A PhD in Ecology or a related field, and the ability to conduct independent ecological research Excellent knowledge of ecological theory, biodiversity research and/or global change ecology Fluency in R and an understanding of advanced statistical techniques Excellent written and oral communication skills in English and the capacity to collaborate effectively within a large and diverse team of researchers A strong publication record and the ambition and capacity to publish in high-impact journals Salary and benefits are according to a full-time public service position in Germany (TV-H E 13, 100%).

The position is a 3-year fixed-term post (with a possible extension), starting in 2018. The date of beginning can be agreed upon flexibly.

The Senckenberg Biodiversity and Climate Research Centre supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment will be Frankfurt am Main, Germany.

The employer is the Senckenberg Gesellschaft fur Naturforschung.

Application details Please include the reference to this position (ref. #11-17019) in the subject line and include a cover letter describing your motivation to apply, a detailed CV including all credentials and certificates.

Your application should also include a research plan that outlines the area(s) you would be interested in pursuing (maximum 1 page and combined with the other documents in a single pdf file).

Please submit your application before November 30th, 2017 via e-mail to: Senckenberg Gesellschaft fur Naturforschung Senckenberganlage 25 60325 Frankfurt am Main E-Mail: recruiting@senckenberg.de For scientific enquiries please contact Dr. Peter Manning, peter.manning@senckenberg.de.

Mit freundlichen GruÃen / Best regards

Isabel Gajcevic, M.A.

Personalsachbearbeiterin

SENCKENBERG

Gesellschaft fur Naturforschung (Rechtsfahiger Verein gemaÃ - 22 BGB) Senckenberganlage 25 60325 Frankfurt am Main

Besucheradresse: VoltastraÃe 1, 60486 Frankfurt am Main (5. Obergeschoss)

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 Bohning-Gaese, Prof. Dr. Uwe Fritz, Prof. Dr. Ingrid Kroncke Prasidentin: Dr. h. c. Beate Heraeus Aufsichtsbehorde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Senckenberg forscht fur Ihr Leben gern! www.200jahresenckenberg.de recruiting <recruiting@senckenberg.de>

StonyBrookU NY EvolutionaryGenomics

The Veeramah Lab at Stony Brook (http://-life.bio.sunysb.edu/ee/veeramahlab/index.html) has an opening for a postdoctoral researcher to begin in December 2017 (later start dates may be negotiable).

The successful applicant will lead a project that was recently funded by NIH for 5 years. Whole genome sequencing will be used to understand adaptation of marine Threespine Stickleback that have recently colonized freshwater lakes. We will study evolutionary trajectories of adaptive alleles by sequencing samples in time-series from young lake populations. The project will involve sample preparation for sequencing, population genetic analyses, and possibly sampling stickleback populations in Alaskan lakes.

The successful applicant should have or will shortly obtain a PhD in the areas of population, evolutionary or anthropological genetics, while at least some computer programming experience (particularly in python, equivalent or lower level languages) is required. Prior experience analyzing 2nd generation sequencing data and/or modeling demographic scenarios with genetic data is desirable.

Applications will be accepted until Dec 1st 2017. Applicants should a submit a State employment application, cover letter, resume, two references and a one page research statement through the official online application:

https://stonybrooku.taleo.net/careersection/-post_docs/jobdetail.ftl?job=1703191&tz=GMT-05%3A00 The official REF# is: 1703191

Queries regarding this position can be made by email to: krishna.veeramah@stonybrook.edu

"krishna.veeramah@stonybrook.edu"
<krishna.veeramah@stonybrook.edu>

Toulouse EvolutionaryBiology

IAST Research Fellowships in Evolutionary Biology,

The Institute for Advanced Study in Toulouse (IAST; www.iast.fr) invites applications for post-doctoral research fellowships in Evolutionary Biology, with a start date of September 1, 2018.

We welcome applications from researchers with research interests in any of the following areas: theoretical models of evolution (applied to family structure, strategic interactions, plasticity, cognition, learning, cultural evolution); related empirical work.

We seek candidates with a strong research background in their own discipline, but willing and able to develop research projects drawing on IAST's substantial interdisciplinary resources, including particularly the proximity of strong groups in economics (Toulouse School of Economics, TSE). We are open to a variety of research methods, including theory, field and laboratory experiments, observational field work, and the analysis of large secondary data sets. All research interests relevant to the broad study of human behavior are welcome, but interests close to those already developed at IAST will be given special consideration.

Eligible applicants Active researchers who have or will have completed their PhD after January 2015 and before September 2018. The IAST offers its researchers an opportunity to devote themselves full time to their research at the start of their careers. Motivated applications will be considered from candidates whose PhDs were completed in 2014 or earlier; please explain your reasons in your cover letter.

Conditions Fellows are provided with office space, computer facilities and a contract for two years, renewable for a third year.

All applications need to be sent through our website: http://www.iast.fr/apply before December 31, 2017

Cynthia Diaz <cynthia.diaz@tse-fr.eu>

TU Braunschweig Metabarcoding

Postdoctoral position in Freshwater Metabarcoding / Molecular Evolution and Ecology Technische Universitat Braunschweig, Zoological Institute

PostDoc position Metabarcoding of freshwater organisms and ancient DNA analysis from sediment cores 2 years, 100% E13, with possible extension for another 2 years.

Application deadline: 20 December 2017 Start of position: February or March 2018

We are seeking a highly motivated Postdoctoral researcher at the TU Braunschweig, Zoological Institute (Evolutionary Biology), for research within the DFG-funded Sino-German Research Training Group (GRK 2309) "Geo-ecosystems in transition on the Tibetan Plateau" (TransTiP).

TransTiP offers a research-oriented doctoral program analyzing different aspects of Earth surface fluxes on the Tibetan Plateau, an area of crucial importance for the global hydrological, energy and element cycles. The program focuses on the dynamics of sediments, soil organic carbon, water, and biodiversity in the light of land use changes and climate change. For more details see: https://www.tu-braunschweig.de/irtg-transtip/-research/projects The postdoctoral researcher will work at the Zoological Institute of TU Braunschweig (Prof. M. Vences lab), in collaboration with the Institute of for Geosystems and Bioindication (Prof. A. Schwalb) of TU Braunschweig and with the Institute for Biochemistry and Biology (Evolutionary Adaptive Genomics; Prof. M. Hofreiter) at the University of Potsdam. http://-www.zoologie.tu-bs.de/index.php/en/evolutionsbiologie http://www.mvences.de https://www.uni-potsdam.de/-de/ibb-genomics/group/hofreiter.html As a core task the researcher will establish, together with two PhD students, a reference library, primers and protocols for barcoding the diversity of freshwater eukaryotes, especially ostracodes and diatoms, in Tibetan plateau water bodies; and as a second step extend this approach to ancient DNA from sediment cores. Furthermore, we encourage the researcher to develop and pursue an own, independent research line in phylogenetics, molecular evolution or molecular ecology, fitting the main scientific interests of the host laboratories.

We will preferably hire a researcher with experience in the fields of environmental DNA / ancient DNA analysis / metabarcoding of eukaryotic or prokaryotic organisms. Expertise with analysis of next-generation sequencing techniques (e.g., Illumina amplicon analysis) and associated bioinformatic tools will be of advantage. Candidates who lack expertise in these methods, but have hands-on experience with other sophisticated molecular laboratory techniques and with lab management and student supervision are also encouraged to apply. Fluent verbal and written English communication skills and first-author papers in peer-reviewed international journals are required.

Applications of women are strongly encouraged. Severely challenged persons will be given preference in case of otherwise equal qualifications. Please send your application (CV, transcript of records, letter of motivation, names of two references) to m.vences@tu-braunschweig.de before 20 December 2017.

Prof. Dr. Miguel Vences Division of Evolutionary Biology Zoological Institute Technical University of Braunschweig Mendelssohnstr. 4 38106 Braunschweig Germany Phone: +49 - 531 391 3237 Fax: +49 - 531 391 8198 E-mail: m.vences@tu-braunschweig.de http://www.mvences.de/ Miguel Vences <m.vences@tu-bs.de>

UAkron EvolutionSpiderSilk

While focused on biomechanics/materials science it has a strong evolutionary foundation.

The University of Akron's Biology Department is seeking applications for a Postdoctoral Research Fellow position to conduct research on the material properties and structures of spider silk & webs in the Blackledge & Dhinojwala laboratories.

We seek a postdoctoral researcher interested in an NSF funded interdisciplinary research project aiming to understand the evolutionary origins of the world's toughest spider silk and its function in giant webs spun by Darwin's bark spider. The successful applicant will join a team of researchers that combines expertise in transcriptomics of silk genes, physiology of silk glands, material properties of spider silks, and ecological function of spider webs to study silk and web evolution within the genus Caerostris. The primary responsibilities of the position include characterizing the material properties of silks and finite element modelling of orb webs. The successful applicant will be eager to work in a highly integrative and interdisciplinary setting, with opportunities for training in both biological and materials research and to interact with the university's Biomimicry Research and Innovation Center. Applicants are therefore encouraged from diverse backgrounds in biology, engineering and materials science. Candidates should have a PhD in a relevant field and a demonstrated track record of peer reviewed publications. The position offers a bi-weekly salary of $1,615.38 plus benefits. The funding for this temporary position is available for up to two years.

Lab websites: http://gozips.uakron.edu/ ˜ tab27/http://blogs.uakron.edu/dhinojwala/ For more information please contact Todd Blackledge (blackledge@uakron.edu)

Applications should include a cover letter, cv, and contact information for three references. Review of applications begins on December 11ˆth and will continue until the position is filled. For complete details and to apply please visit: http://www.uakron.edu/jobs. Job ID# 10519

The University of Akron is an equal education and employment institution. It is the policy of this institution that there shall be no unlawful discrimination against any individual in employment or in its programs or activities at The University of Akron because of race, color, religion, sex, age, national or ethnic origin, sexual orientation, gender identity, disability, genetic information, military status or status as a veteran. The University is also committed to the principles of affirmative action and acts in accordance with state and federal laws.

Todd A. Blackledge Professor & Leuchtag Endowed Chair Department of Biology Integrated Bioscience Program University of Akron Akron, OH 44325-3908

Voice: (330) 972-4264 Fax: (330) 972-8445 Email: blackledge@uakron.edu http://gozips.uakron.edu/˜tab27/ "Blackledge,Todd Alan" <tab27@uakron.edu>

UBarcelona EvolutionaryBiology

Postdoc position in Comparative and Structural Genomics We are looking for a highly motivated candidate that can apply for a “Juan de la Cierva” postdoctoral fellowship from the Spanish Government to join Ruiz-Herrera’s lab.

For more information see: http://www.idi.mineco.gob.es/portal/site/MICINN/ menuitem.dbc68b34d11ccb d5d52ffeb801432ea0/ ?vgnextoidÂ50f4215103f510V gnVCM1000001d04140aRCRD& vgnextchannel= 67a04939e6b42410VgnVCM1000001d0414 0aRCRD&lang_choosen=en The aim of the project is to study mammalian genomic architecture.

Applicants should have a PhD in a relevant area (evolutionary biology, genomics or genetics). We are seeking for someone with a vivid interest in evolution research and a strong background in bioinformatics and or population genetics/ statistical genetics.

Requirements: - PhD degree obtained between 01/01/2013 and 31/12/2017.

- Competitve publication record.

- Skills in bioinformatics and/or programming.

What we offer: - Two years contract.

- The total annual amount stipend will be between euro22,000 and euro25,000 gross, depending on experience.

- Additionally, the grant includes a complementary amount of euro6,000 aimed exclusively at educational and training activities and attendance to meetings.

Ruiz-Herrera’s lab is set at Universitat Aut0noma de Barcelona (UAB), and consists of a cohesive group of national and international researchers. The long-term research goal of our research group is to provide a unified and encompassing view of how genomes are organized and regulated in mammalian cells. Within this framework, the candidate will develop a project on the evolution and function of the structural organization ofmammalian genomes. For further information please see: http://grupsderecerca.uab.cat/evolgenom/ . Likewise, UAB is located close to the city of Barcelona and is one of the major public universities in Spain. The UAB is internationally acknowledged for its quality and innovation in research. It coordinates a potent scientific and technological centre, which comprises all the departments, science and technology services, research centres, institutes and university hospitals affiliated with the UAB.

Complete application packages, including a CV, a brief (1-page) statement of research interests, and the names and e-mail addresses of two referees should be sent to: Dr. Aurora Ruiz-Herrera. Email: aurora.ruizherrera@uab.cat Application deadline: 17th December 2017.

Aurora Ruiz-Herrera Professora Agregada Dept. Biologia Cel.lular, Fisiologia i Immunologia Facultat de Biociencies Campus de la UAB - 08193 Cerdanyola del Valles - Barcelona - Spain http://grupsderecerca.uab.cat/evolgenom/ +34 581 20 51 www.uab.cat “A. Ruiz-Herrera ” <aurora.ruizherrera@uab.cat>

UBath PrizeFellowshipBioinformatics

University of Bath Prize Fellowships in the Faculty of Science, Bioinformatics

Our Prize Fellowships offer early-stage researchers the opportunity to join a cohort of like-minded rising research stars. These two-year research fellowships in our priority research areas are part of a scheme intended to fast-track fellows to a permanent appointment at Bath. As a member of this elite group, you will be on track to become a key member of our research community with a permanent academic position. Our supportive community successfully nurtures ambitious early stage researchers and provides for the requirements of their developing research programme. In the Faculty of Science we will appoint a total of seven Fellows to further strengthen and develop areas of existing research excellence.

Driven by technological advances, the modern life sciences have been transformed by the availability of ever larger datasets. These include huge archives of population data such as patient records, high resolution images of cells, tissues and organs, and the almost incalculable variety of genes, genomes and metagenomes that make up natural biological diversity. The opportunities opened up by these ’Big Data’ bring several challenges and have led to the growth of the interdisciplinary field of bioinformatics that combines computer science, statistics and mathematics to analyse and interpret biological data. Nowhere is this better exemplified than in the field of comparative genomics where analysis of high-throughput sequencing data has already made a considerable impact in understanding the diversity and evolution of organisms and the genomics underlying phenotype variation. The University of Bath has made significant advances in enhancing bioinformatics within several departments. The Prize Fellow can be drawn from multiple disciplines and will have expertise in developing big data tools and interfaces for: querying, manipulating and mining big data; software development; contextualization and integration for hypothesis driven research.

Closing date for applications is 31/12/17; Interview dates are 15th - 26th January 2018 for first stage interviews (via Skype or telephone), and week commencing 5th February for second stage interviews.

Further details can be found at https://-www.bath.ac.uk/jobs/Vacancy.aspx?ref=SF5354;
For informal enquires please contact Prof Sam Sheppard (s.k.sheppard@bath.ac.u

T.B.Taylor@bath.ac.uk

UBath PrizeFellowshipEvolutionaryBiology

University of Bath Prize Fellowships in the Faculty of Science, Evolutionary Biology

Our Prize Fellowships offer early-stage researchers the opportunity to join a cohort of like-minded rising research stars. These two-year research fellowships in our priority research areas are part of a scheme intended to fast-track fellows to a permanent appointment at Bath. As a member of this elite group, you will be on track to become a key member of our research community with a permanent academic position. Our supportive community successfully nurtures ambitious early stage researchers and provides for the requirements of their developing research programme. In the Faculty of Science we will appoint a total of seven Fellows to further strengthen and develop areas of existing research excellence. One appointment will be made within the Evolutionary Biology theme of the Milner Centre for Evolution and the remaining six within the other priority areas.

The Milner Centre for Evolution welcomes applicants in all ares of evolution research but applicants with interests in experimental evolution, statistical approaches to evolution and evolutionary ecology/genomics are especially welcome to apply.

Closing date for applications is 31/12/17; Interview dates are 15th - 26th January 2018 for first stage interviews (via Skype or telephone), and week commencing 5th February for second stage interviews.

Further details can be found at https://-www.bath.ac.uk/jobs/Vacancy.aspx?ref=SF5354
“T.B.Taylor@bath.ac.uk” <T.B.Taylor@bath.ac.uk>

UBritishColumbia Biodiversity

We seek applicants for a 2-year postdoctoral fellowship in the UBC Biodiversity Research Centre.

The next application round begins November 1, 2017. The deadline is January 12, 2018. (Late applications will not be considered.)

The Centre is made up of over 60 faculty members with interests in ecology, evolution, systematics, biodiversity and conservation. Preference will be given to candidates with bold ideas, demonstrated research ability, and strong communication skills. The successful candidate will be expected to conduct original research on core problems in biodiversity, foster interactions within the Centre, run a seminar series, and organize a retreat. Postdoctoral fellows funded by the Biodiversity Research Centre typically interact with several lab groups. Candidates are welcome to contact potential collaborating labs in the Centre to inquire about current and potential research activities, but it is not necessary to apply to work with a specific faculty member.

Starting date: 1 September 2018. Salary: $48,000 per yr. Research stipend: $7,000 per yr. Application requirements: curriculum vitae, a statement of overall scientific goals and interests (approximately 2 pages), and the names and contact information for three references. The statement of goals and interests is free form but we should be able to determine both the general interests and specific projects that the candidate will engage in over the post-doc period.

All of the material should be submitted to biodiversity.centre@ubc.ca as a single PDF (please name your file using this format: Lastname_Firstname_PDF2017.pdf) Closing date for application, 12 January 2018.

The University of British Columbia hires on the basis of merit and is committed to employment equity. We encourage all qualified candidates to apply. Equity and diversity are essential to academic excellence. An open and diverse community fosters the inclusion of voices that have been underrepresented or discouraged. We encourage applications from members of groups that have been marginalized on any grounds enumerated under the B.C. Human Rights Code, including sex, sexual orientation, gender identity or expression, racialization, disability, political belief, religion, marital or family status, age, and/or status as a First Nation, Metis, Inuit, or Indigenous person."

Katie Beall Administrator Faculty of Science | Biodiversity Research Centre The University of British Columbia | Vancouver Campus 115-2212 Main Mall | Vancouver BC | V6T 1Z4 Canada Phone 604 822 0862 brcadmin@biodiversity.ubc.ca http://www.biodiversity.ubc.ca Katie Beall <brcadmin@biodiversity.ubc.ca>

UCalifornia Berkeley GeneDrivePopulationGenetics

POSTDOC POSITIONS 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 two postdoctoral scholars to work on mathematical and computational aspects of gene drive systems in mosquito vectors of malaria, dengue fever and Zika virus. The positions are initially for one year, with the possibility of extension, and are 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 long shared sequence blocks of SNPs and identity by descent, * 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 candidates 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 one of the positions, 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 December 18th, 2017. Inquiries are also welcome. Additional information about the research in the Marshall Lab can be found at 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 Davis HumanGenomics

A new postdoctoral position is available in the Henn Lab at UC Davis < https://www.ucdavis.edu/ > in the Dept.

of Anthropology and the Genome Center. The Henn Lab specializes in human population genetics/genomics and human evolution. Much of our research involves field collection of samples from southern Africa, next-generation sequencing of human genomes and modeling evolution (both phenotype and prehistory) in African populations. Please see *https://ecoevo.stonybrook.edu/hennlab/- [my former SUNY website] for additional information on research projects and publications. We seek a postdoctoral scientist to lead research projects related to African demographic history using next-generation sequence data. A strong computational background is required. Opportunities to participate in workshops, develop independent projects and travel will be available; we have many collaborators both in the US and internationally. UC Davis is an outstanding environment for both anthropology and genomics, and the postdoctoral candidate will spend time at the Genome Center to facilitate interaction. Compensation is based on NIH pay-scales and 3 years of funding are available.

Skills: Experience with scripting languages such as Python or PERL, experience with statistical analysis in R, and a strong background in population genetics are necessary. Knowledge of human evolution is a plus. A PhD in Genetics, Statistics, Anthropology, Biology or related field is required by the start date. Start date February 1, 2018 or thereafter. E-mail a CV and cover letter to Brenna Henn <quercus29@gmail.com>.

Brenna M. Henn

Assistant Professor Dept. of Ecology and Evolution Program in Human Evolutionary Biology 640 Life Sciences Building Stony Brook University, SUNY

brenna.henn@stonybrook.edu

UCalifornia Riverside DataVizPhylogenomics

Postdoc: Interactive and Exploratory Data Visualization Tools for High-Throughput -Omics Datasets

2.5 year postdoctoral position at the University of California, Riverside focused on the development of new data visualization tools within the prototype Phinch framework.

Phinch (http://phinch.org) is an open-source framework for visualizing biological data, funded by a grant from the Alfred P. Sloan foundation. This project represents an interdisciplinary collaboration between Pitch Interactive (http://pitchinteractive.com/ - a data visualization studio in Oakland, CA) and the Bik Lab at UC Riverside (https://biklab.github.io). Typical user applications for Phinch include environmental rRNA amplicons or shotgun metagenomic data, although this framework is being expanded to support any type of sample/observation data represented in a standard format (RNA-seq, gene variants, phenotype character matrices, etc.). The appointed candidate will work with the Pitch Interactive studio to implement novel and interactive visualization features, develop statistical tests as visual plugin tools (e.g. via R shiny apps), and implement new phylogenetic visualizations for microbial ecology datasets. The postdoctoral scholar will also contribute to software documentation and end user training workshops as needed.

Prospective applicants should review project aims outlined in the funded grant proposal (https://doi.org/-10.6084/m9.figshare.5471809.v1) as well as these other related resources:

* Phinch GitHub Wiki https://github.com/-PitchInteractiveInc/Phinch/wiki * Bik HM, Pitch Interactive (2014) Phinch: An interactive, exploratory data visualization framework for -Omic datasets, bioRxiv, doi: http://dx.doi.org/10.1101/009944 (preprint)

Minimum Qualifications:

Postdoctoral applicants should possess a Ph.D. in a biological or computational discipline, demonstrate a strong publication record and ability to conduct independent research. All applicants are expected to develop strong written and verbal communication skills, as well as assist in mentoring undergraduate and graduate students.

Desirable Qualifications:

Proficiency in a standard programming language (Python or Javascript preferred), experience in biological data visualization (e.g. using RStudio or D3.js), and knowledge of common -Omics data types and workflows (e.g. analysis of rRNA amplicon datasets in QIIME, experience with binning/assembly/functional analysis of shotgun metagenomes, large phylogenomic analyses, etc.). Applicants with expertise in phylogenomics, comparative phylogenetics, and/or statistical analysis in R or Python are especially encouraged to apply.

Application and Appointment:

All appointments are initially for one year, and renewable based on performance. Salaries are commensurate with experience and based on minimums set by the University of California postdoctoral union. To apply, submit a curriculum vitae, a 1-page statement of research interests, and contact details for 2-3 academic references to holly.bik@ucr.edu. Review of applications will begin immediately, and will continue until the position is filled.

Please contact Holly Bik (holly.bik@ucr.edu) if you have any questions about this postdoctoral position.

– Holly Bik Assistant Professor Department of Nematology University of California, Riverside 3401 Watkins Drive Riverside, CA 92521 Email: holly.bik@ucr.edu Phone: (+1) 951-827-4230

Web: http://biklab.github.io Twitter: https://twitter.com/hollybik holly.bik@gmail.com

UChicago PopulationGenetics

Post-doctoral Scholar Positions available in:

THEORETICAL POPULATION GENOMICS

Two postdoctoral scholar positions are available in the research group of Matthias Steinrücken in the Department of Ecology and Evolution at the University of Chicago. In the group, we are developing theoretical, computational and statistical methods for population genomics analysis to study neutral and functional genetic variation in the context of complex demographic scenarios. The exact projects for the scholars will be flexible, though based around ongoing research on coalescent and diffusion-based approaches to infer demographic histories, detect local ancestry, and study selection using population genetic data.

The department of Ecology and Evolution has a very collaborative and unique environment with expertise in theoretical and empirical approaches to questions in ecology and evolutionary genetics. Moreover, the University of Chicago provides ample opportunities for interactions with outstanding researchers in overlapping areas, particularly in the departments of Statistics, Human Genetics, and Genetic Medicine.

Candidates should have a PhD in Statistics, Mathematics, Biology, Computer Science, or in a related field with substantial quantitative training. The start date is negotiable, and the salary will be competitive and based on level of experience.

To apply, please send your application to steinrue@uchicago.edu. Your application should include a brief cover letter, a cv, a one-page description of your research interests, and contact information for three references. Applications will be considered on a rolling basis until the positions are filled, but should be received by December 9, 2017 to ensure consideration. Candidates from diverse backgrounds are particularly encouraged to apply. Please see https://voices.uchicago.edu/steinrueckenlab/ to learn more about the group and send any questions regarding the position to steinrue@uchicago.edu.

Matthias Steinrücken, PhD

Assistant Professor

Department of Ecology and Evolution

University of Chicago

https://voices.uchicago.edu/steinrueckenlab/ The University of Chicago is an Affirmative Action/Equal Opportunity/Disabled/Veterans Employer and does not discriminate on the basis of race, color, religion, sex, sexual orientation, gender identity, national or ethnic origin, age, status as an individual with a disability, protected veteran status, genetic information, or other protected classes under the law. Job seekers in need of a reasonable accommodation to complete the application process should call 773-702-5671 or email ACOppAdministrator@uchicago.edu with their request.

Matthias Steinrücken <steinrue@uchicago.edu>

steinrue@uchicago.edu

UColorado Boulder HybridizationGenomics

REVIEW OF APPLICATIONS WILL BEGIN NOV 15, 2017

Applications are invited for a postdoctoral researcher position in the Taylor Lab at the University of Colorado at Boulder (http://www.colorado.edu/lab/taylor/opportunities < https://www.colorado.edu/lab/taylor/opportunities >). The postdoctoral researcher will generate and analyze population genomic and phylogenomic data from North American chickadees, including whole genome and GBS data from two regions of hybridization and whole genome data for all North American taxa. The initial appointment is for one year with the possibility of renewal. Applicants should have completed a PhD or have postdoctoral experience in the fields of Population Genomics, Evolutionary Genomics, Evolutionary Biology, or Computational Biology and have an established record of research productivity and publications in scientific journals. Experience in studies of avian evolution would be an advantage, but is not required.

We are looking for a highly motivated and collaborative individual with lab and computational expertise related to the generation and analysis of high-throughput data. Those with experience studying hybrid zones and/or phylogenomics will be given preference. Proficiency in R, Perl, Python and/or C++ programming is a benefit.

The successful candidate will join the Taylor Lab in the Department of Ecology and Evolutionary Biology (EBIO) at the University of Colorado at Boulder. Research in the Taylor Lab is broadly focused on using avian hybrid zones to understand the genetic bases of traits relevant to speciation and to the maintenance of species barriers. The EBIO Department at CU Boulder has a strong group in evolutionary biology and genomics. The University of Colorado is located in Boulder Colorado, a vibrant city located next to the Front Range of the southern Rocky Mountains.

For further enquiries please contact: Scott Taylor (scott.a.taylor@colorado.edu)

The position will remain open until filled. The start date for this position is flexible, but no later than May 01 2018. REVIEW OF APPLICATIONS WILL BEGIN NOV 15, 2017

To apply please email a CV, cover letter, a brief statement of research goals, and contact information for 3 references to Scott Taylor (scott.a.taylor@colorado). Short-listed individuals will be contacted.

This position is eligible for medical, dental and life insurance, retirement benefits programs, and is eligible for monthly vacation and sick leave accruals.

The University of Colorado Boulder is committed to providing a safe and productive learning, living and working community. To achieve this goal, we conduct background investigations for all final applicants being considered for employment. Background investigations include a criminal history record check, and an EPLS (Excluded Parties List System) check.

The Immigration Reform and Control Act requires that verification of employment eligibility be documented for all new employees by the end of the third day of work.

The University of Colorado is an equal opportunity and affirmative action employer committed to assembling a diverse, broadly trained faculty and staff. In compliance with applicable laws and in furtherance of its commitment to fostering an environment that welcomes and embraces diversity, the University of Colorado does not discriminate on the basis of race, color, creed, religion, national origin, sex (including pregnancy), disability, age, veteran status, sexual orientation, gender identity or expression, genetic information, political affiliation or political philosophy in its programs or activities, including employment, admissions, and educational programs.

– Scott A. Taylor | Assistant Professor Department of Ecology and Evolutionary Biology University of Colorado Campus Box 334 Boulder, CO 80309 Office: C287 Ramaley http://www.colorado.edu/lab/taylor/ Scott Taylor <dr.scott.a.taylor@gmail.com>

UEdinburgh 2 ViralGenomeAnalysis

The Institute of Evolutionary Biology at the University of Edinburgh seeks to appoint two Postdoctoral Researchers to work with Andrew Rambaut, developing computational and statistical approaches to viral genome sequence analysis in real time during an outbreak or epidemic.

Background: In recent viral outbreaks of Ebola, MERS-CoV and Zika, viral genome sequencing revealed critical insights into the evolution and transmission of the virus, offering tantalizing examples of the potential value of this for future outbreak control efforts. To maximize the utility of this information, it needs to be achieved in real-time, providing virus genome data and actionable analysis and interpretation within hours of patients being sampled. The ARTIC project, funded by The Wellcome Trust, will achieve this by producing a mobile virus sequencing system, including statistically rigorous analysis frameworks, to prepare for the next outbreak and ensure that viral genome sequencing is positioned to have full impact on the public health response.

The aim of the project is to create a sample-to-response molecular epidemiology system for acute RNA virus outbreaks in resource-limited locations. Based on the Oxford Nanopore Technology's MinION portable sequencing platform, the system will include a 'lab-in-a-suitcase' for virus isolation and sequencing, in-country bioinformatics of MinION data, real-time phylodynamic analysis, integration of epidemiological data, and interpretation and visualization of the results to inform public health responses. The position advertised here will focus on the computational and statistical aspects of the project including the development of phylodynamic analyses of outbreaks capable of updating in real-time as new data becomes available.

Candidates will have a PhD in a relevant field (computational biology, computer science, mathematical biology or statistics), experience of developing statistical models of molecular epidemiology, phylodynamics and phylogography, and/or demonstrable knowledge and experience of software development, High Performance Computing, and GPGPU development. The candidates will have a track-record of publishing in peer-reviewed, academic journals, excellent communication skills, and the ability to deal with a variety of tasks to set deadlines. The project will involve working with project team members including virologists, bioinformaticians and epidemiologists to create an integrated, practical system for public health emergencies.

The posts are full-time for 5 years.

Informal enquiries to Prof. Andrew Rambaut (a.rambaut@ed.ac.uk).

Full details and application instructions here:

https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id=042022 Andrew Rambaut <a.rambaut@ed.ac.uk>

UFlorida EvolutionSenescence

Postdoctoral Associate in Stem Cell and Regenerative Biology, Whitney Laboratory for Marine Bioscience, University of Florida http://explore.jobs.ufl.edu/cw/en-us/job/504986/postdoctoral-associate The Schnitzler Lab seeks a highly motivated postdoctoral associate to join a team focused broadly on stem-cell mediated tissue regeneration, and the evolution and development of cellular senescence in the colonial cnidarian Hydractinia using modern experimental and computational biology techniques.

The postdoctoral associate will be expected to design and lead research activities related to these topics, including designing and performing experiments, developing and executing protocols, performing data analysis, and writing manuscripts and grants. The postdoc will perform research as part of a team, as well as train and mentor other lab members. The ideal candidate will have extensive experience in molecular and cellular biology techniques such as: DNA and RNA extraction, molecular cloning, in situ hybridization, gene manipulation and editing techniques (RNAi, morpholinos, CRISPR/Cas9), microinjection and/or electroporation of embryos, quantitative PCR, Western blotting, epifluorescence and confocal microscopy. Experience with cellular proliferation and viability assays is preferred. Experience with generating and processing RNA-seq or similar datasets is also preferred. Unix and programming skills are preferred. Experience with cnidarian or other marine invertebrate organisms is preferred.

Information about the Whitney Laboratory can be found at http://www.whitney.ufl.edu/ . Applicants from groups that are traditionally underrepresented in the sciences are strongly encouraged to apply. Application deadline is November 30, 2017.

For further information, please contact Dr. Christine Schnitzler (christine.schnitzler@whitney.ufl.edu)

Christine Schnitzler <christine.schnitzler@whitney.ufl.edu>

UGhent ComputationalPlantNetworks

The Comparative Network Biology lab (Klaas Vandepoele) of the VIB Center for Plant Systems Biology is looking for a Postdoc Computational Network Biology in Plants.

Our mission

Our objective is to extract and validate biological knowledge from large-scale experimental data sets using data integration, comparative sequence and expression analysis, and network analysis. In our lab, we combine computational methods with experimental data to generate new insights about gene function, gene regulation and comparative genome biology.

In this project, our objective is to * delineate high-quality biological networks in different plant species * develop new methods to accurately translate biological networks between different species (model species & crops) with different levels of genome complexity

Job description

* Fully funded Postdoc position for 2 years (start date March 2018 or later). * You get the freedom to design and execute a personal research project addressing some of the objectives listed above. * Through (inter)national collaborations with wetlab scientists, computational results can be experimentally validated! * Perform co-supervision of research projects of PhD students in the lab. * Access to a diverse set of training programs at VIB (both scientific & soft skills) * Reporting of results through publications in peer-reviewed international journals. * Attending and presenting your results

at international scientific events.

Your profile

* You have PhD degree in Bioinformatics, Computational Biology or related. * You are enthusiastic about scientific research and have a strong interest in studying plant biology using genomics and systems biology approaches. * Through international peer-reviewed publications, you have a track record in plant genomics or systems biology research (people only having publications describing experimental/wetlab work will not be retained). * You are fluent with Linux/Unix and have good knowledge of Python or another programming/scripting language. * You have good communication and writing skills. * You are proficient in English.

How to apply?

Motivated candidates are asked to apply online (https://vibvzw.jobsoid.com/j/10785/postdoc-computational-network-biolo gy-in-plants). Please make sure your application includes a letter of motivation, a detailed CV and the contact information of 2 references (including e-mail addresses and phone numbers). Applications will be accepted until 31 January 2018.

best regards,

Klaas Vandepoele - Professor Comparative Integrative Genomics VIB-UGent Center for Plant Systems Biology Ghent University Technologiepark 927 - 9052 Ghent - Belgium Tel. +32(0)9 331 38 22

Lab website: http://bioinformatics.psb.ugent.be/cig/ Twitter: http://twitter.com/plaza_genomics Klaas Vandepoele <klaas.vandepoele@psb.vib-ugent.be>

UHamburg PDF PhD EvolBiol

I have a PhD position and a post doc position opening with me at the University of Hamburg. Both are at the interface of evolutionary biology and biological oceanography.

PhD position

About the University and Institute At the Universitat Hamburg more than 4300 scientists including 700 full professors teach and conduct research in 8 faculties representing a broad spectrum of disciplines. The research profile in Mathematics, Informatics, Natural Sciences and Medicine has a focus on Climate, Earth and Environment', ,Matter and Universe', Structure and Function of Biomolecules' and Neurosciences'. The MIN faculty is located at the heart of Hamburg surrounded by the pulsating life of the international metropolitan with its inspiring environment.

The Institute for Hydrobiology and Fisheries Science (IHF) conducts interdisciplinary research in all fields of marine science with a focus of understanding the functioning and sensitivity of marine ecosystems under different pressures, e.g. climate variability/climate change, eutrophication and fisheries.

The Position: - The PhD student will design, carry out, and analyse a long-term selection experiment and/or use natural samples from environmental gradients to conduct their experiments in order to disentangle how environmental variability and biotic complexity impact the evolutionary potential of marine phytoplankton.

- Plans for the experimental set-up will be finalised after discussions between the student, group leader, and collaborating scientists from related disciplines, but must involve an element of biotic complexity

-The candidate will partake in scientific cruises (2 weeks each, Baltic Sea and North Sea); the main experiments will be based in the laboratory

-Associates will be expected primarily to conduct research and teach

-The associate will have the opportunity to pursue further academic qualifications

Requirements: -A university degree in a relevant field marine biology/ biological oceanography, ecology and evolution, or a related field

-The candidate will have a grasp of either plankton ecology, microbiology, marine biology or evolutionary biology and should demonstrate a strong willingness to develop interdisciplinary skills spanning these areas

-Excellent laboratory skills (e.g. sterile working techniques, cell culture) are expected

-Knowledge of statistical programming would be desirable

-It is a prerequisite that the candidate be willing to cooperate with colleagues from other disciplines

-The candidate will have to be fluent in English or fluent in German with very good knowledge of English

For further information, please contact Jun-Prof. Elisa Schaum (elisa.schaum@uni-hamburg.de) or consult our website at https://www.biologie.uni-hamburg.de/ihf Application deadline: Dec 20th2017

Post-Doc position Background: The position is located at the laboratory for Plankton Ecology, within the Institute for Hydrobiology and Fisheries Science, (also in collaboration with the Centre for Earth System Research and Sustainability). The research focus in this group is, through experimental evolution, on factors that modulate the adaptive potential of large marine phytoplankton populations under aspects of climate change, and, through physiological experiments, on the ecological and biogeochemical repercussions of climate change on phytoplankton communities. The position will investigate the role of marine viruses in shaping phytoplankton communities under climate change scenarios.

Whether this is primarily through the lens of molecular biology, physiology, or both, will depend on the skill sets and interests of the applicant. The successful candidate is expected to have a keen interest in micro-evolutionary processes, interactions between different phytoplankton species, between phytoplankton and their associated viruses, as well as in the repercussions of the changing role of phytoplankton in biogeochemical cycles.

The University:

At the Universitat Hamburg more than 4300 scientists including 700 full professors teach and conduct research in 8 faculties representing a broad spectrum of disciplines. The research profile in Mathematics, Informatics, Natural Sciences and Medicine has a focus on Climate, Earth and Environment', ‚Matter and Universe', Structure and Function of Biomolecules' and Neurosciences'. The MIN faculty is located at the heart of Hamburg surrounded by the pulsating life of the international metropolitan with its inspiring environment.

The Institute for Hydrobiology and Fisheries Science (IHF) conducts interdisciplinary research in all fields of marine science with a focus of understanding the functioning and sensitivity of marine ecosystems under different pressures, e.g. climate variability/climate change, eutrophication and fisheries.

The Position: * The position will investigate the role of marine viruses in shaping

— / —

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

---

UKoblenz AnimalBiodiversity

University of Koblenz-Landau, Institute for Integrated Natural Sciences

Postdoctoral Research Assistant in Animal Ecology

Application deadline: 31.01.2018

The Department of Zoology, Institute for Integrated Natural Sciences, at the University of Koblenz-Landau invites applications for a

Postdoctoral Research Assistant.

Starting date: April 1st 2018.

Duration: 3 years (with the possibility of extension for another 3 years).

Salary: German salary scale (TV-L 13, 100%).

Teaching obligation (in German or English): 4 hours per week.

We are seeking a highly motivated and productive candidate who is interested in and capable of developing his/her own independent research profile. We will consider a wide spectrum of candidates working in the fields of animal ecology or animal biodiversity research. Applicants working on hot topics in biodiversity research with state-of-the-art approaches are particularly encouraged to apply. Areas of interest include for example: Organismal responses to environmental change (e.g. climate or land-use change); conservation biology; dispersal / movement ecology; adaptation to environmental stress; thermal adaptation; population and landscape genetics.

The successful candidate will hold a Ph.D. in animal ecology / biodiversity research and will have a strong publication record and background in ecology. He/she will have broad experience in experimental design and according statistical analyses. Excellent English communication skills are essential. Prior postdoc experience and experience in acquiring third-party funding will be advantageous.

Our department works mainly in the field of evolutionary ecology, focusing on life-history evolution, stress adaptation, and reproductive biology. For further information please visit https://www.researchgate.net/profile/Klaus_Fischer . The University of Koblenz-Landau is an equal opportunity employer.

Applications should include (1) a cover letter with short statements of motivation and research interests, (2) scientific CV with degree certificates, (3) list of publications, (4) list of externally acquired funds (if any), (5) a short statement of future research plans, and (6) contact details of two academic referees. Applications should be submitted electronically as a single PDF file to bewerbung@uni-koblenz-landau.de before February 1st, 2018. Please mention the call number (198/2017) in your application and in the header of your email.

For any enquiries please contact Klaus Fischer via e-mail.

Prof. Dr. Klaus Fischer

e-mail: klausfischer@uni-koblenz.de

Prof. Dr. Klaus Fischer Institut für Integrierte Naturwisssenschaften

Abteilung Biologie Universität Koblenz-Landau Universitätsstraße 1 D-56070 Koblenz

Phone: +49-261-287-2238

Klaus Fischer <klausfischer@uni-koblenz.de>

ULaval EvolutionaryCellBiology

Postdoctoral position in Evolutionary Cell Biology at Université Laval (Quebec City, Canada) A postdoctoral position (2 years) is available in the Landry Laboratory. The ideal applicant would have a strong expertise in molecular biology, biochemistry, or proteomics with interest for and/or basic skills in bioinformatics (Python, R). The projects are mainly experimental but candidates with a strong computational background who are willing to learn and perform experimental research are encouraged to apply. Previous work in yeast genetics and genomics would be an asset. Potential projects are related to recently published work (see below) and include, but are not limited to, the evolution and function of new genes and the organization and evolution of protein-interaction networks.

Université Laval is one of the most important research universities in Canada and is located in Quebec City (https://en.wikipedia.org/wiki/Quebec_City), a lively city with a vibrant culture that offers an exceptional quality of life.

Interested applicants should send a CV, a list of publications, a statement of interest (1 page) and the name of three referees in a single PDF file to landrylaboratory@gmail.com. The positions will remain available until filled. Starting dates could be between January 2018 and July 2018.

Recent representative publications: Marsit S, Leducq JB, Durand Ã, Marchant A, Filteau M, Landry CR. Evolutionary biology through the lens of budding yeast comparative genomics. Nat Rev Genet.2017 Oct;18(10):581-598.

Diss G, Gagnon-Arsenault I, Dion-Coté AM, Vignaud H, Ascencio DI, Berger CM, Landry CR. Gene duplication can impart fragility, not robustness, in the yeast protein interaction network. Science. 2017 Feb 10;355(6325):630-634.

Caron D, Byrne DP, Thebault P, Soulet D, Landry CR, Eyers PA, Elowe S. Mitotic phosphotyrosine network analysis reveals that tyrosine phosphorylation regulates Polo-like kinase 1 (PLK1). Sci Signal. 2016 Dec 13;9(458):rs14.

Leducq JB, Nielly-Thibault L, Charron G, Eberlein C, Verta JP, Samani P, Sylvester K, Hittinger CT, Bell G, Landry CR. Speciation driven by hybridization and chromosomal plasticity in a wild yeast. Nat Microbiol. 2016 Jan 11;1:15003.

Filteau M, Hamel V, Pouliot MC, Gagnon-Arsenault I, Dubé AK, Landry CR. Evolutionary rescue by compensatory mutations is constrained by genomic and environmental backgrounds. Mol Syst Biol. 2015 Oct 12;11(10):832 Filteau M, Diss G, Torres-Quiroz F, Dubé AK, Schraffl A, Bachmann VA, Gagnon-Arsenault I, Chrétien AÃ, Steunou AL, Dionne U, Côté J, Bisson N, Stefan E, Landry CR. Systematic identification of signal integration by protein kinase A. Proc Natl Acad Sci U S A. 2015 Apr 7;112(14):4501-6.

Nguyen Ba AN, Strome B, Hua JJ, Desmond J, Gagnon-Arsenault I, Weiss EL,Landry CR, Moses AM. Detecting functional divergence after gene duplication through evolutionary changes in posttranslational regulatory sequences. PLoS Comput Biol. 2014 Dec 4;10(12):e1003977.

Goldman A, Roy J, Bodenmiller B, Wanka S, Landry CR, Aebersold R, Cyert MS. The calcineurin signaling network evolves via conserved kinase-phosphatase modules that transcend substrate identity. Mol Cell. 2014 Aug 7;55(3):422-435.

Christian Landry, PhD Professor Canada Research Chair in Evolutionary Cell and Systems Biology Département de biologie Département de biochimie, de microbiologie et de bio-informatique Institut de Biologie Intégrative et des Systèmes Université Laval Québec (Québec) G1V 0A6 Canada

http://landrylab.ibis.ulaval.ca/ Christian Landry

<Christian.Landry@bio.ulaval.ca>

UMichigan SpeciesDelimitation

NSF Funded Postdoctoral Position

Application deadline: December 1, 2017

A two-year postdoctoral position is currently available in the Knowles Lab, in collaboration with Jeet Sukumaran and Craig Moritz, to work on conceptual issues regarding species delimitation. Specifically, this postdoctoral position focuses on empirical applications of genetic-based delimitation, which will be coupled with evaluations of method performance using computer simulations. Although the postdoc will not be required to program, the ideal candidate should have experience with scripting and analysis of genomic datasets, as well as a conceptual interest in species delimitation. The postdoc will be based in Ann Arbor.

Please send CV and inquires to L. Lacey Knowles (knowlesl@umich.edu), briefly explaining your past experience with coalescent simulations and their application (e.g., phylogeographic, phylogenetics, species delimitation analyses), as well as your general proficiency with scripting and analysis of genomic data.

– L. Lacey Knowles Robert B. Payne Collegiate Professor Dept. of Ecology and Evolutionary Biology Curator of Insects, Museum of Zoology University of Michigan Ann Arbor MI 48109-1079

"knowlesl@umich.edu" <knowlesl@umich.edu>

UMinnesota EvolutionarySystems

Grand Challenges in Biology Postdoctoral Program

College of Biological Sciences

University of Minnesota

Application deadline: February 1, 2018

Position start date: May-August 2018 (specific date negotiable)

Rationale

Understanding and predicting the behavior of complex biological systems requires a framework that can integrate across levels of biological organization, can capture nonlinear feedbacks in dynamical systems, and can incorporate and facilitate mechanistic understanding. This is the challenge of the future of biology. Meeting this challenge requires a multidisciplinary approach that relies heavily on innovations in quantitative fields such as mathematics, computer science, statistics, and engineering. It also requires strong integration (or re-integration) of molecular biology with organismal biology. Meeting the food, water, and energy needs of a growing human population, while minimizing adverse impacts of habitat alteration, climate change, invasive species, overexploitation, and pollution on human health and ecological systems - operate at scales from molecules to ecosystems, and there is a pressing need to develop the science that can cross these scales. The University of Minnesota is developing research and curricular initiatives focused on addressing grand challenges, and this program is part of CBS' contribution to the university-wide programs.

Program Aims

The overall aim of the Grand Challenges in Biology (GCB) Postdoctoral Program is to stimulate synergistic interactions between faculty and postdoctoral associates interested in collaborating on multidisciplinary research that addresses societally relevant problems. Postdoctoral projects are for two years (assuming satisfactory progress toward research goals in year one). Postdoctoral associates will be encouraged to participate in grant proposal development workshops and other professional development activities offered at UMN and CBS and are permitted to serve as Principal Investigators on grant proposals. While in residence, the postdoctoral associates will be expected to be visible members of CBS, actively engaging with faculty, undergraduate- and graduate students and contributing to furthering the collaborative culture of CBS.

Application Process

To apply:

Visit http://humanresources.umn.edu/jobs Click the appropriate maroon link in the center of the page

Enter 320761 in the Keywords box

Click "Search"

Applications must be submitted through the UMN employment site.

Applicants should develop a 2-year research project under the guidance of two or more faculty advisors, at least one of whom must be a faculty member in the College of Biological Sciences (CBS). The other advisor(s) may be from a different department within CBS, from any other College at UMN or from a local entity external to the university (e.g., private company, government agency, NGO). Since an important aim of the program is to jumpstart the formation of new teams, the faculty advisors should not have an already established record of collaboration with each other (as evidenced by jointly authored publications).

Uploaded applications materials must include:

CV

1-page description of previous or current research

3-page (maximum) description of proposed research containing: a statement of the problem to be addressed; methods/approach; relevance of the work in relation to grand challenges in biology; contributions of the collaborating partners; literature cited (does not count toward the 3-page limit)

letters of support from each of the proposed faculty advisors who will be involved in the project as well as the names and contact information for two external persons (not from UMN) who may be asked to submit letters of recommendation

The expected salary will be $47,500 plus benefits. In addition, the postdoctoral scholar will receive $5,000 per year for research supplies and research-related travel. It is expected that necessary office and laboratory space, access to large equipment and any other research needs will be provided by faculty advisors.

Additional Details

Positions are initially for two years with the possibility of renewal for a third year pending progress review.

Early-career scientists with a high potential to springboard their careers to future faculty positions are especially encouraged to apply.

Applications will be evaluated by a search committee representing CBS's disciplines. This same committee, or a subset thereof, will also be responsible for evaluating postdocs' performance at the end of the first year and in connection with eventual renewal for a third year.

Applicants should have completed all of the requirements necessary to attain a Ph.D. degree and be able to be on campus to start employment by the agreed start date.

Graduates of UMN are eligible to apply for these positions, but we also hope to recruit a strong pool of external applicants.

— / —

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

UMinnesota MaizeGenomics

Position: Post-doctoral Research Associate

Location: University of Minnesota, Department of Agronomy and Plant Genetics

Research Area: Maize Genomics

Qualifications: Ph.D. in Genomics, Bioinformatics, Applied Quantitative Genetics, Plant Breeding, or related field. Strong programming and data management skills are preferred as well as excellent written and oral communication skills.

A post-doctoral position is available in the field of genomics applied to maize as part of an NSF Plant Genome project "Dissecting natural mechanisms of genome content variation and the impact on phenotypic variation". The candidate will be responsible for leading computational analyses related to understanding diversity in the maize pan-genome. The research associate is expected to analyze large datasets and lead preparation and publication of peer-reviewed manuscripts that present research findings from the project.

Experience working with next-generation sequence data, quantitative genetics or statistical modeling and analysis of large data sets is required. Prior experience analyzing complex omics data is desirable. Ideal candidates will be highly motivated to publish, able to lead an independent research project, have documented ability to successfully complete research publications, and clearly describe skills that they have to offer and skills that they would like to acquire during their tenure as a post-doctoral researcher. Expertise in maize genetics or similar and documented ability to coordinate collaborative research is highly desirable.

For inquires about the position and research focus, please contact Candice Hirsch (cnhirsch@umn.edu; (612) 301-9522). To apply, send a letter of application, a full curriculum vita, and contact information for three references to Candice Hirsch (cnhirsch@umn.edu).

Suzanne McGaugh <smcgaugh@umn.edu>

UMinnesota PopulationGenomics

Mexican cave tetras offer a unique opportunity to study how recombination, selection, drift, and introgression shape genomic divergence. Cave tetras experience vastly different selection pressures than do conspecifics living in surface waters. Distinct phenotypes and behavioral differences have evolved and are maintained in the cavefish populations, while in some caves, substantial gene flow between surface and cavefish is ongoing. There are multiple, independent origins of cavefish in separate caves, providing a naturally replicated experiment. The McGaugh lab is recruiting a postdoc to 1) analyze resequenced genomes for complex demography, admixture, and local adaptation in repeatedly evolved cavefish and 2) conduct multiple high-resolution QTL maps of sleep loss and circadian deregulation in repeatedly evolved cavefish.

Start-date is flexible, and there is opportunity for independent projects from functional genetics to modeling. Review of applications will begin Nov 10, and continue until a suitable candidate has been found. Interested applicants should send a preliminary inquiry with CV and references smcgaugh@umn.edu Applicants with a strong computational background or molecular/function genetic background are encouraged to apply. The initial position is available for one year, with renewal for additional years pending performance.

For more information on the McGaugh lab see https://sites.google.com/site/mcgaughlab/ Principal Duties and Responsibilities 90% Computational genomics, sample collection, writing manuscripts, animal husbandry and DNA extraction Analyzing next-generation sequencing data, keeping detailed notes and logs of the analyses, and keeping well-annotated code that was written for those analyses to ensure future replication of the work.

Conduct phenotyping, genotyping, and analyses of fish for a large-scale QTL experiment.

Submit permits, conduct field-work, and extract DNA for population genomic analyses.

Maintain fish and basic molecular lab work to confirm results of next generation sequence analysis.

Participate in small projects that may or may not be directly related research, but aid in other's projects in the lab and help generate preliminary data for grant submissions. This may also include mentoring of undergraduate and graduate students.

Write and submit manuscripts that present results of the analysis conducted in the McGaugh lab. Help in the preparation of other lab-wide manuscripts and analyses for those manuscripts.

5% Lab maintenance, safety, supplies and systems administration In charge of daily function and operation of the McGaugh lab including the purchasing of supplies, maintenance of a safe and productive physical and computational environment.

5%- Lab citizen Attend lab meetings (and do associated readings), attend relevant lectures and training sessions. Assist other lab/community members.

Minimum Qualifications A PhD in genomics, evolution, genetics, or related fields.

Experience with next-gen sequence data and a unix/command line interface.

Experience with or willingness to learn scripting/programming languages including R, python, and/or C++ Demonstrated ability to produce high-quality publications A desire to help lead an integrative and motivated group of young scientists Patience, dedication, flexibility, and enthusiasm Excellent communication skills

Preferred Qualifications Strong knowledge of population genetics, genomics Interest in aging, stress, and recombination.

Experience with international fieldwork and caving At least minimal understanding of Spanish or willingness to learn basics prior to fieldwork.

The Twin Cities offer a range of arts and entertainment, and an amazing restaurant scene. The University of Minnesota also houses one of the most comprehensive computing environments (Minnesota Supercomputing Institute) and abundant bioinformatics training opportunities. The UofM is a collaborative atmosphere and with concentration of population, quantitative, and evolutionary geneticists.

https://cbs.umn.edu/academics/departments/pmb/directory https://cbs.umn.edu/academics/departments/eeb/directory https://cbs.umn.edu/academics/departments/gcd/directory https://agronomy.cfans.umn.edu/department-directory/faculty Assistant Professor Ecology, Evolution, and Behavior University of Minnesota 234 Cargill Building for Microbial and Plant Genomics Campus Delivery Code 6127 1500 Gortner Avenue Saint Paul, MN 55108-1023 phone: 612-624-6143

Suzanne McGaugh <smcgaugh@umn.edu>

UoGuelph PDF PhD 2MSc FishGenetics

Positions are available for one postdoc and two MSc and one Ph.D. positions to investigate the foraging ecology and genetics of two cleaner fish species that forage on parasitic lice attached to Atlantic salmon.

The postdoctoral position begins in May 2018 and is funded for two years. The two MSc. positions begin in January or May 2018 and are funded for two years. The Ph.D. position begins in January or May 2018 and is funded for four years.

The project is led by Professor Elizabeth Boulding (Integrative Biology, U. Guelph) with co-investigator Professor Emeritus Larry Schaeffer (Animal Biosciences, U. Guelph). Our industrial collaborators are led by Dr. K.P. Ang of Kelly Cove Salmon Ltd. (KCS) a division of Cooke Aquaculture Inc. (CAI). They include Dr. J.A.K. Elliott, Dr. M. Herlin, F. Powell from KCS, and Dr. T. M. Jonassen from Akvaplan-Niva, Norway.

The objective of this NSERC Strategic Project is to provide a sustainable and pedigreed source of cleaner fish to reduce lice densities found on Atlantic salmon living in marine sea cages in Eastern Canada. This project will develop highly-repeatable methods of measuring the functional responses of two proven cleaner fishes: the lumpfish (Cyclopterus lumpus) and the cunner (Tautogolabrus adspersus). An outcome of this project will be a breeding program for lice-eating performance by lumpfish and by cunners at two existing hatcheries operated by CAI. It will also deepen our understanding of the reciprocal evolution of early mutualisms between facultative cleaner fishes and their clients.

MSc. student position 1 (behavioural ecology of fishes) will help develop methods of predicting lice-cleaning performance of cunners in marine sea cages from observations of their performance in indoor tanks. This will involve comparing condition-dependent performance among different families of cunners from different geographical regions that have been reared in a common environment. Cunner lice-removal performance in marine sea cages will be assessed using video-footage and by examining their stomach contents.

MSc student position 2 (molecular ecology/bioinformatics) will help develop DNA markers to estimate pedigrees for cleaner fish families spawned in the hatcheries. This position will involve high throughput DNA extraction, and bioinformatics using a high-performance computer cluster. This research will identify DNA markers that show larger than expected amounts of genetic divergence among cunner populations and among lumpfish populations from different geographical areas.

Ph.D. student (applied evolution/behavioural ecology of fishes) will help develop methods of predicting lice-cleaning performance of lumpfish in marine sea cages from their performance in tanks. This will involve comparing condition-dependent performance among different families of lumpfish from different geographical regions that have been reared in a common environment. Lumpfish lice-removal performance in marine sea cages will be assessed using video-footage and by examining their stomach contents. Relationships between traditional and DNA barcoding of stomach contents will be compared for lumpfish and for cunners and used to develop non-lethal methods of monitoring the prevalence of lice in their diets. This may lead to a deeper understanding of environmental factors affecting facultative lice-cleaning performance in the field.

Postdoctoral fellow (with experience in fish applied evolution/applied ethology/behavioural ecology) will help the graduate students develop repeatable methods of measuring posing and other co-operative behaviors by client fish that facilitate parasite-removal by cleaner fishes. Their own project will involve assisting with salmon lice tank challenges of pedigreed Atlantic salmon and measuring posing rates near cleaner fish refuges. It will also involve video-assisted field observations of client behavior near cleaner-fish refuges within marine sea cages. The postdoc will be trained to estimate breeding values for lice-cleaning performance by the cleaner fish and for posing performance by their Atlantic salmon clients. Creating a breeding nucleus containing only cleaner fish and client fish with high breeding values for performance traits would be predicted to increase the reciprocal co-evolution of this mutualism in marine sea cages.

Please apply for the postdoctoral, Ph.D. or MSc. positions by sending an email to Dr. Boulding (boulding@uoguelph.ca) with attachments containing: 1) your curriculum vitae/resume, 2) an electronic transcript of all your university grades, 3) a list of referees with their email addresses and telephone numbers, 4) pdf reprints of your scientific publications (if any), and 5) a statement that you are willing to travel from Guelph to New Brunswick and Newfoundland for fieldwork as needed. She will then request references from the referees of qualified applicants.

Applicants for a M.Sc. or Ph.D. position need to be eligible for

— / —

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 AncientDNA

Deadline to apply is 15.11.2017

Postdoctoral Research Fellow in Ancient DNA and Evolutionary Genomics A two-year position as a postdoctoral research fellow in the field of ancient DNA (aDNA) and evolutionary genomics is available at the Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biosciences.

The Postdoctoral fellow will be part of a multidisciplinary, international team led by Dr Bastiaan Star, working on the project Catching the Past: Discovering the legacy of historic Atlantic cod exploitation using ancient DNA funded by the Research Council of Norway. The position is affiliated with CEES, a former national centre of excellence (CoE). Expected start date is April 2018. No one can be appointed for more than one Postdoctoral Research Fellowship at the University of Oslo.

The University of Oslo is Norway'Âs oldest and highest rated institution of research and education with 28 000 students and 7000 employees. Its broad range of academic disciplines and internationally esteemed research communities make UiO an important contributor to society. The Centre for Ecological and Evolutionary Synthesis (CEES) is a Centre of Excellence (CoE) based at the Department of Biosciences, University of Oslo. CEES combines a broad spectrum of disciplines (population biology, genomics, statistics, mathematical modelling) to foster the concept of ecology as a driving force of evolution via selective processes, with a corresponding influence of evolutionary changes on ecology. CEES has over 160 members (Professors (20), postdocs/researchers (45), PhDs (25), Master'Âs students (25) and technical and administrative staff) and many guest researchers. The members represent 30 nationalities and constitute a vibrant and creative research environment. CEES coordinate several international networks. The budget = 150 million NOK (about 50 externally funded research projects). CEES is chaired by Professor Nils Chr. Stenseth.

Project description Humans have used the natural resources of the oceans for thousands of years. The main aim of this project is to investigate if the intensive, long-term exploitation of Atlantic cod has affected its pan-European population demography or has led to evolutionary change. By extracting DNA from ancient fish remains (up to 10,000 years old), we compare the genome-wide data of specimens that predate extensive human influence to extensive modern reference databases comprising hundreds of individuals. In addition, we aim to reconstruct the early origin of long-distance fishing trade by analysing material from different types of archaeological sites (representing centres of export and import). By identifying the biological source population of bones from a large number of import sites, we will investigate the extent and range of early Viking Age and medieval fish trade (see for instance http://www.pnas.org/content/114/34/9152.full). Knowledge of the chronology of such long-distance trade yields fundamental insights into historic exploitation patterns.

In this project, we have access to unique biological material from different countries that will be analysed using high-throughput, whole-genome sequencing approaches. The successful applicant will join a multi-disciplinary, international team that brings together experts from the fields of biology, archaeology and zooarchaeology. The research fellow'Âs main task will be the comparative genomic analyses of hundreds of individually sequenced ancient genomes. These data will be interpreted in close dialog with project partners and archaeological sample providers. The ideal candidate will make a major contribution to the planned research, but may also develop her/his own complementary lines of research that reflect the candidate's own expertise and interests, and that fit within the project's main goals. This project forms a collaboration between the CEES at the University of Oslo, the Institute for Marine Research (IMR), University Museum of Bergen, University of Gothenburg, University of Cambridge and the University of Copenhagen.

Requirements Applicants must hold a PhD-degree (or other corresponding education equivalent to a Norwegian doctoral degree) with a background within population genomics and/or evolutionary genomics. The candidate should be able to document strong skills in the analyses of genome-wide data using phylogenetic or population genetic approaches. Experience with ancient DNA, analytical or experimental, is a distinct advantage. Applicants should have a strong publication record for their career stage.

We seek a highly motivated, enthusiastic person with the ambition to gain insight and publish papers in leading, international journals, with interpersonal skills and the capability to work in close collaboration with others. The candidate will work in close collaboration with the rest

— / —

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

UOstrava CzechRepublic HumanEvolution

We are looking for a postdoc candidate for an internal grant application at the University of Ostrava, Czech Republic. Our team lead by Pavel Flegontov focuses on using computational methods and large autosomal datasets to study the history of human populations. We currently work on the settlement of the American Arctic (see our preprint: https://www.biorxiv.org/content/early/2017/10/13/203018). We also investigate the relationship of language families and ethnic groups around the Bering Strait, ancient populations of Chukotka, Indian and negrito ancestry across Southeast Asia, and Jewish population history. We have tight collaborations with leading researchers in the field: David Reich (Harvard Medical School, Boston, MA), Johannes Krause and Stephan Schiffels (Max Planck Institute for the Science of Human History, Jena, Germany), Ron Pinhasi (University of Vienna, Austria).

The postdoc will receive a net salary of 1200 ’V 1500 EUR per month for 3 years. The cost of living is low in Czechia, and average net salary is below 1000 EUR.

An applicant must have at least 1 publication in the genetic anthropology field in an international scientific journal (studies on both uniparental and autosomal markers are acceptable). To apply, please send an email with a CV attached to pflegontov[at]gmail.com until November 20, 2017. A two-tier selection process will consist of 1) skype interviews between November 20 and November 27, 2) approval of a successful candidate by the university board. The final funding decision will be announced on December 18, 2017.

You can check full list of the publications at the following link: http://www1.osu.cz/~flegontov/ N. Ezgi Altinisik ezgimo.com

Ezgi Altinisik <ezgialtinisik@gmail.com>

UPennsylvania 2 EvolutionaryGenomics

Title: UPenn.Intragenomic_Conflict

Postdoc opportunity: Cell Biological Basis of Intragenomic Conflict

The Levine Lab (https://web.sas.upenn.edu/levine-lab/) at the University of Pennsylvania is recruiting two postdoctoral research fellows to start spring or summer 2018. Our lab integrates evolutionary genetics and cell biology to investigate intra-genomic conflict between host genomes and their selfish genetic elements. We study how these escalating molecular 'arms races' shape the fundamental, chromatin-dependent processes of telomere protection and inter-generational sex chromosome transmission. To experimentally elucidate the molecular mechanisms of selfish element cheating and host suppression, we harness CRISPR/Cas9-mediated gene manipulation to unleash otherwise cryptic conflicts in contemporary genomes. Drosophila is our primary model; however, we have recently initiated projects in the genus, Mus.

The Levine Lab is housed in UPenn's Department of Biology (www.bio.upenn.edu), a diverse, interactive community with breadth and depth in evolutionary genetics and genomics, cell biology, and molecular genetics. The Levine Lab is also a core member of the Epigenetics Institute at the Perelman School of Medicine (https://hosting.med.upenn.edu/epigenetics/), a group of 29 lab groups dedicated to mechanistic dissection of epigenetic regulation in healthy and disease states.

The Levine Lab aims to recruit applicants with EITHER a PhD in evolutionary genetics/genomics (but motivated to learn chromatin biochemistry and cell biology) OR a PhD in chromatin biology (but motivated to learn evolutionary genomics). Please send a cover letter (including statement of research goals), CV, and a list of three references as a single PDF to: levinelab.upennpostdoc@gmail.com. Applications will be reviewed starting November 20th.

Mia Levine Assistant Professor Department of Biology Epigenetics Institute University of Pennsylvania 204B Carolyn Lynch Laboratories 433 South University Avenue Philadelphia, PA 19104-6018

m.levine@sas.upenn.edu 215-573-9709

"Levine, Mia Tauna" <m.levine@sas.upenn.edu>

UPittsburgh MicrobiomeExptEvolution

POSTDOC: Intercellular communication in the microbiome (University of Pittsburgh)

The Wright Lab (http://wrightlabscience.com) is seeking an enthusiastic postdoctoral associate to lead an exciting project aimed at understanding the language of intercellular communication in the microbiome. The successful candidate will apply methods that have recently been developed in the Wright Lab for high-throughput interrogation of intercellular signaling molecules. The project will involve deciphering the molecular basis of microbial communication with small molecule mass spectrometry and bioinformatics. This research provides the opportunity to elucidate the context-dependent language that microorganisms use to communicate and apply that knowledge to manipulate the microbiome.

The Wright Lab is a rapidly growing experimental evolution and comparative genomics hybrid wet/dry lab at the University of Pittsburgh. We are affiliated with the Department of Biomedical Informatics, and collaborate closely with other experimental evolution and microbiology labs on campus. Our lab offers opportunities to gain experience giving presentations, lecturing, mentoring students, & writing proposals and papers. We are part of a broader effort to make the University of Pittsburgh a leader in applying evolution to the improvement of medicine. The university consistently ranks in the top 10 nationally for biomedical research funding. Pittsburgh, PA is often voted the most livable city in the US featuring eclectic neighborhoods, diverse culinary and entertainment opportunities, as well as easy access to natural areas (http://www.coolpgh.pitt.edu/).

QUALIFICATIONS: Qualifications for this position include a PhD in microbiology, ecology, chemistry, evolutionary biology, or a related field. Ideal candidates would have experience in mass spectrometry, biosynthesis, proteomics, signaling, or microbial ecology, as well as a willingness to learn 3D printing. The candidate should 1) be fluent in written and spoken English, 2) be able to work independently and as a member of a team, 3) be hard-working, motivated, and eager to learn, & 4) have an interest in the microbiome.

TO APPLY: Please email applications (including cover letter, curriculum vitae, & names and email addresses for 3 professional references) to Dr. Erik Wright (eswright@pitt.edu). The position is available starting as early as January 2018 for 1 year, renewable up to 3 years contingent upon satisfactory performance. Salary is commensurate with experience and includes a comprehensive benefits package. Review of applications will begin immediately and continue until the position is filled.

Erik Wright Assistant Professor Department of Biomedical Informatics University of Pittsburgh Pittsburgh, PA (412) 383-4458 http://www.dbmi.pitt.edu/person/erik-s-wright-phd-ms "ESWRIGHT@pitt.edu" <ESWRIGHT@pitt.edu>

UppsalaU ComputationalGenetics

Post doc in Computational Genetics, Uppsala University

The Department of Medical Biochemistry and Microbiology at Uppsala University seeks applicants for a 1+1 year Post doc position in Computational Genetics. The starting date is flexible (any time during 2018). Review of applications will start immediately and the position will remain open until a suitable candidate has been found.

The Post-doc will work with the Virginia lines - a chicken population developed during a long-term (60 year) bi-directional, single-trait selection experiment. The adaptive trait is highly polygenic and selection has primarily acted on standing variants available at the onset of selection. In-depth explorations of the adaptive loci have revealed that most are complex with either tightly linked adaptive variants, multiple segregating haplotypes and/or interactions between loci. The major focus of the Post-doc will be to further dissect the genetic architecture of the adaptive trait in and model its contributions to long-term adaptation and individual phenotypes. A newly developed dataset including approximately 4000 phenotyped, pedigreed and individually low-coverage sequenced individuals from a 19 generation deep advanced intercross line between the divergently selected lines is available for this work.

The responsibilities in the Post-doc project includes standard bioinformatics work with short-read sequence data, development of software and pipelines (in R) for haplotyping, genotype imputation and linkage/association analyses to explore the genome-wide genetic basis of the adaptive trait in the deep intercross line. The Post-doc will also be involved in work to develop and explore ways to model and reveal how complex polygenic architectures contribute to long-term selection responses and individual phenotypes.

Candidates for the position must have a Ph.D. by time of employment. A suitable educational background will likely include computational biology/bioinformatics as part of, for example, PhD studies or Post-doctoral work in human/animal/plant quantitative/population/evolutionary genetics, systems biology or equivalent. Interested candidates are encouraged to submit a letter of interest explaining their motivation for working on this project and suitability for the position. This should be accompanied by a C.V. and a description of relevant undergraduate and graduate projects that the applicant has been involved in.

The letter of interest, or any questions about the position, should be directed to Prof. Ãrjan Carlborg, Department of Medical Biochemistry and Microbiology, Uppsala University; orjan.carlborg@imbim.uu.se. Review will begin as soon as received and continue until the position is filled.

Selected references of relevance to the project are1-6: 1. Carlborg, Ã., Jacobsson, L., Ãhgren, P., Siegel, P. & Andersson, L. Epistasis and the release of genetic variation during long-term selection. Nat Genet 38, 418-420 (2006).

2. Le Rouzic, A., Siegel, P. B. & Carlborg, Ã. Phenotypic evolution from genetic polymorphisms in a radial network architecture. BMC Biol. 5, 50 (2007).

3. Johansson, A. M., Pettersson, M. E., Siegel, P. B. & Carlborg, Ã. Genome-wide effects of long-term divergent selection. PLoS Genet 6, e1001188 (2010).

4. Pettersson, M., Besnier, F., Siegel, P. B. & Carlborg, Ã. Replication and explorations of high-order epistasis using a large advanced intercross line pedigree. PLoS Genet 7, e1002180 (2011).

5. Sheng, Z., Pettersson, M. E., Honaker, C. F., Siegel, P. B. & Carlborg, Ã. Standing genetic variation as a major contributor to adaptation in the Virginia chicken lines selection experiment. Genome Biol. 16, 219 (2015).

6. Zan, Y. et al. Artificial Selection Response due to Polygenic Adaptation from a Multilocus, Multiallelic Genetic Architecture. Mol Biol Evol 34, 2678-2689 (2017).

Ãrjan Carlborg <orjan.carlborg@imbim.uu.se>

UPuertoRico EvolutionaryGenomics

JOB DESCRIPTION

Postdoc in evolutionary and functional genomics. An EPSCoR-funded postdoctoral position is available in the laboratory of Dr. Riccardo Papa in the Department of Biology of the University of Puerto Rico, RÃo Piedras Campus, and in collaboration with Dr. Brian Counterman of the Department of Biological Sciences of Mississippi State University. The laboratory has a rich background in studying the natural history of Heliconius butterflies, with a focus on whole genome sequencing and performing functional assays to go after the developmental and genetic architecture of color pattern development in butterflies. These regions provide exciting candidates for further validation using functional approaches such as ATAC-seq, ChIP-seq and CRISPR to better understand the pathways involved in color pattern development and their evolution.

SPECIAL REQUISITES

The candidate must have completed Ph.D. degree within the last 5 years, preferably in genomics, population genetics or statistical genetics. The position requires skills in the more bioinformatical areas of biology, and a strong record of research in these areas. High motivation and mobility will be necessary to collaborate with the Smithsonian Tropical Research Institute (STRI, Panama; Owen McMillan), Cornell University (US; Robert Reed), George Washington University (US; Arnaud Martin) and Cambridge University (UK; Chris Jiggins). The work will focus on bioinformatics methods to analyze genomic sequencing and functional genomic data. Specifically, this includes building pipelines to assemble and analyze whole genome resequencing data using multiple platforms and obtain and analyze ATAC-seq and ChIP-seq data. Strong knowledge of the Heliconius system is preferred but not required.

IMPORTANT INFORMATION

To apply, please submit (i) a cover letter including motivation and research interests, (ii) a full CV that includes all requisites for the position, and (iii) contact information for two references electronically, and (iv) copies of all academic degrees *(diplomas and certifications). Review of applications will start immediately and will continue until the position is filled. Inquiries about the position can be directed to brenda.santiago@upr.edu.

APPLICATIONS SUBMITED WITH INCOMPLETE INFORMATION WILL NOT BE CONSIDERED. CANDIDATES WITH A PH.D. DEGREE OF 5 YEARS OR MORE ARE NOT ELIGEBLE FOR THIS POSITION.

Please email your application to:

Riccardo Papa

rpapa.lab@gmail.com

Riccardo Papa <rpapa.lab@gmail.com>

UToronto Evolution

The Department of Ecology and Evolutionary Biology at the University of Toronto invites applications for a Departmental Postdoctoral Fellowship.

Area of Research: Ecology and/or Evolution, broadly defined.

Description of duties: The Fellow will collaborate with the advisor(s) on research that is mutually agreed upon by all parties and the Fellow will publish the results in scientific journals.— The Fellow will be a fully participating member in the Department. The Fellow may be asked to organize a workshop for graduate students, postdocs and faculty.

Salary: $40,500/year

Pleasenote that should the minimum rates stipulated in the collective agreement fall below the rates stated in this posting, the minimum rates stated in the collective agreement shall prevail. Required qualifications:— Applicants must have a PhD in ecology and/or evolution or a related area of study, and field-specific qualifications as set by the faculty advisor(s).

Application Instructions All individuals interested in this position must first contact and obtain the agreement of a—faculty advisor (or co-advisors); full-time faculty members at the St. George (downtown) campus of the University of Toronto are eligible to serve as advisors (see the list at the bottom of this page for a list of potential supervisors). Afterwards, applicants must submit a cover letter clearly indicating the proposed faculty advisor(s) and the date that they will be available to begin the position, a curriculum vitae, copies of 2 publications, and a short (1-3 pages) description of past research accomplishments and future research plans. Applicants should include names and e-mail addresses for two potential referees. All application materials must be submitted as PDF(s) in a single email to: Elizabeth Rentzelos chairsec.eeb@utoronto.ca by the closing date.

Closing date: December 10, 2017

Supervisor: Member(s) of the EEB faculty (St. George campus) who has/have agreed to contribute to the salary of this postdoctoral fellow and to cover her/his research expenses.

Expected start date: As early as Feb 1, 2018—and no later than Sept 1, 2018

Term: 12 months with the potential for a second, renewed term, assuming suitable progress.

FTE:—— 100%

The normal hours of work are 40 hours per week for a full-time postdoctoral fellow (pro-rated for those holding a partial appointment) recognizing that the needs of the employee's research and training and the needs of the supervisor's research program may require flexibility in the performance of the employee's duties and hours of work.

The University of Toronto is a leading academic institution in Canada with over 60 faculty members specializing 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, and the School of the Environment. The University owns a nearby field station dedicated to ecological and evolutionary research (the Koffler Scientific Reserve, www.ksr.utoronto.ca). The department also has a partnership with the Ontario Ministry of Natural Resources that helps provide access to infrastructure, including lab facilities in Algonquin Provincial Park (www.harkness.ca), funding, and long-term data sets. Genomic analyses are supported by a number of high-performance computing resources, multi-lab bioinformaticians, as well as staff at the Centre for the Analysis of Genome Evolution and Function. Employment as a Postdoctoral Fellow at the University of Toronto is covered by the terms of the CUPE 3902 Unit 5 Collective Agreement. This job is posted in accordance with the CUPE 3902 Unit 5 Collective Agreement. 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.

List of potential advisors for the EEB Postdoctoral Fellow: Aneil Agrawal, Spencer Barrett, Belinda Chang, Asher Cutter, Hélène Cyr, Marie-Josée Fortin, Benjamin Gilbert, Don Jackson, Marty Krkosek, Luke Mahler, Nicole Mideo, Chelsea Rochman, Helen Rodd, Njal Rollingson, Locke Rowe, Tammy Sage, Marla Sokolowski, John Stinchcombe, Art Weis, Stephen Wright Please see the EEB website for information about their research programs: http://www.eeb.utoronto.ca/people/d-faculty.htm Note: eligible applicants might also want to apply for the Arts and Science Postdoctoral Fellowship Program at the U of Toronto (this deadline is Dec. 6, 2017):

— / —

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 Mississauga PlantDefenceEvolution

Prof. Marc Johnson's EvoEco Lab (www.evoeco.org) is seeking applications for a Post-Doctoral Researcher to study Plant Defence Evolution against herbivores and pathogens at the University of Toronto Mississauga (UTM). The successful candidate will examine the mechanisms and evolutionary processes affecting adaptive and non-adaptive evolution of plant chemical and non-chemical defences. The specific topic of research will depend on the successful candidate's interests, but could for example include the population genomics of defence, macroevolution evolution of defence, the effects of sexual reproduction on defence, and more. The Johnson lab uses many natural and agricultural systems to study plant defence evolution (Arabidopsis, Oenothera, Trifolium, Glycine, Brassica, etc.), and there is opportunity to use these systems or to develop a new system, depending on the candidate's interests and expertise. The post-doctoral researcher will have the opportunity to integrate experiments, population genomics, evolutionary genetics, plant chemistry, and modeling approaches. This project is ideally suited to individuals seeking to perform productive cutting-edge research while building collaborations across traditional disciplines. We are interested in all outstanding post-doctoral applicants with an interest and expertise in plant evolutionary biology or the evolution of plant-animal interactions; previous work in plant defence evolution specifically is an asset but not a requirement. To learn more about the Johnson Lab's research on plant defence evolution please visit www.evoeco.org or see:

Anstett et al. 2016. Can genetically based clines in plant defence explain greater herbivory at higher latitudes? Ecology Letters 18:1376-1386.

Thompson, K. A., and M. T. J. Johnson. 2016. Anti-herbivore defenses and natural selection on floral traits. Evolution 70:796-810.

Hollister et al. 2015. Recurrent loss of sex is associated with accumulation of deleterious mutations in Oenothera. Mol Biol Evol 32:896-905.

Johnson et al. 2015. Coevolution Between Plant Reproduction and Defense Against Herbivores. AREES 46:191-213.

Johnson et al. 2014. Macroevolution of plant defenses against herbivores in the evening primroses. New Phytologist 203:267-279.

Agrawal et al. 2012. Insect herbivores drive real-time ecological and evolutionary change in plant populations. Science 338:113-116.

Johnson et al. 2009. Plant sex and the evolution of plant defenses against herbivores. PNAS 106:18079-18084.

In addition to being a part of the EvoEco Lab (www.evoeco.org), the post-doctoral researcher will be a member of the Department of Biology (http://www.utm.utoronto.ca/biology) and the Department of Ecology and Evolutionary Biology (http://www.eeb.utoronto.ca).

The UTM campus has excellent facilities for plant-insect research (wet and dry lab infrastructure, growth chambers, greenhouses), housing, and 225 acres of fields, forests, many trails and a wild salmon/trout river for recreation. Toronto and Mississauga are world-class cities that are interconnected and culturally diverse. They boast an abundance of restaurants, excellent transit systems, a diversity of cultural activities (theatres, sports, bars, clubs), and an abundance of parks and water.

Starting salary: Commensurate with experience + benefits Start date: Flexible, but preferably before Sept. 1, 2018 Duration: 1- 3 years (conditional on favourable annual performance review) Application Deadline: Review of applications will commence Dec. 6. Please send applications to marc.johnson@utoronto.ca Applications should include: i) a cover letter, ii) CV, iii) PDFs of top three publications, and iv) contact information for three references.

This job is posted in accordance with the CUPE 3902 Unit 5 Collective Agreement. The normal hours of work are 40 hours per week for a full-time postdoctoral fellow recognizing that the needs of the employee's research and training and the needs of the supervisor'Âs research program may require flexibility in the performance of the employee'Âs duties and hours of work. The position will regularly require evening and/or weekend work. 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.

Marc T. J. Johnson, Ph.D. Director, Centre for Urban Environments (CUE) Associate Professor Depts. of Biology & EEB University of Toronto Mississauga www.evoeco.org (lab) www.urbanenvironment.ca (CUE) twitter: @evoecolab

— / —

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 Mississauga UrbanEvolutionaryEcol

Prof. Marc Johnson's EvoEco Lab (www.evoeco.org) is seeking applications for a Post-Doctoral Researcher to study Urban Evolutionary Ecology at the University of Toronto Mississauga (UTM). The successful candidate will examine how urbanization influences adaptive and non-adaptive evolution in plants or plant-animal interactions. We presently use several systems to study urban evolution (Trifolium repens, Impatiens capensis, Brassica rapa) and there is opportunity to use these systems or to develop a new system, depending on the candidate's interests and expertise. The post-doctoral researcher will have the opportunity to integrate experiments, genomic and modeling approaches. This project is ideally suited to individuals seeking to perform productive cutting-edge research while connecting with a global network of collaborators and the public. We are interested in all outstanding post-doctoral applicants with an interest and expertise in plant evolutionary biology or plant-animal interactions; previous work in urban systems is not a requirement.

To learn more about the Johnson Lab's research on urban evolutionary ecology please see:

Johnson, M. T. J., and J. Munshi-South. 2017. The evolution of life in urban environments. Science 358: DOI: 10.1126/science.aam1832.

Thompson, K. A., M. Renaudin, and M. T. J. Johnson. 2016. Urbanization drives the evolution of parallel clines in plant populations. Proc. R. Soc. London Ser. B 283:20162180.

Johnson, M. T. J., K. A. Thompson, and H. S. Saini. 2015. Plant evolution in the urban jungle. Am. J. Bot. 102:1951-1953.

In addition to being a part of the EvoEco Lab, the post-doctoral researcher will be a member of the new Centre for Urban Environments (www.urbanenvironment.ca), the Department of Biology (http://www.utm.utoronto.ca/biology), and the Department of Ecology and Evolutionary Biology (http://www.eeb.utoronto.ca).

The UTM campus has excellent facilities for research (wet and dry lab infrastructure, growth chambers, greenhouses), housing, and 225 acres of fields, forests, many trails and a wild salmon/trout river for recreation. Toronto and Mississauga are world-class cities that are interconnected and culturally diverse. They boast an abundance of restaurants, excellent transit systems, a diversity of cultural activities (theatres, sports, bars, clubs), and an abundance of parks and water.

Starting salary: Commensurate with experience + benefits Start date: Flexible, but preferably before Sept. 1, 2018 Duration: 1- 3 years (conditional on favourable annual performance review) Application Deadline: Review of applications will commence Dec. 6. Please send applications to marc.johnson@utoronto.ca Applications should include: i) a cover letter, ii) CV, iii) PDFs of top three publications, and iv) contact information for three references.

This job is posted in accordance with the CUPE 3902 Unit 5 Collective Agreement. The normal hours of work are 40 hours per week for a full-time postdoctoral fellow recognizing that the needs of the employee's research and training and the needs of the supervisor's research program may require flexibility in the performance of the employee's duties and hours of work. The position will will regularly require evening and/or weekend work.

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.

Marc T. J. Johnson, Ph.D. Director, Centre for Urban Environments (CUE) Associate Professor Depts. of Biology & EEB University of Toronto Mississauga www.evoeco.org (lab) www.urbanenvironment.ca (CUE) twitter: @evoecolab twitter (CUE): @CUE_UofT

marc.johnson@utoronto.ca

UUtah EvolutionaryGenomics

POSTDOCTORAL FELLOW POSITION:

EVOLUTIONARY GENOMICS AT THE UNIVERSITY OF UTAH

Postdoctoral position available in the laboratories of Dr. Mike Shapiro and Dr. Denise Dearing in the Department of Biology, University of Utah. We seek a highly motivated colleague to identify the genetic and physiological mechanisms that facilitate the ingestion of dietary toxins by herbivorous vertebrates. Our current research focuses on identifying and understanding the genomic changes associated with creosote feeding in herbivorous woodrats (Neotoma).

Please visit our websites for more information about the labs: http://www.biology.utah.edu/shapiro http://biologylabs.utah.edu/dearing Requirements:

1. Ph.D. in genetics, genomics, evolutionary biology, or a closely related field

2. Track record of productivity

3. Demonstrated ability and willingness to work both independently and collaboratively

4. Excellent written and oral communication skills

A strong background in genomics and transcriptomic analyses of vertebrates is preferred.

To apply, please submit the following materials:

1. CV, including a list of publications

2. Statement that includes your research experience and interests, as well as your preferred start date on or after February 1, 2018

3. Names of three referees who will be willing to submit letters of reference upon request

For full consideration, please submit application materials by December 1, 2017.

Please email application materials in PDF format to Mike Shapiro: shapiro@biology.utah.edu

Informal inquiries are welcome prior to formal application.

Recent publications from our labs relevant to this position include:

Malenke JR, Skopec MM, Dearing MD. (2014) Evidence for functional convergence in genes upregulated by herbivores ingesting plant secondary compounds. BMC Ecology. 14:23.

Magnanou E, Malenke J, Dearing MD. (2013) Hepatic gene expression in herbivores on diets with natural and novel plant secondary compounds. Physiological Genomics. 45:774-785. DOI: 10.1152/physiolgenomics.00033.2013.

E.T. Domyan, Z. Kronenberg, C. Infante, A.I. Vickrey, S.A. Stringham, R. Bruders, M.W. Guernsey, S. Park, J. Payne, R. Beckstead, G. Kardon, D.B. Menke, M. Yandell, M.D. Shapiro. (2017) Molecular shifts in limb identity underlie development of feathered feet in two domestic avian species. eLife 5:e12115.

A.I. Vickrey, E.T. Domyan, M.P. Horvath, M.D. Shapiro. (2015) Convergent evolution of head crests in two domesticated columbids is associated with different missense mutations in EphB2. Molecular Biology and Evolution 32: 2657-2664. doi: 10.1093/molbev/msv140.

M. D. Shapiro, Z. Kronenberg, C. Li, E.T. Domyan, H. Pan, M. Campbell, H. Tan, C.D. Huff, Haofu Hu, A.I. Vickrey, S.A. Nielsen, S.A. Stringham, Hao Hu, E. Willerslev, M. T. P. Gilbert, M. Yandell, G. Zhang, J. Wang. (2013) Genomic diversity and evolution of the head crest in the rock pigeon. Science 339: 1063-1067.

SCIENTIFIC AND CULTURAL ENVIRONMENT

The Department of Biology comprises a diverse and vibrant group of laboratories, with research interests ranging from environmental biology to biochemistry. The genetics and genomics biology communities are strong on the University of Utah main campus and medical school and offer numerous opportunities for collaboration. The evolutionary genetics and genomics community on campus is especially strong. Both PIs have a strong record of mentoring and success in placing trainees.

The University of Utah is located in beautiful (and affordable) Salt Lake City, with easy access to world-class entertainment and recreation. Salt Lake City and nearby Park City are home to the annual Sundance Film Festival and a vibrant year-round cinema scene, as well as outstanding restaurants and brewpubs. Several national parks are located within a just few hours$B!G(B drive, and the university is within a 40-minute drive of at least six major alpine skiing and snowboarding resorts, including venues of the 2002 Olympics. Hiking and mountain biking trails begin essentially on campus. Outside Magazine recently called Salt Lake City

$B!H(Bone of the nation's most underrated outdoor meccas.$B!I(B The city is also a major airline hub, with non-stop flights throughout North America and Europe.

Denise Dearing <denise.dearing@utah.edu>

UWashington EvolutionaryGenomicsFlyBrain

The Promislow lab (http://www.promislowlab.org) at the University of Washington in Seattle is seeking an enthusiastic, independent postdoctoral researcher to work on an NIH-funded project on the systems biology of neurodegeneration in Drosophila. This collaborative project between the Promislow, Pallanck and Tuthill labs combines metabolomics and single-cell sequencing, neurophysiology and behavior, and mitochondrial biology to understand the maintenance and downstream consequences of genetic variation for age-related neurodegeneration. The long-term goal in all our studies is to better understand the proximate and evolutionary causes and consequences of aging in natural populations. More details about this project can be found at http://www.flyseq.com . The successful applicant will have the opportunity carry out both empirical and computational studies. This project integrates quantitative genetics, single-cell genomics, metabolomics, neurobiology, physiology, and network analysis. The ideal candidate will have experience in one or more of these fields.

The position is initially available for two years, and can be extended for additional years, but the University of Washington policy is to offer a one year appointment with subsequent renewals. Start date is flexible, though ideally in the Fall 2017 or Winter 2018.

Applications should be sent by Nov 17, 2017 by email to Daniel Promislow (promislo@uw.edu). Applicants are requested to send a single PDF file that includes a cover letter with names and contact information of three references, a CV and one or two representative publications.

The University of Washington is an affirmative action, equal opportunity employer. The University is building a culturally diverse faculty and staff and strongly encourages applications from women, minorities, individuals with disabilities and covered veterans.

Daniel Promislow Professor, Departments of Biology and Pathology University of Washington Seattle, WA 98195 promislo [at] uw.edu http://www.promislowlab.org Daniel Promislow <danielpromislow@gmail.com>

Daniel Promislow <danielpromislow@gmail.com>

Vienna PopGen

Genomic architecture of adaptation

A postdoctoral position is available at the Institute of Population Genetics, Vetmeduni Vienna (Austria). The research focus of the Institute of Population Genetics is on understanding the genetics of adaptation in sexual organisms. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including experimental evolution, quantitative genetics, functional genetics, empirical population genetics, bioinformatics and statistics.

The successful candidate will be part of a team of scientists studying adaptation of experimental Drosophila populations, which are exposed to temperature stress. She/he can build on several highly replicated Drosophila populations that have evolved under various temperature regimes. With up to 15 replicate populations from different founder populations evolving for more than 100 generations, we host one of the best data sets currently available for a genuinely outcrossing species. The postdoc will integrate data from whole genome time-series sequencing, RNA-Seq and targeted phenotyping to understand the genetic architecture of adaptation to a new thermal environment.

We are looking for candidates with good quantitative training and experience in handling large data sets. A background in population genetic data analysis and/or quantitative genetics is a bonus, but not required. Active contribution to fly work during common garden experiments is expected, as well as a keen interest in linking the data to the biology of the fly.

The position is available starting from February 2018, but the exact starting date is negotiable. The application should be emailed to christian.schloetterer@vetmeduni.ac.at <christian.schloetterer@vu-wien.ac.at> as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be received by 3.12.2017 to ensure full consideration.

Background:

1. S. U. Franssen, N. H. Barton, C. Schlötterer, Re-

construction of haplotype-blocks selected during experimental evolution. *Molecular Biology and Evolution*, (2016).

2. S. U. Franssen, V. Nolte, R. Tobler, C. Schlötterer, Patterns of linkage disequilibrium and long range hitchhiking in evolving experimental *Drosophila melanogaster* populations. *Molecular Biology and Evolution* *32*, 495-509 (2015).

3. C. Schlötterer, R. Kofler, E. Versace, R. Tobler, S. U. Franssen, Combining experimental evolution with next-generation sequencing: a powerful tool to study adaptation from standing genetic variation. *Heredity* *114*, 431-440 (2015).

4. N. Barghi, R. Tobler, V. Nolte, C. Schlötterer, *Drosophila simulans*: a species with improved resolution in evolve and resequence studies. *G3* *7*, 2337-2343 (2017).

5. F. Mallard, V. Nolte, R. Tobler, M. Kapun, C. Schlötterer, A simple genetic basis of adaptation to a novel thermal environment results in complex metabolic rewiring in *Drosophila*. *BioRxiv*, DOI: 10.1101/174011 (2017).

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://www.vetmeduni.ac.at/en/population-genetics/ Vienna Graduate School of Population Genetics http://www.popgen-vienna.at Christian Schlötterer <christian.schloetterer@vetmeduni.ac.at>

WashingtonStateU EvolutionaryGenomics

WashingtonStateU.EvolutionaryGenomics.Hostpathogenevolution

POSTDOCTORAL RESEARCHER Washington State University School of Biological Sciences

We are seeking a postdoctoral researcher 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 this unique infectious tumor across Tasmania and consequent endangerment of the iconic Tasmanian devil. Reference genomes are available for both tumor and devil and population genomic data have already been collected for >3500 Tasmanian devil individuals. 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 across Tasmania. 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 December 4, 2016 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 January and May, 2018. Salary and benefits are competitive. Position is for 1 year, with continuation for an additional year 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>

WashingtonStateU TasmanianDevilEvolution

POSTDOCTORAL RESEARCHER Washington State University School of Biological Sciences We are seeking a postdoctoral researcher 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 this unique infectious tumor across Tasmania and consequent endangerment of the iconic Tasmanian devil. Reference genomes are available for both tumor and devil and population genomic data have already been collected for >3500 Tasmanian devil individuals. 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 across Tasmania. 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 November 30, 2017 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 January and May, 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>

Wissenschaftskolleg Berlin Fellowship

GAIN TIME TO THINK! 2018/19 COLLEGE FOR LIFE SCIENCES FELLOWSHIPS DEADLINE: — JANUARY 7, 2018 Call for Applications https://cfls-application.wiko-berlin.de/

The College for Life Sciences, a junior program of the Wissenschaftskolleg zu Berlin (Institute for Advanced Study), offers young life-sciences scholars from around the world an opportunity to take a break from the lab and gain time to work and develop their own projects and immerse themselves in an intellectually and culturally diverse environment.

Each year the Wissenschaftskolleg welcomes internationally recognized senior as well as promising junior scholars in all fields of knowledge, including the humanities, the social sciences and the arts and we invite you to become part of this “learning community”. Our goal is to promote a kind of science that transcends disciplinary boundaries and goes beyond established issues and approaches.

Through the College for Life Sciences we promote scientists at the beginning of their career, i.e. postdocs, junior group leaders, lecturers, assistant, associate and junior professors.

The fellowships are intended for residencies of 3-6 months during the academic year 2018/19, i.e. September 2018 June 2019.

BENEFITS OF THE FELLOWSHIP * Three to six months’ residency at the Wissenschaftskolleg in Berlin * A full stipend based on your previous salary * Studio accommodation on campus * Freedom to pursue a project of your choice * Insight into new areas of knowledge and research cultures * Integration into a unique international community of Fellows * Access to Berlin’s excellent scholarly and scientific community * Access to the Wissenschaftskolleg’s outstanding library and IT services We do not offer any lab space. For more details please visit: www.wiko-berlin.de/cfls APPLICATION AND REQUIREMENTS Please apply by January 7, 2018 with a project outline (about 1000 words), a letter stating your motivation for wishing to obtain a fellowship (about 500 words), your complete curriculum vitae, and a list of your publications here: https://cfls-application.wiko-berlin.de/ You are completely free to choose the project that you will pursue at the Wissenschaftskolleg; we impose no thematic presettings whatsoever.

You must have obtained your doctorate by the start of your fellowship, and we also require that you have at least one lead-author publication in a peer-reviewed journal. There are no restrictions regarding your discipline of origin in the life sciences, nationality, or age etc. Applications from scientists working at institutions in Berlin cannot be taken into consideration. If you have been a principal investigator for longer than five years, though, you are advised to apply for a regular fellowship at the Wissenschaftskolleg.

Dr. Ulrike Pannasch Wissenschaftliche Koordinatorin Academic Coordinator College for Life Sciences ulrike.pannasch@wiko-berlin.de

WISSENSCHAFTSKOLLEG ZU BERLIN INSTITUTE FOR ADVANCED STUDY Wallotstrasse 19 14193 Berlin Tel.: +49 30 89 00 1 - 255 Fax: +49 30 89 00 1 - 100 www.wiko-berlin.de/cfls

Dr. Ulrike Pannasch Wissenschaftliche Koordinatorin/Academic Coordinator College for Life Sciences Wissenschaftskolleg zu Berlin / Institute for Advanced Study Wallotstr. 19, 14193 Berlin Tel. +49 - 30 - 89 001 - 255http://www.wiko-berlin.de/institution/college-for-life-sciences/ Ulrike Pannasch <paul@wiko-berlin.de>

WorkshopsCourses

Berlin AdvancedPython Nov13-17 deadline

Dear all,

we have the last 3 spots available for the course: "Advanced Python for biologists" and the registration deadline is next Friday (20th October; https://www.physalia-courses.org/courses/course12/)

Dates: 13-17 November 2017

Where: Berlin (Germany)

Instructor: Dr. Martin Jones (founder, Python for Biologists; http://www.physalia-courses.org/instructors/t1/)

Overview

This course is aimed at people who already have a basic knowledge of Python and are interested in using the language to tackle larger problems. In it, we will look in detail at the parts of the language which are particularly useful in scientific programming, and at the tools Python offers for making development faster and easier. The course will use examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) take advantage of the advanced language features in their own programs and (2) use appropriate tools when developing software programs.

Who should attend

This course is aimed at researchers and technical workers with a background in biology and a basic knowledge of Python. The Advanced course is aimed at people who want to develop bigger or more complicated programs in Python, or to learn more about the language, or to explore different approaches (object-oriented, functional) to programming. The material covered is very general purpose and can be applied to any kind of problem.

Requirements

Students should have enough biological/bioinformatics background to appreciate the examples and exercise problems (i.e. they should know what a protein accession number, BLAST report, and FASTA sequence is). They should also have basic Python experience (the Introduction to Python for Biologists course will fulfil these requirements). Students should be familiar with the use of lists, loops, functions and conditions in Python and have written at least a few small programs from scratch.

For the detailed program, please visit our website: https://www.physalia-courses.org/courses-workshops/-course12/curriculum-12/ 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

https://groups.google.com/forum/#!forum/physalia-courses

Berlin AnalysisGenomicData Mar19-23

Exploratory multivariate analysis and visualization of genomic data

https://www.physalia-courses.org/courses-workshops/-course29/ Berlin, 19-23 March 2018

Instructors:

Dr. Sebastien Le (Agrocampus Ouest, FR)

Dr. Aubry Marc (University of Rennes1, FR)

Overview

This course is divided into two parts.

First, a detailed overview of the classical exploratory methods conceived for multivariate data: Principal Components Analysis, Correspondence Analysis, and Multiple Correspondence Analysis. From a unified theoretical framework, we will see how these methods are linked, as well as their specificities in terms of interpretation, due to the nature of the data they are dealing with. From a practical point of view, we will see how they can be applied to genomic data, and how they can be used to obtain meaningful information. We will see notably, how we can add supplementary information to get a better understanding of the data.

Second, an overview of methods that handle multivariate data, when variables are structured according to groups: generalised canonical analysis, and Multiple Factor Analysis. These methods are really useful when different points of view on the same set of individuals have to be compared. It is the case for instance, when one has at his disposal gene expressions on the one hand,

and chemical measures on the other hand.

The methods will be presented from a geometrical point of view. The concepts of quality of representation, active versus illustrative variables, automatic description of the dimensions provided by the analyses will be discussed.

Format

Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group. Computing will be done using a combination of tools installed on the attendees laptop computer and web resources accessed via web browser.

Who should attend

Researchers who would like to investigate multivariate and heterogenous data from an exploratory point of view. Researchers who would like to invest in methods capable of handling multi-block data, in the sense that data are structured into groups of variables.

WHERE

Botanisches Museum, Königin-Luise-Straße 6-8, Berlin

For the detailed program, please visit our website: https://www.physalia-courses.org/courses-workshops/-course29/ 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

https://groups.google.com/forum/#!forum/physalia-courses Carlo Pecoraro <info@physalia-courses.org>

Berlin AppliedBioinformaticsWithR Jan22-26

Dear all,

we still have a few spots available for the course “Applied Statistics and Bioinformatics with R and Bioconductor”, which will take place in Berlin from the 22nd to the 26th of January 2018.

Registration deadline: December 20th , 2017.

https://www.physalia-courses.org/courses-workshops/-course19/ Instructors

Dr. Levi Waldron and Dr. Ludwig Geistlinger from the Waldron lab for computational biostatistics CUNY School of Public Health in New York City (http://-waldronlab.org/)

Overview

This course will provide biologists and bioinformaticians with practical statistical and data analysis skills to perform rigorous analysis of high-throughput biological data. The course assumes some familiarity with genomics and with R programming, but does not assume prior statistical training. It covers the statistical concepts necessary to design experiments and analyze high-dimensional data generated by high-throughput sequencing, including: exploratory data analysis, principal components analysis, unsupervised clustering, batch effects, linear modeling for differential expression, gene set analysis.

Labs

Each day will include a hands-on lab session, that students should attempt and hand in before the following day by committing to the course Github repository. A selection of labs will be reviewed the following day.

Program

Monday 22nd ’V Classes from 09:30 to 17:30

Session 1 ’V Introduction

Lecture 1: Data distributions

* random variables * distributions

Lecture 2: Statistical inference and sampling

* populations and samples * Central Limit Theorem * t-distribution

Lab 1: Introduction to R and Bioconductor

Lab 2: Creating graphics

Tuesday 23nd 'V Classes from 09:30 to 17:30

Session 2'V Hypothesis testing

Lecture 1: hypothesis testing concepts

* type I and II error and power * confidence intervals * multiple hypothesis testing: false discovery rate, family-wise error rate

Lecture 2: hypothesis testing in practice

* hypothesis tests for categorical variables (chi-square, Fisher's exact) * Monte Carlo simulation * permutation tests * bootstrap simulation * exploratory data analysis

Lab: bootstrap simulation and permutation tests

Wednesday 24th 'V Classes from 09:30 to 17:30

Session 3 - Linear modeling

Lecture 1: linear modeling

* linear regression and multiple regression * model matrix and model formulae

Lecture 2: generalized linear models for count data

* intro to generalized linear models * logistic regression and log-linear models * Poisson and Negative Binomial error models * Zero-inflated models

Lab: RNA-seq differential expression workflow

Thursday 25th 'V Classes from 09:30 to 17:30

Session 4 - Unsupervised methods

Lecture 1: distances and PCA

* distance in high dimensions * singular value decomposition * principal components analysis and multidimensional scaling

Lecture 2: unsupervised clustering

* unsupervised clustering * batch effects

Lab 1: applications of unsupervised methods to shotgun metagenomics microbiome data analysis

Lab 2: option to work on students'Â own data.

Friday 26th 'V Classes from 09:30 to 17:30

Session 5 - Gene set and multi-omics data analysis

Lecture 1 - gene set enrichment analysis

* background on gene set testing * types and interpretations of gene set tests * advantages and pitfalls of gene set testing

Lab 1 - gene set analysis with applications to gene expression and multi-omics experiments

Lab 2 - multi-omics data analysis

Lab 3 - option to work on students'Â own data.

For more information about the course, please visit our website:https://www.physalia-courses.org/courses-workshops/course19/ Full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Best regards,

Carlo

–

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org

http://www.physalia-courses.org/ Twitter: @physacourses

mobile: +49 15771084054

https://groups.google.com/forum/#!forum/physalia-courses

Berlin GeneSetEnrichmentPathwayAnalysisInR Mar12-16

Squeezing biology out of statistics: Gene set and pathway analysis in HT data

Berlin, 12-16 2018

https://www.physalia-courses.org/courses-workshops/course3/ Instructor: January Weiner (Staff scientist, Max Planck Institute for Infection Biology)

Course summary

High throughput (HT) techniques such as transcriptomics or metabolomics are of great significance in many areas of biology. However, the path from a boring list of differentially expressed genes to a biological understanding of the results is not straightforward.

This course offers computational techniques that go beyond a simple technical or statistical analysis. It covers techniques for the analysis of gene set enrichments, pathway analysis, gene ontologies, functional analysis of metabolomic profiling and making use of correlations and coexpression networks. A prominent part of the course will be devoted to data visualization and visual data exploration.

The students will gain the ability to independently process and analyse HT data sets, select the appropriate tools, functionally interpret the results as well as learn the paradigms of computational biology and statistics which will allow them to efficiently communicate with computational biologists.

"As an incentive, each student will receive a set of gene expression profiles for a different organism, and during the course they will use these to generate species-specific gene expression modules and test their utility. If we are successfull, we will attempt a joint publication."

Course prerequisites

In general, the course is aimed at biologists who would like to take their data analysis in their own hands. While an aptitude for computational work is necessary, the main goal of the course is the application of biological and statistical knowledge to HT sets with as little effort as necessary.

- basic computer skills (a rudimentary knowledge of programming principles in any language is recommended, but not mandatory) - basic understanding of statistics - basic understanding of molecular techniques for generating high throughput data

The students should be comfortable with using a computer and have at least a rudimentary understanding of computer programming. However, no specific skills are necessary; the students will learn basic R programming in this course.

Basic skills in statistics are necessary. The students should understand the concepts of statistical hypothesis testing and p-values. However, an in-depth introduction to these concepts will also be provided.

Target student skills

- understanding of computational problems associated with high- throughput data analysis - statistical problems and solutions in functional analysis of HT data - overview of commonly used functional analysis techniques (GSEA, gene ontologies, MSigDB, tmod, metabolic profiling) - multivariate techniques and machine learning - Communication skills in statistics and computational biology

After the course, the student should be able to prepare, analyse and functionally interpret a HT data set, including multivariate and machine learning techniques.

Course scheme

On each day, the course will consist of four parts:

- Lecture: theoretical introduction to the days focus - Hands-on guide: guided practical session in R where students replicate the analysis performed by the teacher. While the lecture is general, here specific R techniques and R packages are introduced - Guided self-study: students are given excercises and problems to solve and work on them individually under the guidance of the teacher - Individual project work: each student will receive a transcriptomic (RNASeq or microarray) data set to analyse throughout the course - Lecture: wrap-up and side notes; preparation for the following day

Course plan

- Day 1: Introduction to statistical reasoning and R - Lecture: "Statistics gone wrong: basics of statistical problems in HT applications" - Hands-on guide: working with R: first steps - Guided self-study: using R for data loading and basic statistical calculations - Individual project work: loading data for the individual project - Lecture: "So you have a list of thousand gene names: why do we do HT analyses?"

- Day 2: Data preparation and a functional analysis primer - Lecture: "Methods of pathway and functional analysis in gene set enrichment analyses" - Hands-on guide: gene set enrichment techniques in R and other frameworks - Guided self-study: comparing results of different gene set enrichment techniques - Individual project work: biological interpretation of the results - Lecture: "Common mistakes in functional analysis of HT data"

- Day 3: Making your own modules - Lecture: "Gene expression, co-expression and correlations" - Hands-on guide: making your own modules - Individual project work

- Day 4: Multivariate approaches to functional analyses

— / —

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 LinuxForBiologists Mar12-16

Dear all,

We are happy to announce that the 3rd edition of our course "Introduction to Linux and workflows for biologists" will be held in Berlin (Germany) from the 12th to the 16th of March 2018.

https://www.physalia-courses.org/courses-workshops/course1/ Registration deadline: 9th February 2018.

There is a limited number of spots for this course and attendees will be seated on a first-come, first-served basis.

Instructor:

Dr Martin Jones (Founder, Python for biologists) http://www.physalia-courses.org/instructors/t1/ Overview

Most high-throughput bioinformatics work these days takes place on the Linux command line. The programs which do the majority of the computational heavy lifting genome assemblers, read mappers, and annotation tools are designed to work best when used with a command-line interface. Because the command line can be an intimidating environment, many biologists learn the bare minimum needed to get their analysis tools working. This means that they miss out on the power of Linux to customize their environment and automate many parts of the bioinformatics workflow. This course will introduce the Linux command line environment from scratch and teach students how to make the most of its tools to achieve a high level of productivity when working with biological data.

Intended audience

This course is aimed at researchers and technical workers with a background in biology who want to learn to use the Linux operating system and the command line environment. No previous experience of Linux is required.

Venue

Botanischer Garten und Botanisches Museum (BGBM) Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin.

Course content

Monday 12th - Classes from 09:30 to 17:30

Session 1 - The design of Linux

Session 2 - System management

–

Tuesday 13th - Classes from 09:30 to 17:30

Session 3 - Manipulating tabular data

Session 4 - Constructing pipelines

–

Wednesday 14th - Classes from 09:30 to 17:30

Session 5 - EMBOSS

Session 6 - Using a Linux server

–

Thursday 15th - Classes from 09:30 to 17:30

Session 7 - Combining methods

Session 8 - Combining methods

–

Friday 16th - Classes from 09:30 to 17:30

Session 9 - Customization

Session 10 - Customization

–

For more information please visit our website: https://www.physalia-courses.org/courses-workshops/course1/ https://www.physalia-courses.org/courses-workshops/course4/ For the full list of our courses and Workshops, please visit our website: https://www.physalia-courses.org/courses-workshops/ Best regards,

Carlo

–

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org

http://www.physalia-courses.org/ Twitter: @physacourses

mobile: +49 15771084054

https://groups.google.com/forum/#!forum/physalia-courses

Berlin Phylogenomics Jun4-8

Course “Phylogenomics”

(https://www.physalia-courses.org/courses-workshops/course21/)

Berlin, 4th - 8th June 2018

Our instructor:

Dr. Michael Matschiner, University of Basel (Switzerland) https://www.physalia-courses.org/instructors/t27/ —–

Topic:

Phylogenetic inference and divergence-time estimation with genomic data sets

—–

Overview

Recent advances in sequencing technology, and the rapid increase in the availability of genetic data, have revolutionized the field of phylogenetics. While genomic data promise unprecedented insights into the evolution of the tree of life, they also pose new challenges that must be addressed to avoid misleading results and to fully leverage the potential of the genome-scale data sets. These challenges include the identification of orthologuous sequences that are suitable as phylogenetic markers, the selection of appropriate models of sequence evolution, and the detection of gene-tree discordance due to incomplete lineage sorting and introgression. In this workshop I will present theory and exercises to infer time-calibrated phylogenies from multi-locus, RADseq, and whole-genome data sets while accounting for these confounding factors.

—–

Format

The course will be delivered over the course of five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group. Computing will be done using tools installed on the attendees laptop computer.

—–

Who should attend

This workshop is aimed at researchers, PhD or postdoc level planning to infer phylogenetic relationships and divergence times from multi-locus, RADseq, or whole-genome data.

Attendents should have basic knowledge of UNIX and will need to use the command line on their laptops. Familiarity with a scripting language such as Ruby, Python, or Perl will be helpful but is not required.

—–

For the detailed program, please visit our website: https://www.physalia-courses.org/courses-workshops/-course21/curriculum-21/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ –

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org

http://www.physalia-courses.org/ Twitter: @physacourses

mobile: +49 15771084054

https://groups.google.com/forum/#!forum/physalia-courses

Berlin RADseq Dec4-8 LastCall

Dear all,

we have the last 3 spots left for the course "RADseq data analysis" (https://www.physalia-courses.org/-courses-workshops/course16/), which will be held in Berlin from the 4th to the 8th of December 2017.

Our instructors are:

Dr. Julian Catchen (University of Illinois, USA)

Dr. Josie Paris (University of Sussex, UK)

—–

Topic:

Reduced representation genome sequencing (RADseq) data analysis for population genetics, association studies and phylogenetics

—–

Overview

Reduced representation genome sequencing methods are revolutionizing evolutionary analyses of non-model organisms. Several data generation and data analysis protocols have been developed to generate thousands of sequence variants in hundreds of individuals at relative low cost and speed. In this course, we will introduce the different approaches for obtaining reduced representation genome sequencing data and will specially focus on the data analysis. We will cover all necessary steps to obtain genome variants from short read data that are informative for population genetics, phylogenetic and association studies.

—–

Format

The course will be delivered over the course of five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group.

—–

Who should attend

This course is aimed at researchers and technical workers who are generating and/or analyzing reduced representation genome sequencing data (RAD-seq, ddRAD, 2bRAD, GBS,$B!D(B). Examples demonstrated in this course will involve primarily non-model organisms and examples of applications of this data type for different purposes will be covered. Attendees should have a background in biology. We will dedicate one session to some basic and advanced Linux concepts. Attendees should have also some familiarity with genomic data such as that arising from NGS sequencers.

—–

For the detailed program, please visit our website: https://www.physalia-courses.org/courses-workshops/-course16/curriculum-16/ 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

https://groups.google.com/forum/#!forum/physalia-courses

Berlin RNAseqTrinity Jun11-15

Genome-free RNA-seq assembly and transcriptome analysis leveraging Trinity

11-15 June 2018, Berlin (Germany)

http://www.physalia-courses.org/courses/course11/ Instructors:

Brian Haas (Senior Computational Biologist at the Broad Institute)

Dr. Nicolas Delhomme (UmeÃ¥ Plant Science Center, Sweden)

Course Overview:

RNA-Seq technology has been transformative in our ability to explore gene content and gene expression in all realms of biology, and de novo transcriptome assembly has enabled opportunities to expand transcriptome analysis to non-model organisms. This workshop provides an overview of modern applications of transcriptome sequencing and popular tools and algorithms for exploring transcript reconstruction and expression analysis in a genome-free manner, leveraging the Trinity software and analysis framework. Attendees will perform quality assessment of Illumina RNA-Seq data, assemble a transcriptome using Trinity, quantify transcript expression, leverage Bioconductor tools for differential expression analysis, and apply Trinotate to functionally annotate transcripts. Additional methods will be explored for characterizing the assembled transcriptome and revealing biological findings.

Intended Audience:

This workshop is aimed primarily at biologist researchers that have basic bioinformatics skills and are pursuing RNA-Seq projects in non-model organisms. Attendees will gain skills needed to successfully approach transcriptome sequencing, de novo transcriptome assembly, expression analysis, and functional annotation as applied to organisms lacking a high quality reference genome sequence. Attendees are also invited to bring a subset of their own data. .

Teaching format:

The workshop will be delivered over the course of four and a half days, with each session entailing lectures followed by practical hands-on sessions. Most all computing will be done on the cloud and attendees will use their own laptop computers with the Google Chrome web browser providing all the necessary interfaces to the cloud computing environment, including the linux command terminal.

Assumed background for the participants:

Basic experience with linux command-line execution and execution of bioinformatics tools would be helpful. We will begin the course with a review of basic linux commands and operations as a refresher. No programming or scripting knowledge is required.

Program:

Monday 11th Classes from 09:30 to 17:30

Session 1- Intro to the Trinity RNA-Seq workshop

* Intro to RNA-Seq * Intro to next-gen sequence analysis * Overview of unix and workshop setup

o Practical: exploring the computational infrastructure

* Read quality assessment and trimming

o Practical: using FASTQC and TRIMMOMATIC

Tuesday 12th Classes from 09:30 to 17:30

Session 2-Trinity de novo assembly, expression quantitation, and assembly QC

* Overview of Trinity de novo transcriptome assembly

o Practical: assemble rna-seq data using Trinity

* Intro to expression quantification using RNA-Seq

o Practical: quantify expression for Trinity assembly

* Initial data exploration: assembly quality, and QC samples and replicates

o Practical: using IGV

o Practical: replicate correlation matrix and PCA

Wednesday 13th Classes from 09:30 to 17:30

Session 3- Differential expression analysis

* Overview of statistical methods for differential expression (DE).

o Practical: using Bioconductor tools for DE analysis.

* Transcript clustering and expression profiling

o Practical: generating heatmaps and extracting transcript clusters.

Thursday 14th Classes from 09:30 to 17:30

Session 4-Functional annotation and Functional enrichment studies

* Overview of methods for functional annotation

o Practical: applying Trinotate to find coding regions in transcripts and predict biological function.

* Overview of functional enrichment analysis

o Practical: applying GOseq to identify significantly enriched Gene Ontology categories among transcript clusters.

Friday 15th Classes from 09:30 to 17:30

Session 5- Review and custom data analyses

—-

For the more information about the Workshop, please visit our website: https://www.physalia-courses.org/courses-workshops/course21/curriculum-11/ https://www.physalia-courses.org/courses-workshops/course21/curriculum-21/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ –

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org mailto:info@physalia-courses.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

Crete ComputationalMolEvol May6-17 2018

LAST CHANCE REMINDER:-

Dear Community,

The 10th summer school on Computational Molecular Evolution organized by Alexis Stamatakis, Ziheng Yang, Nick Goldman, Cilia Antoniou, and Laura Emery will take place from May 6 - 17 2018 in Crete, Greece again.

Please visit the course web-site for further details, application deadline is 20 November. Please feel free to circulate this message.

http://meetings.embo.org/event/18-computational-evolution Nick Goldman

Nick Goldman http://www.ebi.ac.uk/research/goldman European Molecular Biology Laboratory tel: +44-(0)1223-492530 European Bioinformatics Institute tel: +44-(0)1223-494522 Wellcome Genome Campus, Hinxton, Cambridge CB10 1SD, UK

"goldman@ebi.ac.uk" <goldman@ebi.ac.uk>

Europe EvolutionaryBiology

Erasmus Mundus Master Program in Evolutionary Biology (MEME)

MEME is a two-year research oriented master program for talented and motivated students who are interested in understanding evolution in all its facets. It intends to provide an optimal preparation for subsequent doctoral studies and eventually a career in academic research.

The MEME program addresses the driving forces of evolution at all levels of organismal organization (from cells and individuals to populations and ecosystems), and allows students to study all kinds of organisms (microorganisms, plants, animals) in all kinds of habitats (marine as well as terrestrial) with a diversity of approaches (field, lab, theory). The focus of the program is not only on how evolution shaped life on our planet in the past, but also on how understanding the principles underlying evolution can provide new insights and help to cope with present-day challenges in a variety of fields, including ecology, epidemiology, physiology, immunology, genetics/genomics, bioinformatics, economics and the social sciences.

To offer a program of such broad scope, four European universities (University of Groningen, Netherlands; University of Montpellier, France; Ludwig Maximilians University of Munich, Germany; Uppsala University, Sweden), have joined forces with Harvard University (USA). Together, this consortium has put together an attractive multidisciplinary program that meets highest standards. All students have to study at (at least) two partner universities, and they will receive a double degree from two partner universities they have attended.

A limited number of full scholarships is available for European and non-European students and these will be awarded in a selective procedure. Details on the program and the selection procedure can be found on www.evobio.eu . Starting date: 1 September 2018

Application deadline: 1 February 2018

Please alert your students to this great opportunity!

More information and how to apply - please see www.evobio.eu Questions about the contents of the program:

Franjo Weissing (f.j.weissing@rug.nl)

Questions about the requirements and the application procedure:

Maartje Giesbers (m.c.w.g.giesbers@rug.nl)

—

Postal address: Dr. Maartje Giesbers Administrative Coordinator MEME

Groningen Institute for Evolutionary Life Sciences University of Groningen P.O. Box 11103 9700 CC Groningen Visiting address: Nijenborgh 7, room 05-04

Phone +31 50 363 8462 Email m.c.w.g.giesbers@rug.nl

Working days: Monday, Tuesday, Thursday, Friday

Maartje Giesbers <m.c.w.g.giesbers@rug.nl>

Finland MathematicalEvolution Aug2018

Applications are now invited to THE HELSINKI SUMMER SCHOOL ON MATHEMATICAL ECOLOGY AND EVOLUTION 2018

Dear Colleagues,

We are glad to invite applications to the 2018 edition of The Helsinki Summer School on Mathematical Ecology and Evolution, an EMS-ESMTB School in Applied Mathematics. The school will be held between 19 and 26 August 2018 in Turku, Finland, and will be part of the EMS Year of Mathematical Biology < http://euro-math-soc.eu/year-mathematical-biology-2018 >.

The core program consists of five series of lectures:

Karl Sigmund (University of Vienna): Evolutionary game theory

Odo Diekmann (Utrecht University): Renewal equations in population biology

Sebastian Schreiber (University of California, Davis): Coexistence in variable environments

Ellen Baake (University of Bielefeld): Probabilistic models and ancestral processes in population genetics

Mick Roberts (Massey University of New Zealand): Ecology of infectious diseases

All young researchers working in mathematical ecology can apply from all countries, especially from Europe and the Mediterranean. The school is aimed at graduate students of mathematics, but we also welcome students of biology with sufficient background in mathematics, as well as advanced undergraduates and postdocs.

For more information and details of the application procedure, please visit the school's webpage https://wiki.helsinki.fi/display/BioMath/The+Helsinki+Summer+School+on+Mathematical+Ecology+and+Ev With best regards, Eva Kisdi (eva.kisdi@helsinki.fi)

FU Berlin ProgrammingForEvolBiol Mar5-21

Course on Programming for Evolutionary Biology

When: March 5th - March 21st 2018

Location: Berlin, Germany

Application deadline: December 31st 2017

Detailed information about the course content and how to apply: http://evop.bioinf.uni-leipzig.de/ In this intensive 17 days course, students will learn how to survive in a Linux environment, get hands-on experience in two widely used programming languages (Python and R), and statistical data analysis. The classes will be given by experts in the field and consist of lectures and exercises with the computer. The aim of the course is to provide the students with the necessary background and skills to perform computational analyses with a focus on solving research questions related to genomics and evolution. The philosophy of the course will be "learning by doing", which means that the computational skills will be taught using examples and real data from evolutionary biology for the exercises. During the course, students will also propose projects of their own interest and perform them as final projects in small groups under the supervision of a teaching assistant. This summer school is open for students from all countries and targeted toward PhD students and postdocs of evolutionary biology or related research fields with no or little programming experience who want to become proficient in computational evolutionary biology in a couple of weeks.

The course takes place at the Free University of Berlin.

– Dr. Katja Nowick

Professur fÂÂ^{1}r Humanbiologie www.nowick-lab.info
Current address: Max-Planck-Institute for Molecular Genetics Ihnestrasse 73 14195 Berlin Germany

Phone 1: +49 30 84131170

Katja Nowick <katja.nowick@fu-berlin.de>

Leicester ExomeSeq Dec04-05

Places are still available on the upcoming Exome Variants, Copy Number Calling, Variant Annotation and Reporting Workshop hosted by BBASH at the University of Leicester.

Course dates: 4th-5th December 2017

Venue: University of Leicester - College Court Conference Centre, Leicester, UK (http://collegecourt.co.uk/)

Instructors: Matthew Blades (BBASH, University of Leicester, UK) Robert Hastings (University of Leicester, UK) Peter Causey-Freeman (University of Leicester, UK) — Course description: The course provides an introduction to calling variants and copy number alterations from exome sequencing—data alignments, variant annotation, variant effect prediction and reporting recommendations. The course will be delivered using a mixture of lectures and computer based hands on practical sessions using real data.

Target audience and pre-requisites: This course is aimed at clinicians and wet-lab biologists who are involved in research projects that will require the handling and analysis of DNA-seq, exome data and sequence—variation. A significant proportion of the course will be computer-based using command line tools in the Unix environment and applicants will require a grasp of basic skills such as file navigation and management. Experience with R will be helpful, though all R scripts will be provided and guidance given on code alterations. This workshop is the second in a two-part course in conjunction with our Introduction to DNA-seq workshop on 20th-21st November. Attendance at the November workshop is not a pre-requisite, but experience will be required with the topics covered therein (aligning reads to a reference genome and BAM refinement - see link below).

For further information/registration: https://-www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/bbash/training/workshop-webpages/-dna-seq-ngs-dec2017 For information/registration for our Introduction to DNA-seq workshop (November): https://www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/bbash/training/workshop-webpages/-dna-seq-ngs-nov2017 The Organisers Chiara Batini (University of Leicester, UK) Matthew Blades (BBASH, University of Leicester, UK) Benjamin Hunt (University of Leicester, UK) Robert Hastings (University of

Leicester, UK) Peter Causey-Freeman (University of Leicester, UK)

"bh177@leicester.ac.uk" <bh177@leicester.ac.uk>

MNHN Paris DnaBarcodesInTheGenomicEra Mar5-9

The course Integrative taxonomy and taxonomic expertise: DNA barcodes in the genomic era will be from the 5th to the 9th of March, 2017 at the MNHN of Paris, France.

This course is also part of the DEST- Taxonomy training program ([http://www.taxonomytraining.eu/]).

The course is in English. To register, please fill the form on the website of the course (https://sites.google.com/-site/coursbarcode/inscription-1) before the 8th of January, 2018.

If you have any question, please contact: Line Le Gall (legall@mnhn.fr) Nicolas Puillandre (puillandre@mnhn.fr) Sarah Samadi (sarah@mnhn.fr)

Nicolas PUILLANDRE <nicolas.puillandre@mnhn.fr>

NHM London BotanicalTaxonomicPrinciples Mar12-16

Short course on taxonomic principles and tools in botanical research, 12-16 March 2018, Natural History Museum, London.

Applications are open for a short course on plant taxonomy and identification funded by the UK's Natural Environment Research Council (NERC).

The course is taught by NHM taxonomic specialists and makes use of the outstanding botanical collections of the Museum. Specialist training is offered in vascular plants (flowering plants and ferns), bryophytes, lichens and marine macroalgae (red, brown and green seaweeds).

The course comprises two days of lectures and demonstrations and three days of practical sessions, comprising one day in the field and two days in the herbarium/laboratory.

The course is available to environmental science researchers and PhD students. There are 25 spaces available, and priority will be given to those with NERC funding.

The deadline for applications is 18th December 2018.

For more details see: http://www.nhm.ac.uk/our-science/courses-and-students/short-course-taxonomic-principles-botanical-research.html Mark Carine <M.Carine@nhm.ac.uk>

NIMBioS UTennessee Selection Jun18-22

The National Institute for Mathematical and Biological Synthesis (NIMBioS) is now accepting applications for its Tutorial, The Search for Selection, to be held June 18-22, 2018, at NIMBioS.

Objectives: Biologists are obsessed (indeed, seduced) by the search for signatures of selection in organismal features of interest, ranging from specific traits to genome-wide signatures. A vast number of approaches have been suggested in this search for selection, including genomic-based signatures of recent or ongoing selection, tests based on either excessive amounts or nonrandom patterns of divergence (in both fossil sequences and functional genomics data) and the more classical Lande-Arnold fitness estimates (direct association of phenotypic values with fitness estimates) and their modern extensions (such as aster models). Given the breadth of such searches, a large amount of machinery has been developed, but is rarely presented in a unified fashion. This tutorial presents an integrated overview of all these approaches, highlighting common themes and divergent assumptions.

The goal of this tutorial is to expose investigators from all branches of biology to this rich menagerie of tests. It is applicable for population geneticists, genome biologists, evolutionary ecologists, paleontologists, functional morphologists, and just about any biologist who ponders on how to formally demonstrate that a feature (or features) of interest might have been shaped by selection.

The intended audience is advanced graduate students, postdocs, and faculty with an interest in searching for targets of selection, be they particular genomic sequences or particular traits. Given the breadth of this topic, we expect students from functional genomics, population and evolutionary genetics, ecology, paleobiology, functional morphology, and statistics (as well as other fields). The background required is some basic introduction to population and/or quantitative genetics.

Location: NIMBioS at the University of Tennessee, Knoxville Organizer: Bruce Walsh, Ecology & Evolutionary Biology, Univ. of Arizona For more information about the tutorial and a link to the online application form, go to http://www.nimbios.org/tutorials/selection Participation in NIMBioS tutorials is by application only. Individuals with a strong interest in the topic are encouraged to apply, and successful applicants will be notified within several weeks after the application deadline. NIMBioS will cover lodging (5 nights) and provide breakfast and lunch each day at NIMBioS. If needed, limited financial support for travel expenses is available.

Application deadline: February 1, 2018 The National Institute for Mathematical and Biological Synthesis (NIMBioS) (http://www.nimbios.org) brings together researchers from around the world to collaborate across disciplinary boundaries to investigate solutions to basic and applied problems in the life sciences. NIMBioS is sponsored by the National Science Foundation, with additional support from The University of Tennessee, Knoxville.

“Walsh, James Bruce - (jbwalsh)” <jbwalsh@email.arizona.edu>

Online LandscapeGenetics Jan17-May9

Online Landscape Genetics Graduate Student Course Available Jan 17 ’V May 9, 2018, Wed 8:30 ’V 10:30 PST (also can be taken at any time using taped lectures)

Cost $500 individuals, $1000 Groups

Course Organizers: Helene Wagner, Melanie Murphy, and Lisette Waits Co-Instructors: Niko Balkenhol, Jeff Bowman, Sam Cushman, Marie-Josee Fortin, Caren Goldberg, Nusha Keyghobadi, Erin Landguth, Stephanie Manel, Sean Schoville, Kim Selkoe, Steve Spear, and others

Course description This course on Landscape Genetics provides a unique opportunity for interdisciplinary training and provides an overview of the field of landscape genetics. The course caters to students in basic and applied ecology, conservation and population genetics, landscape ecology, evolutionary biology and conservation biology. A key objective of landscape genetics is to study how landscape modification and habitat fragmentation affect organism dispersal and gene flow across the landscape. Landscape genetics requires highly interdisciplinary specialized skills making intensive use of technical population genetic skills and spatial analysis tools (spatial statistics, GIS tools and remote sensing).

Landscape Genetics will be concurrently offered at multiple universities across the globe, giving students the opportunity to learn from international experts and work with peers from outside institutions. For students who are not members of the participating institutions, we are offering a web-based online course to reach a broader audience. Each course meeting will start with a live web-cast lecture (no special software required) by an expert on the topic that introduces foundations and methods and highlights points for discussion in local seminar groups.

After breaking out into local course group discussion (including a discussion group for online course students), a web-based discussion across campuses will wrap up the weekly topic. Students who are unable to make it to live- cast of lectures can view taped lectures. In addition, students can choose to participate in an optional lab section using R and/or interdisciplinary group term projects with web-based collaboration across institutions. The final two options are provided to help students develop analytical skills in Landscape Genetics. Students who participate in group projects will have the option of applying to attend a project synthesis meeting in Coeur d’ÂAlene, Idaho in May 2018.

Course website: https://sites.google.com/site/-dgs2018landscapegenetics/ How to register? Please register here by Dec 30th: https://goo.gl/forms/-iEMKsRSbkp8KN25l1. A link to the registration form can also be found on the course website.

Faculty who would like to add a local section of the course at their university can register as a group or multiple students at one institution can register as a group to decrease cost/student.

Lisette Waits, PhD Distinguished Professor Department Head Fish and Wildlife Sciences University of Idaho Moscow, ID 83844-1136 (208) 885-7823

lwaits@uidaho.edu

Oslo GalaxyAdministration Jan8-12

We are pleased to announce that registration is now open for the European Galaxy Administrator Workshop.

- Mon 8 January 2018 to Fri 12 January 2018 CET - UiO, Oslo, Norway - https://www.elixir-europe.org/events/-european-galaxy-administrator-workshop Participants will learn how to install, configure, customize, and extend their own Galaxy servers. Topics include tool configuration, authentication and user management, using heterogeneous storage and compute services, and many other topics that will enable you to get your own Galaxy server up and running, performing well, and used by your community. Have a look at the programme (https://github.com/elixir-no-nels/dagobah-training/-blob/2018-oslo/README.md) to see more details on the planned content of the workshop.

Maximum number of participants is limited to 30, and we will manage registrations to allow for geographical distribution and proritize participants with responsibility of administrating galaxy servers. After registering you will get a second confirmation if/when a slot has been allocated to you.

Although located in Europe, and named to reflect this, the workshop is definitely open to a world-wide audience. The workshop is a result of the collaboration between the Elixir Galaxy WG and the Galaxy Project, and so far known, this is the only Galaxy Admin workshop planned for 2018.

Participants are to cover their own travel and accomodation, while the workshop participation is free of charge.

Instructors

Björn Grüning (Elixir Galaxy WG, Elixir Germany, University of Freiburg) Marius van den Beek (Elixir Galaxy WG, Institute Curie, France) Nicola Soranzo (Elixir Galaxy WG, Earlham Institute, UK) Enis Afgan (Galaxy Project, Johns Hopkins University, USA) Abdulrahman Azab (Elixir Norway, USIT, University of Oslo, Norway)

About Galaxy

Galaxy is an open, web-based platform for data-intensive biomedical analysis used by tens of thousands of researchers around the world. It supports ad hoc exploration and analysis through scalable and repeatable data analysis pipelines for large research studies. Galaxy is available in over 90 free and publicly accessible web servers, on commercial and national cloud infrastructures, and is locally installed at hundreds, if not thousands, of research organisations around the world.

– https://galaxyproject.org/ https://usegalaxy.org/ clementsgalaxy@gmail.com

Portugal cE3c DeadlinesDec

Subject: Portugal-cE3c-Course: three advanced courses with deadlines December 2017

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the four courses with closer deadlines. Additional informations at:

http://ce3c.ciencias.ulisboa.pt/training/?cat Course Hands on Functional Diversity: from Ecological Indicators to Ecosystem Services

organized by Laura Concostrina-Zubiri, Paula Matos, Alice Nunes et al. | January 15-19 2018 @ Lisbon, Portugal

Objectives: Under the general framework of Global Change Ecology, the goal of this five days intensive course is to provide the participants with the most recent and practical knowledge on the use of Functional Diversity. This includes the selection of functional traits and calculation of Functional Diversity Indexes. Examples of the application of this knowledge will be given regarding Ecological Indicators and Ecosystem Services.

See the PROGRAMME at:

http://ce3c.ciencias.ulisboa.pt/training/?cat Course INSTRUCTOR (among others)

Laura Concostrina-Zubiri

(http://ce3c.ciencias.ulisboa.pt/member/laura-concostrina-zubiri)

(cE3c collaborator, leader of a Marie Curie project)

Intended audience

This course will be open to a maximum number of 20 participants, being directed to MSc or PhD students in Biology, Environmental Sciences, Ecology or related areas, postdocs and professionals working in related topics.

Minimum formation: Bachelor in Biology, Natural Science or related areas

The course is free for a maximum of 10 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL, UP) and Biology and Ecology of Global Changes (BEAG UL, UA). For information of fees for other participants see the programme details.

Deadline for applications: December 15^th 2017

Candidates should send a short CV and motivation letter explaining why they are interested in the course to Laura Concostrina-Zubiri (lczubiri@fc.ul.pt)

For additional details about the course click here:

http://ce3c.ciencias.ulisboa.pt/training/?cat Course Introduction to Big Data - knowledge extraction from biological databases

by Teresa Nogueira - January 17th to January 19th 2018 @ Lisbon, Portugal

Objectives

During recent decades we have witnessed a great development of bioinformatics that has led to the accumulation of a huge amount of biological information. The Bioinformatics and computational Biology aim at dealing with this large volume of data so that biological information can be extracted, generating scientific knowledge. Handling and mining big data is currently a subject of great interest and importance. This course aim at familiarizing the attendees with the Unix/Linux environment and shell scripting. The participants will develop and implement querying algorithms in order to generate metadata for analysis.

Course INSTRUCTOR

Teresa Nogueira (cE3c collaborator)

http://ce3c.ciencias.ulisboa.pt/member/teresa-nogueira Intended audience: The course will be open to a maximum of 20 students, being directed to PhD or MSc students, postdocs, and professionals working in Molecular Biology, Biochemistry, Genetics and related topics.

Minimum formation: bachelor degree in Biology, Biochemistry or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below).

Deadline for applications: December 15^th 2017

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:

teresainogueira@gmail.com

Course Scientific Writing and Communication

Organized by Gabor Lövei| January 22 - 26 2018 @ Lisbon, Portugal

Objectives The objective of this course is to introduce participants to the details of communication and writing scientific publications. The main emphasis is on the most common form, the “primary scientific paper”, but other forms will be covered. Matters related to oral presentations, poster preparation and proposal writing will also be discussed. Thus participants will become familiar with the forms of presenting new findings to various scientific forums.

Course INSTRUCTOR

— / —

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

---

Roscoff EvolutionNetworkBioinformatics Jun24-30

Introduction to the concepts and methods of networks in evolutionary studies (sequence similarity networks, genome networks and multipartite graphs)

—This free summer school will be held in Roscoff, France, between June 24th 2018 (date of arrival) and June 30th (date of departure).

—This school is designed in priority for biologists and bioinformaticians (completing a PhD degree or currently post-doctoral fellows, as well as researchers), who wish to learn the bases of network analyses.

—The main notions (regarding various types of networks, the relevance of their analyses, and some bases in graph theory) will be introduced by short theoretical classes, followed by practical case-studies, introducing the basics in programming required to run such network analyses as well as to use the existing software/tools. Our goal is that, by the end of this summer school, all applicants will be qualified to perform network analyses of their own datasets.

—More precisely, we will focus on the following concepts and methods:

—- Introgressive evolution and large-scale diversity studies.

—- Construction and analysis of sequence similarity networks (construction and sorting of connected components, definition of gene families, search for composite genes, implementation of centrality measures)

—- Construction and analysis of genome networks (construction of weighted genome networks, implementation of their diameter, shortest paths, analyses of labeled nodes, etc.)

—- Construction and analysis of gene-genome bipartite graphs (detection of connected components, and their articulation points, and twins)

—In addition, 9 conferences on networks and evolution will be delivered by leading European and American scientists— during this school.

Monday June 25th:

Pr. James McInerney (U. Manchester, UK): Networks and public goods : reticulate evolution in prokaryotes

Dr. Philippe Gambette (U. Marne, France): The different types of networks used in evolutionary study : how they are made and what they are useful for

Dr. Eric Bapteste (UPMC, France): Introduction to sequence similarity networks

Tuesday June 26th:

Pr. Debashish Bhattacharya (U. Rutgers, USA): Reticulate evolution in eukaryotes

Pr. Michel Habib (U. Paris 7, France): Graph centralities and graph comparisons

Dr. Damien Eveillard (U. Nantes, France): Cooccurrence networks and the evolution of geochemical cycles in the environment

Friday June 29th:

Pr. Tal Dagan (U. kiel, Germany): Directed bipartite graphs and LGT mediated by phages

Dr. Mehdi Layeghifard (U. Toronto, Canada): Metagenomic networks

Marc-André Sélosse (MNHN, France): The living world as a network

This summer school is funded by ERC grant (FP7/2007-2013 Grant Agreement # 615274). Hence, registration is free, housing and food (breakfast, lunch) are also fully covered. Applicants will only need to fund their travel to Roscoff and their evening dinners.

—10 places only are available, with a mandatory requirement: applicants must show basic computer skills (i.e. to be familiar with Linux environment and with at least one programming language, preferably Python).

—Applications are to be submitted asap, and no later than January 15th 2018, by email to :

—eric.bapteste@upmc.fr , and contain a brief letter describing why this class will be of significant interest for the applicant and his/her future studies.

—Applicants will be selected based on their motivation, and their resume, including the names of two scientific referees for PhD and postdoctoral fellows.

— We are excited to meet you soon in Roscoff.

—Eric Bapteste + Philippe Lopez + Eduardo Corel

Eric Bapteste <epbapteste@gmail.com>

SaoPaulo Evolution Dec5-19

Dear All

the V ELAEVO (Escuela Latinoamericana de Evolución - Latin-American School on Evolution) will be held in Sāo Paulo University (USP) this next December 5th in a 2 week Graduate course format. Students from all over the world are welcome to attend and enroll to use the course credits in their own graduate programs. Instructors Gabriel Marroig, Diogo Meyr, Jason Wolf and Julien Ayroles will cover the following topics:

Introduction to Quantitative Genetics Genetic Architecture of quantitative traits Molecular Basis of variation and evolutionary response Characterizing genetic Architecture (QTL and GWAS) Multiple traits and Pleiotropy Gene interaction (Epistasis) Modularity and Integration Evolvability and Constraints Environmental variation and genotype-environment interaction Measuring Natural Selection Micro- and Macroevolution Towards and integrative approach: genes, expression and quantitative traits data

More details can be found here:

https://lem-usp.github.io/elaevo/ Gabriel Marroig Professor Titular Depto. Genética e Biologia Evolutiva Instituto de Biociências - USP "gmarroig@usp.br" <gmarroig@usp.br>

Scotland PhylogenticDataAnalysis Jan28-Feb2 FinalCall

"Phylogenetic data analysis using R"

FINAL CALL - LAST FEW PLACES

Delivered by Dr. Emmanuel Paradis

www.prstatistics.com/course/introduction-to-phylogenetic-analysis-with-r-phyg-phyl02/ This course will run from 28th January - 2nd February 2018 at SCENE field station, Loch Lomond, Glasgow.

The main objectives of the course are to teach the theoretical bases of phylogenetic analysis, and to give the ability to initiate a phylogenetic analysis starting from the files of molecular sequences until the interpretation of the results and the graphics. The introduction will cover a brief historical background and an overview of the different methods of phylogenetic inference. Different kinds of data will be considered, but with a special emphasis on DNA sequences. The software used will be based on R and several specialized packages (particularly ape and phangorn). Other software will be used (e.g., MUSCLE or Clustal) called from R. Overall, the course will cover almost all aspects of phylogenetic inference from reading/downloading the data to plotting the results. This course is intended for PhD and postgraduate students, researchers and engineers in evolutionary biology, systematics, population genetics, ecology, conservation.

Course content is as follows Day 1 - Refresher on R: data structures, data manipulation with the indexing system, scripts, using the help system. - Introduction to phylogenetic inference. - Basics on phylogenetic data (sequences, alignments, trees, networks, "splits") and other data in R. - Reading / writing data from files or from internet. - Matching data. Manipulating labels. Subsetting data. - Main package: ape. Day 2 - Plotting and annotating trees. - Theory of sequence alignment. Comparing alignments. Graphical analyses of alignments. - Main packages: ape (with MUSCLE and Clustal). Day 3 - Theory and methods of phylogeny reconstruction. - Parsimony methods. - Evolutionary distances. - Distance-based methods: General principles and the main methods (NJ, BIONJ, FastME, MVR). - Methods for incomplete distances matrices (NJ*, BIONJ*, MVR*). Methods for combining several matrices (SDM). - Main packages: ape, phangorn. Day 4 - Theory of maximum likelihood estimation. - Application to phylogeny reconstruction. - Substitution models. - Tree space and topology estimation. - Main packages: ape, phangorn. Day 5 - Tree comparison, consensus methods. - Topological space and distances. - Bootstrap. - Bayesian methods.

Please email any inquiries to oliverhooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

PRstatistics upcoming courses - email for details oliverhooker@prstatistics.com for details

1. November 20th - 25th 2017 APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS #ABME SCENE, Scotland, Dr. Matt Denwood http://www.prstatistics.com/course/applied-bayesian-modelling-ecologists-epidemiologists-abme03/ 2. November 27th - December 1st 2017 INTRODUCTION TO PYTHON FOR BIOLOGISTS #IPYB Margam Discovery Centre, Wales, Dr. Martin Jones http://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb04/ 3. December 4th - 8th 2017 ADVANCING IN STATISTICAL MODELLING USING R #ADVR Margam Discovery Centre, Wales, Dr. Luc Bussiere, Dr. Tom Houslay, Dr. Ane Timenes Laugen, http://www.prstatistics.com/course/-advancing-statistical-modelling-using-r-advr07/ 4. January 29t - February 2nd 2018 INTRODUCTION TO BAYESIAN HIERARCHICAL MODELLING #IBHM SCENE, Scotland, Dr. Andrew Parnell http://www.prstatistics.com/course/introduction-to-bayesian-hierarchical-modelling-using-r-ibhm02/ 5. January 29th - February 2nd 2018 PHYLOGENETIC DATA ANALYSIS USING R #PHYL SCENE, Scotland, Dr. Emmanuel Paradis https://www.prstatistics.com/-course/introduction-to-phylogenetic-analysis-with-r-phyg-phyl02/ 6. February 19th - 23rd 2018 MOVEMENT ECOLOGY #MOVE Margam Discovery Centre, Wales, Dr Luca Borger, Dr Ronny Wilson, Dr Jonathan Potts https://www.prstatistics.com/course/-movement-ecology-move01/ 7. February 19th - 23rd 2018 GEOMETRIC MORPHOMETRICS USING R #GMMR

— / —

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

Sweden ParentalCareSexualSel Feb26-Mar3

WORKSHOP INVITATION

INTERPLAY BETWEEN PARENTAL CARE AND SEXUAL SELECTION

Dear Colleagues,

We are glad to invite you to our Workshop that will take place between 26th February and 3rd March 2018 in Fiskebäckskil, Sweden.

We aim to bring together evolutionary biologists and behavioral ecologists interested in different aspects of the interplay between parental care and sexual selection. The main goal is to provide a relaxed atmosphere where researchers with diverse backgrounds, at different career stages, and that use different approaches (from theoretical models to empirical data in a great variety of organisms) can exchange ideas, discussing in details the recent developments in the field and proposing future directions. We believe that addressing the complexity of the interaction between parental care and sexual selection from multiple viewpoints has a great potential to optimize chances for breakthrough ideas. Besides, the workshop will provide the perfect forum for researchers (especially young scientists) to network with other specialists in the field.

The event will start with a reception on Monday 26th February, will include 3 full days of talks from invited speakers and attendees, 1 night of poster exhibition, and a last full day of general discussion of relevant sub-themes in the field, conducted in small groups self-organized by the participants. Talks will comprise 12 min of presentation, followed by a 13 min long discussion session so that each participant will enjoy a total of 25 min to interact with the specialist audience. In particular, we ask participants to present results or ideas from on-going research instead of already published papers, given that the main focus of the workshop is the discussion of fresh perspectives and initiatives.

Confirmed invited speakers include:

Professor Suzanne H. Alonzo

University of California - Santa Cruz, USA

Dr. Lutz Fromhage

University of Jyväskylä, Finland

Professor Wolfgang Goymann

Max Planck Institute for Ornithology, Germany

Dr. Irja Ida Ratikainen

Norwegian University of Science and Technology, Norway

Professor Nick Royle

University of Exeter, UK

The Workshop will take place at the Lovén Centre Kristineberg (http://loven.gu.se/english/-about_the_loven_centre), a marine research station beautifully located in Fiskebäckskil, suitably secluded at the mouth of the Gullmarn fjord, and easily accessible. Social events will include informal hangouts at night, walks to explore the village, a farewell dinner on Friday night, and the premiere exhibition of a documentary on male-only care, featuring emus, pipefishes, midshipman fishes, poison frogs and harvestmen (http:/-/www.rotatingplanet.com/animal_dads.php).

There are no registration fees. Accommodation and meals for 40 participants will be covered by the financial support of the Gothenburg Centre for Advanced Studies in Science & Technology *(GoCAS)* and the Royal Swedish Academy of Sciences (*KVA).* Participants will only be charged for the costs of their social events and the transportation to the event venue.

Application deadline: Monday, 15 January 2018.

A website with detailed information will soon be launched and announced here, but inquiries and further information on the event may be directed to Dr. Gustavo S. Requena (gs.requena@gmail.com)

We look forward to hearing from you.

Best regards,

Gustavo S. Requena

Postdoctoral Fellow

Universidade de Sāo Paulo

http://campuspress.yale.edu/gsrequena/ *Charlotta Kvarnemo*

Professor

University of Gothenburg

https://sites.google.com/site/kvarnemolab/home Gustavo Requena <gs.requena@gmail.com>

Sweden SexualSelection Feb26-Mar03

WORKSHOP INVITATION

INTERPLAY BETWEEN PARENTAL CARE AND SEXUAL SELECTION

Dear Colleagues,

We are glad to invite you to our Workshop that will take place between 26th February and 3rd March 2018 in Fiskebäckskil, Sweden.

The main goal of this workshop is to provide a relaxed atmosphere where researchers interested in different aspects of the interplay between parental care and sexual selection will exchange ideas, discuss the recent developments in the field, and propose in details future directions. We embrace diversity as a way to enrich scientific discussions and we will prioritize attendees with diverse backgrounds, at different career stages, and that use different organisms and methodological approaches to address their questions. Besides, the workshop will provide the perfect forum for researchers (especially young scientists) to network with other specialists in the field.

The event will start with a reception on Monday 26th February, will include 3 full days of talks from invited speakers and attendees, 1 night of poster exhibition, and a last full day of general discussion of relevant sub-themes in the field, conducted in small groups self-organized by the participants. We ask participants to present results or ideas from on-going research instead of already published papers, given that the main focus of the workshop is the discussion of fresh perspectives and initiatives.

Confirmed invited speakers include:

Professor Suzanne H. Alonzo

University of California - Santa Cruz, USA

Dr Lutz Fromhage

University of Jyväskylä, Finland

Professor Wolfgang Goymann

Max Planck Institute for Ornithology, Germany

Dr. Irja Ida Ratikainen

Norwegian University of Science and Technology, Norway

Professor Nick Royle

University of Exeter, UK

There are no registration fees. Accommodation and meals for 40 participants will be covered by the financial support of the Gothenburg Centre for Advanced Studies in Science & Technology *(GoCAS)* and the Royal Swedish Academy of Sciences (*KVA).* Participants will only be charged for the costs of their social events and the transportation to the event venue.

For more details, access: https://parentalcaresexualselection.wordpress.com/ *Application deadline: Monday, 08th January 2018.*

We look forward to hearing from you.

Best regards,

Gustavo S. Requena

Postdoctoral Fellow

Universidade de Sāo Paulo

http://campuspress.yale.edu/gsrequena/ *Charlotta Kvarnemo*

Professor

University of Gothenburg

https://sites.google.com/site/kvarnemolab/home Gustavo Requena <gs.requena@gmail.com>

Switzerland WholeGenomeSeqAnalysis Feb4-9

Reminder: Winter School on Whole Genome Seq. Analysis and Annotation registration closes 10.11.17

The Winter School is an intensive 5-day workshop that combines lectures and practicals on whole genome assembly using short and long reads, 3D genome assembly, whole genome sequence annotation and manual gene annotation. The instructors include developers of some of the most widely used WGS analysis programs including BUSCO, APOLLO, JUICEBOX and MAKER.

For more information please visit the website (http://www.adaptation.ethz.ch/education/wgs-winter-school-2018/registration.html). For further enquires please email Jessica Stapley at monte-verita@env.ethz.ch

Jessica Stapley Fellow, Adaptation to a Changing Environment (ACE)

Institute of Integrative Biology, ETH Department of Environmental Sciences Universitätstrasse 16 ETH Zentrum, CHN G 31.2 CH-8092 Zürich

email: jessica.stapley@env.ethz.ch web: http://jessicastapley.com/ twitter: @jessstapley Tel: +41-44-632 8399

Jessica Stapley <jessica.stapley@env.ethz.ch>

Texas BenthicInvertMetagenomics Jan15-19

2nd Benthic Invertebrate Taxonomy, Metagenomics, and Bioinformatics (BITMaB-2) Workshop

January 15-19, 2018

Texas A&M University-Corpus Christi Harte Research Institute for Gulf of Mexico Studies 6300 Ocean Drive, Corpus Christi, Texas 78412 USA

Workshop Application Form: https://goo.gl/forms/RL5P6EAOzfQG16kq2 (EXTENDED application deadline November 20, 2017):

Full Workshop Announcement: https://docs.google.com/document/d/1Sky4bKzrxF4ImwrKCEcgdzFzLSjyhnWustoUELyyT8Q/edit

Background: Morphological identification of benthic meiofauna and macrofauna samples is labor intensive, time consuming, and costly. A more efficient method, using DNA markers from metagenomic sequencing of sediment samples to characterize benthic communities, is being developed. For this purpose, a reference library for whole genomes of widely distributed infauna species of the Gulf of Mexico is currently being populated. While still in its infancy, we are anticipating that this new methodology will become a standard procedure for ecological surveys and environmental monitoring procedures.

Purpose: The BITMaB-2 workshop is designed to train graduate students and researchers in the full spectrum involved in this new cutting edge methodology, including sample preparation, taxonomy of common benthic meiofauna and macrofauna taxa of the Gulf of Mexico, metagenomics, and bioinformatics. There is no registration fee for BITMaB-2.

Objectives: There are two objectives of this workshop. First, we intend to produce meio- and macrofaunal specimens from which we will generate draft genomes in support of the development of the eukaryotic genomes reference databases. We strive to include as many unique families/phyla represented in the GoM as possible. A complication for many groups is that fresh material will be required to find and identify individual specimens. As such this workshop will focus on samples collected each morning during the workshop from relatively shallow sediments. This aspect of the workshop will be led by taxonomic experts and provide an opportunity for training students, at all levels. The anticipated outcome for this activity is to provide valuable experiences for many students and to produce as many potential reference samples competent for genome sequencing analysis as possible during the week. The taxonomy experience will take place in the facilities at the Harte Research Institute.

Holly Bik Assistant Professor Department of Nematology University of California, Riverside 3401 Watkins Drive Riverside, CA 92521 Email: holly.bik@ucr.edu Phone: (+1) 951-827-4230

Web: http://biklab.github.io Twitter: https://twitter.com/hollybik holly.bik@gmail.com

---

UK ModellingEvolution Dec4-8

PARTFUNDED SCHOLARHPS for the course “Advancing in statistical modelling for evolutionary biologists and ecologists using R”

PR STATISTICS ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE “Advancing in statistical modelling for evolutionary biologists and ecologists using R (ADVR07)”

SCHOLARSHIPS CONTRIBUTE TOWARDS COURSE FEES WITH 5 PLACES AVAILABLE AT 330.00 (Fees have been subsidised by 40% from 550.00).

Applications should be sent to oliverhooker@prstatistics.com and contain the following. 1. Full name 2. Institute name 3. PhD subject title or Post doc research questions 4. Do you hold a funded position 5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Monday 13th November 2017 and decisions will be made by Tuesday 14th November 2017

We still have 'normal' places available for anyone else interested.

Full course details are given below

"Advancing in statistical modelling for evolutionary biologists and ecologists using R"

Delivered by Dr. Luc Bussiere and Dr. Tom Houslay

https://www.prstatistics.com/course/advancing-statistical-modelling-using-r-advr07/ This course will run from 4th - 8th December 2017 at Margam Park Discovery Centre, Wales, UK

Course only and all inclusive packages are available.

Course Overview: This course will provide an introduction to working with real-life data typical of those encountered in the field of evolutionary biology and ecology. The course will be delivered by Dr. Luc Bussiere and Dr. Tom Houslay who are—both practicing academics in the field of evolutionary biology.——This five day course will consist of series of modules (each lasting roughly half a day) covering—model selection and simplification, generalised linear models, mixed effects models,— and non-linear models. Along the way you will gain in depth experience—in data 'wrangling', data and model visualisation and plotting, as well as exploring and understanding model diagnostics.—Classes will comprises of a mixture of lectures and practicals designed to either build required skills for future modules or to perform a family of analyses that is frequently encountered in the biological literature. Course content is as follows

Monday 4th Course introduction; techniques for data manipulation, aggregation, and visualisation; introduction to linear regression. Packages: {tidyr}, {dplyr}, {ggplot2}

Tuesday 5th Linear models (diagnostics, collinearity, scaling, plotting fitted values); fitting and interpreting interaction terms; model selection and simplication; general linear models and ANCOVA. Packages: {stats}, {car}

Wednesday 6th Generalized linear models (logistic and Poisson regression); predicting using model objects and visualizing model fits. Packages: {broom}, {visreg}, {ggplot2}

Thursday 7th Mixed effects models in theory and practice; visualising fixed and random effects. Packages: {lme4}, {broom}, {ggplot2}, {sjPlot}

Friday 8th Fitting nonlinear functions (polynomial & mechanistic models); brief introduction to more advanced topics & combining methods (e.g., generalised linear mixed effects, nonlinear mixed effects, and zero-inflated and zero-altered models). Packages: {nlsTools}

Please email any inquiries to oliverhooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Other up-coming courses are as follows

1. November 6th - 10th 2017 LANDSCAPE GENETIC DATA ANALYSIS USING R #LNDG Margam Discovery Centre, Wales, Prof. Rodney Dyer http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg02/ 2. November 20th - 25th 2017 APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS #ABME SCENE, Scotland, Dr. Matt Denwood http://www.prstatistics.com/course/applied-bayesian-modelling-ecologists-epidemiologists-abme03/ 3. November 27th - December 1st 2017 INTRODUCTION TO PYTHON FOR BIOLOGISTS #IPYB Margam Discovery Centre, Wales, Dr. Martin Jones http://www.prinformatics.com/course/-introduction-to-python-for-biologists-ipyb04/ ——

4. December 4th - 8th 2017 ADVANCING IN STATISTICAL MODELLING USING R #ADVR Margam Discovery Centre, Wales, Dr. Luc Bussiere, Dr. Tom Houslay, Dr. Ane Timenes Laugen,

— / —

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 NicheModellingUsingR Mar12-16

Niche modelling using R (ENMR02)

https://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr02/ 12th March 2018 - 16th March 2018

Course Overview: The course will cover the base theory of ecological niche modelling and its main methodologies. By the end of this 5-day practical course, attendees will have the capacity to perform ecological niche models and understand their results, as well as to choose and apply the correct methodology depending on the aim of their type of study and data. Ecological niche, species distribution, habitat distribution, or climatic envelope models are different names for similar mechanistic or correlative models, empirical or mathematical approaches to the ecological niche of a species, where different types of ecogeographical variables (environmental, topographical, human) are related with a species physiological data or geographical locations, in order to identify the factors limiting and defining the species'Â niche. ENMs have become popular due to the need for efficiency in the design and implementation of conservation management. The course will be mainly practical, with some theoretical lectures. All modelling processes and calculations will be performed with R, the free software environment for statistical computing and graphics (http://www.r-project.org/). Attendees will learn to use modelling algorithms like Maxent, Bioclim, Domain, and logistic regressions, and R packages for computing ENMs like Dismo and Biomod2. Also, students will learn to compare different ecological niche models using the Ecospat package.

Monday 12th 'V Classes from 09:00 to 17:00 Elementary concepts on Ecological Niche Modelling Module 1: Introduction to ENM theory. Definition of ecological niche model; introduction to species ecological niche theory, types of ecological niches, types of ENM, diagram BAM, ENMs as approximations to species'Â niches. Module 2: Problems and limitations on ENM. Assumptions and uncertainties, equilibrium concept, niche conservatism, autocorrelation and intensity, sample size, correlation of environmental variables, size and form of study area, thresholds, model validation, model projections. Module 3: Methods on ENM. Mechanistic and correlative models. Overlap Analysis, Biomod, Domain, Habitat, Distance of Mahalanobis, ENFA, GARP, Maxent, Logistic regression, Generalised Linear Models, Generalised Additive Models, Generalised Boosted Regression Models, Random Forest, Support Vector Machines, Artificial Neural Network. Module 4: Conceptual and practice steps to calculate ENM. How to make an ENM step-by-step. Module 5: Applications of ENM. Ecological niche identification, Identification of contact zones, Integration with genetical data, Species expansions, Species invasions, Dispersion hypotheses, Species conservation status, Prediction of future conservation problems, Projection to future and past climate change scenarios, Modelling past species, Modelling species richness, Road-kills, Diseases, Windmills, Location of protected areas.

Tuesday 13th 'V Classes from 09:00 to 17:00 Prepare environmental variables and run ecological niche models with dismo package. Module 6: Preparing variables. Choosing environmental data sources, Downloading variables, Clipping variables, Aggregating variables, Checking pixel size, Checking raster limits, Checking NoData, Correlating variables. Module 7: Dismo practice. How to run an ENM using the R package dismo.

Wednesday 14th 'V Classes from 09:00 to 17:00 Run ecological niche models with Biomod2 package and Maxent. Module 8: Biomod2 practice. How to run an ENM using the R package Biomod2. Module 9: Maxent practice. How to run an ENM using the R packages dismo and Biomod2 as well as Maxent software.

Thursday 15th 'V Classes from 09:00 to 17:00 Compare ecological niche models with ecospat. Module 10: Ecospat practice. Compare statistically two different ecological niche models using the R package Ecospat. Module 11: Students'Â talks. Attendees will have the opportunity to present their own data and analyse which is the best way to successfully obtain an ENM.

Friday 16th 'V Classes from 09:00 to 16:00 Run ecological niche models with your own data. Module 12: Final practical. In this practical, the students will run ENM with their own data or with a new dataset, applying all the methods showed during the previous days.

1. November 27th 'V December 1st 2017 INTRODUCTION TO PYTHON FOR BIOLOGISTS #IPYB Margam Discovery Centre, Wales, Dr. Martin Jones http://www.prinformatics.com/course/-introduction-to-python-for-biologists-ipyb04/ —– 2. December 4th - 8th 2017 ADVANCING IN STATISTICAL MODELLING USING R #ADVR

— / —

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 PhylogeographyNicheEvolution Apr30-May4

Dear Brian can you please post the following to course and workshops page please. A considerable portion of this course is devoted to phylogeography, niche evolution etc so very relevant to an evolutionary audience.

Thank you in advance, Oliver

Quantitative geographic ecology, modelling genomes, niches, and communities (QGER01)

https://www.prstatistics.com/course/quantitative-geographic-ecology-using-r-modelling-genomes-niches-and-communities-qger01/ 30th April 2018 - 4th May 2018

Dr. Dan Warren and Dr. Matt Fitzpatrick

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 - 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

Monday 30th Organisation and Introductions. Spatial data in R. Point data, vector data, and raster data. GBIF, the Global Biodiversity Information Facility. Interacting with Google Maps. Working with raster and vector data.

Tuesday 1st Ecological vs. historical biogeography. ENM / SDM concepts and assumptions Dismo Conceptual and practical issues with ecological inferences from distribution data. Simulating species occurrence data.

Wednesday 2nd Testing ecological and evolutionary hypotheses via Monte Carlo methods. ENMTools R package. Ecospat Questions of taxonomic scale. Incorporating niche conservatism into the modelling process.

Thursday 3rd Introduction to community-level modeling Background on GDM and GF Review of data formats and data preparation - Community-level data - Genomic data Model fitting and testing Interpreting model results, including turnover functions Model testing / validation / variable selection

Friday 4th Predictions & Applications of GDM / GF Transforming grids Visualizing spatial variation in community / genetic composition - Dissimilarity between locations - Projecting patterns under climate change

Please send enquiries to oliverhooker@prstaititcs.com

Other upcoming courses

1. November 6th - 10th 2017 LANDSCAPE GENETIC DATA ANALYSIS USING R #LNDG Margam Discovery Centre, Wales, Prof. Rodney Dyer http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg02/ 2. November 20th - 25th 2017 APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS #ABME SCENE, Scotland, Dr. Matt Denwood http://www.prstatistics.com/course/applied-bayesian-modelling-ecologists-epidemiologists-abme03/ 3. November 27th - December 1st 2017 INTRODUCTION TO PYTHON FOR BIOLOGISTS #IPYB Margam Discovery Centre, Wales, Dr. Martin Jones http://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb04/ —— 4. December 4th - 8th 2017

— / —

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

---

Weggis Switzerland AdaptationBioinformatics Feb11-17

Reminder: Winter School of Bioinformatics for Adaptation Genomics (B@G4 2018).

Registration closes 19.11.2017

For more information: http://www.adaptation.ethz.ch/education/bag-winter-school-2018.html Winter School - Bioinformatics for Adaptation Genomics (B@G4 2018)

DATE: February 11-17, 2018

Given the positive experiences of the previous three editions of the B@G Winter School that received enthusiastic feedback from both the instructors and the students, we are happy to announce that the School will take place again with a similar program and format.

AIMS AND OBJECTIVES The application of next-generation sequencing (NGS) technologies to non-model organisms is now well-established and has unlocked new frontiers for research on adaptation genomics. Despite recent technological developments enabling an increasing number of projects to use genome-scale data, the analysis of such complex data sets still raises substantial hurdles for researchers with primarily a biological background. Bioinformatic pipelines offer an invaluable resource to process genomic data, but their underlying rationale often remains hard to understand, which poses significant challenges for their rigorous use and for the accurate interpretation of the results. The B@G Winter School provides an opportunity for researchers to penetrate the 'black box' behind the complex bioinformatics approaches available for investigating adaptation genomics throughout the analytical pipeline; from the programs and assumptions necessary to produce a high-quality SNP dataset to the in-depth interpretation of methods designed to address key evolutionary questions. B@G teachers are established scientists with a primary role in the development of widely used bioinformatic software, and will provide insights into the foundations of the algorithms and suggest best practice in experimental design and analysis.

AUDIENCE The School is primarily aimed at evolutionary biologists and bioinformaticians who want to gain deeper knowledge on state-of-the-art methods used to detect evolutionary patterns from genome-wide nucleotide data. Applications from early career researchers (motivated Master students, PhD and post-doctoral level), as well as faculty with a background in ecology, genetics, or bioinformatics, will be considered. The workshop is particularly aimed at candidates with experience of the Unix environment and with preliminary knowledge on analytical pipelines for genomic data. Participants will be requested to bring their own laptop with which to connect to a server for the practical sessions. Classes will include lectures on the theoretical background of the programs and practical demonstrations given by the instructor followed by hands-on exercises performed by the participants under guided supervision.

VENUE The school will be hosted at the Alexander & Gerbi Hotel in Weggis, Switzerland (http://www.alexander-gerbi.ch).

COST Total fee for participants is 750.- CHF. This includes tuition and accommodation in double rooms with full board (Breakfast, Lunch, Dinner and coffee breaks) at the Alexander & Gerbi Hotel during the workshop. A limited number of single rooms may be available upon request at an additional fee of 300.- CHF.

REGISTRATION The workshop will be limited to 30 participants. We ask that all interested participants submit a cover letter (1 page max) detailing their research interests, their level of bioinformatics experience, and motivation for attending the workshop, as well as their CV (2 pages max) to BioinfAdapt@env.ethz.ch by November 19th 2017. Participants will be notified of the outcome of the selection process by December 4th 2017.

SCHOOL LECTURERS Prof. Dr. Jonathan Puritz - University of Rhode Island, USA Website: http://www.marineevoeco.com Mr. Erik Garrison - Wellcome Trust Sanger Institute, UK Website: http://hypervolu.me/ ˜ erik/erik_garrison.html Prof. Dr. Anders Albrechtsen - Copenhagen University, Denmark Website: http://popgen.dk/albrecht/web/WelcomePage.html Prof. Dr. Daniel Wegmann - University of Fribourg, Switzerland Website: http://www.unifr.ch/biochem/index.php?id=789 Dr. Simone Tiberi - University of Zurich, Switzerland Website: https://sites.google.com/view/simonetiberi ORGANISERS Dr. Simone Fior, ETH Zurich, Switzerland (simone.fior@env.ethz.ch) Dr. Martin C. Fischer, ETH Zurich, Switzerland (martin.fischer@env.ethz.ch) Prof. Dr. Alex Widmer, ETH Zurich, Switzerland (alex.widmer@env.ethz.ch)

— / —

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

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 notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating 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.