EvolDir

January 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.

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Conferences

AsconaSwitzerland PopGenomicsFungalPathogens May7-11 AbstReminder

AsconaSwitzerland.PopGenomicsFungalPathogens.May7-11.Abstracts.Reminder

POPULATION GENOMICS OF FUNGAL AND OOMYCETE PATHOGENS OF ANIMALS AND PLANTS

7-11 May 2017

Monte Verita Conference Center, Ascona, Switzerland

Conference website: http://www.path.ethz.ch/-education/population-genomics-of-fungal-and-oomycete-diseases-of-animals-a.html

Conference email inquiries to: ascona_2017@usys.ethz.ch

CONFERENCE OVERVIEW:

The population genomics of fungal and oomycete pathogens is a rapidly growing area of research. New datasets, new sequencing methodologies and new analytical methods are enabling a deeper understanding of the evolutionary processes driving the emergence of fungal and oomycete pathogens. This conference aims to enrich our understanding of the processes driving the evolution of plant, animal and human pathogens, with an over-riding goal of identifying the genomic changes responsible for adaptation to novel hosts and environments. A secondary goal will be to determine how the relevant genes (and their underlying functions) vary along ecological/agronomic gradients associated with host specialization, including quantitative adaptation to host resistance. The conference will be oriented around genome-based approaches, including; 1) using population genomics to understand pathogen emergence and host specialization, 2) using genome-wide association studies to identify key genes and genomic regions associated with pathogen local adaptation, 3) using population genomics to understand pathogen divergence/speciation, 4) developing new analytical methods for population genomic analyses.

CONFIRMED SPEAKERS:

Daniel Croll (University of Neuchatel, Switzerland)

Barbara Dunn (Stanford University, USA)

Matthew Fisher (Imperial College London, UK)

Tatiana Giraud (CNRS-Universite Paris Sud, France)

Pierre Gladieux (INRA BGPI, France)

Michael Hood (Amherst College, USA)

Hanna Johannesson (Uppsala University, Sweden)

Sophien Kamoun (The Sainsbury Laboratory, John Innes Center, UK)

Anna-Liisa Laine (University of Helsinki, Finland)

Gianni Liti (IRCAN, France)

Bruce McDonald (ETH Zurich, Switzerland)

Joseph Spatafora (Oregon State University, USA)

Jason Stajich (University of California Riverside, USA)

John Taylor (University of California Berkeley, USA)

~30 additional speakers will be chosen from among the submitted abstracts.

VENUE:

~75 conference participants will be able stay on-site at the Monte Verita conference center. The remaining ~35 participants will be able to find accommodation in the nearby city of Ascona. All lunches and dinners will take place at the Monte Verita conference center. More details, including off-site housing options, will be provided on the conference website.

REGISTRATION:

The cost of attending this 4-day meeting will be approximately $900-1200 for each conference delegate depending on the chosen accommodations. This cost includes a $100 registration fee, all meals and lodging. Pre-registration is required (https://www.ethz.ch/content/-dam/ethz/special-interest/usys/ibz/plant-p athology-dam/documents/Ascona_2017/Application_form_for_Population_Genomics_Meeting_Ascona_May_2017.pdf). Applicants should submit a 250-word abstract for an oral and/or poster presentation. The form can be downloaded on the conference website.

Pre-registration closes on 31 December 2016.

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Austin Texas SMBE AbstractsOpen Jul2-6

SMBE 2017 | Abstracts Open

We are delighted to announce that the abstract system for the Annual Meeting of the Society for Molecular Biology and Evolution 2017 is now open! We are accepting abstracts via the official SMBE 2017 website. Just follow the link below or click here to find out more.

Taking place from 2nd - 6th July, 2017, in Austin, USA, SMBE 2017 is an opportunity to join your colleagues and present your work internationally to world leaders and experts within the industry.

Registration for SMBE 2017 will open during December, please keep an eye on our registration page for updates.

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SMBE 2017 Website < http://ch1-marketing.mci-group.com/t/112066/49707052/23983/0/ > |Registration < http://ch1-marketing.mci-group.com/-t/112066/49707052/23986/0/ > | Industry < http:/-/ch1-marketing.mci-group.com/t/112066/49707052/-23988/0/ > | Contact < http://ch1-marketing.mci-group.com/t/112066/49707052/23989/0/ >| Unsubscribe

SMBE 2017 <SMBE2017@mci-group.com>

BatonRougeLA SocietyOfSystematicBiologists Jan7-10

NOTE: The regular registration period has been extended by one day, but will be closing this Friday, Dec. 16th. After Friday, registration rates will increase and hotel rooms may not be available at the discounted rate.

Society of Systematic Biologists (SSB) Standalone Meeting January 8-10, 2017 Baton Rouge, LA

Following on the tremendous success of the 2015 Standalone Meeting in Ann Arbor, SSB is pleased to announce its next Standalone Meeting in Baton Rouge, LA, scheduled for January 8-10, 2017, and hosted by Louisiana State University. This meeting will feature a wide variety of workshops, lightning talks, as well as society-wide debates and discussions. The Society is committed to promoting the involvement of students and other early-career researchers by offering travel awards and a welcoming atmosphere. The meeting will offer many opportunities for meaningful interactions, with a maximum capacity of 300 attendees.

Meeting registration will cover attendance at all workshops, coffee breaks, talks, and debates, as well as an evening reception at the LSU Museum of Natural Science. NSF program directors will also be available to discuss the future of support for research in systematic biology.

Outstanding venues have been reserved for the meeting, including the newly renovated Hilton Capitol Center hotel and the beautiful Manship Theatre at the Shaw Center for the Arts, both in downtown Baton Rouge. These venues are in close proximity to a wide variety of excellent restaurants and cultural attractions. Attendees are strongly encouraged to book lodging as part of the group reservation at the Hilton (see below for details).

Full details, including a detailed schedule, are available on the meeting webpage: https://ssb2017.github.io/ Follow @jembrown and @systbiol on Twitter for meeting updates.

Dedicated nursing and lactation rooms will be available during the meeting.

Confirmed workshops will offer training directly from the developers of popular software tools including Arbor, Bayou, BioGeoBears, Dendropy, RevBayes, Phrapl, and TreeScaper.

Confirmed debate and discussion leaders include:

Frank Burbrink (AMNH) Scott Edwards (Harvard University) Matt Hahn (Indiana University) Mark Holder (University of Kansas) Emily Jane McTavish (University of California, Merced) Gavin Naylor (College of Charleston) Rachel Schwartz (University of Rhode Island) Anne Yoder (Duke University)

Register here:

https://www.regonline.com/registration/checkin.aspx?MethodId=3D0&EventSessionId=-cf93b99f12c94b34a0ed4d8a5a433db0&EventId=1884549 Individuals registering first will be given preference for available spaces in workshops and lightning talk sessions.

Hotel rooms are available at a special group rate and can be booked here:

http://www.hilton.com/en/hi/groups/personalized/-B/BTRCPHF-SSB-20170105/index.jhtml SSB has recently expanded its membership options and members can register for the meeting at a reduced rate. Go here to become an SSB member:

http://www.oxfordjournals.org/our_journals/sysbio/-access_purchase/price_list.html "jembrown@lsu.edu" <jembrown@lsu.edu>

Blossin InsectImmunity Aug28-Sep1

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We would like to announce the Ecological Immunology Workshop 2017 on:

Insect immunity: genomics, microbiome, applications

28th August to 1st September 2017 in Blossin (close to Berlin), Germany.

This workshop will bring together researchers interested in ecological immunology with a focus on insects, and with diverse scientific backgrounds ranging from molecular biology to ecology. The hallmark of these workshops, started in 2001, is the open atmosphere fostering free exchange by keeping it an affordable, small conference (100 participants). The format consists of eighteen invited speakers, contributed talks and a dedicated poster.

Long breaks provide plenty of opportunity for informal exchange. Past workshops have initiated new collaborations and ideas focusing on frontier research that has not been published. The premises are basic but in a beautiful location conducive to the success of the meeting. We will be located at a lakeside, which at this time of the year offers great swimming and canoeing, and a small private bar at the harbour [http://www.blossin.de] . Program and invited speakers

Genomics and functional work in the wild

Seth Barribeau, University of Liverpool Nicole Gerardo, Emory University Brian Lazzaro, Cornell University Hinrich Schulenburg, University of Kiel Ann Tate, University of Texas Lumi Viljakainen, University of Oulu Chris Wheat, University of Stockholm

Host-symbiont interactions affecting host immunity

Nichole Broderick, University of Connecticut Ewa Chrostek, MPI Infection Biology Ellen Decaesteker, University of Leuven Abdelaziz Heddi, INSA-Lyon Martin Kaltenpoth, University of Mainz David Schneider, Stanford University

Applying ecological immunology

Lena Bayer-Wilfert, University of Essex Astrid Groot, University of Amsterdam Dino McMahon, Free University Berlin Brian Weiss, Yale University Ken Wilson, University of Lancaster

Important dates Registration will open on 15th January 2016 The deadline for abstract submission of oral and poster presentations is 31st March 2017

Registration fee will include accommodation and catering (all meals)

We will announce the website with more information shortly before registration will open.

We are looking forward to welcoming you at the Ecological Immunology Workshop 2017.

Kind regards,

Organizing Committee Jens Rolff, Free University of Berlin Oliver Otti, University of Bayreuth Paul Schmid-Hempel, ETH Zurich

If you have any questions concerning the meeting please do not hesitate to e-mail us: oliver.otti@uni-bayreuth.de (program) magdalena.nagel@fu-berlin.de (travel and registration)

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web: Otti's homepage < http://www.bayceer.uni-bayreuth.de/toek1/de/mitarbeiter/mit/-mitarbeiter_detail.php?id_obj=106154 >

Oliver Otti <oliver.otti@uni-bayreuth.de> Oliver Otti <oliver.otti@uni-bayreuth.de>

Edinburgh ProtistEvolution Apr3-Apr6

Dear all,

The Protistology-UK society will be organising two sessions at the next Annual Conference 2017 of the Microbiology Society that will take place in Edinburgh from Monday 3 April to Thursday 6 April 2017: - Annual Meeting of Protistology-UK society: Intracellular infection and endosymbiosis within protists Invited speakers include Martin Embley, John Archibald, Yousef Abu Kwaik, David Bass, Eva Nowack, Jean-Michel Claverie, Chris Lowe and others. - Aquatic microbiology: New model organisms and new challenges (sponsored by the Moore Foundation) Invited speakers include John Dolan, Chris Lane, Thomas Mock, Angela Falciatore, Virginia Edgcomb, Ross Waller, Susanne Menden-Deuer, Alexandra Z. Worden and many others.

In addition, there are going to be numerous other sessions that might be of interest of researchers in the evolutionary field including but not restricted to: > Microbial genomics: whole population to single cell > Evolution and virus populations > Anaerobes in infection

More information about the meeting and abstract submission: http://www.microbiologysociety.org/events/-annual-conferences/index.cfm/annual-conference-2017 The submission deadline for poster and oral presentations will close at 23:59 (UK time) on Monday 12 December 2016. Abstracts can be submitted online through the Society's website, where you will find full details of the conference programme and guidelines for submission. Decisions on successful abstracts will be made in early 2017.

The 2017 Conference will be the first time that the Society awards four sets of poster prizes. The first set will be awarded by the Editors of our journals, the second chosen by members of the Early Career Microbiologists' Forum, while our Principle Investigators will select the third. The fourth "People's Choice" award will be decided upon by delegates at the event.

To support attendance, the Society offers grants for delegates at different stages of their careers. For full details, please see our dedicated grants page: http://www.microbiologysociety.org/grants-prizes/index.cfm We look forward to receiving your abstracts (only a week to go), and hope to see you in Edinburgh.

Kind regards,

Anastasios Tsaousis

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Orcid: http://orcid.org/0000-0002-5424-1905 tsaousis.anastasios@gmail.com

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Edinburgh WildlifeForensics Jun5-9

Dear colleagues,

The Society for Wildlife Forensic Science is an international organisation promoting the use of forensics in law enforcement across wildlife crime. I'm writing to draw your attention to the Society's 2017 meeting that will be held from 5-9th June in Edinburgh, UK, which may be of particular interest to Evoldir subscribers working on population genetics of species involved in the illegal wildlife trade.

Forensics has been receiving increasing attention within the wildlife law enforcement community, with inclusion in numerous high level national and intergovernmental strategies, as well as the development of new laboratory facilities around the world.

The meeting will bring together the world's leading wildlife forensic scientists and includes a special 1-day International Symposium where we will bring together Policy, Enforcement and Scientific experts to discuss the use of forensics in relation to transnational crime, IUU fishing, illegal timer trade and national wildlife crime. This event will be opened by the Scottish government Cabinet Secretary for Environment, Climate Change and Land Reform, Ms Roseanna Cunningham, with a keynote address from the Secretary General of CITES, Mr John Scanlon.

Please visit the website for more information and to register your attendance (https://www.wildlifeforensicscience.org/2017-meeting/), discounts apply for early registration (until 31st January 2017). Spread the word to colleagues you think may be interested in this meeting.

Many thanks,

Lucy

Dr Lucy Webster Wildlife DNA Forensics - Diagnostics, Wildlife & Molecular Biology Section Science and Advice for Scottish Agriculture (SASA) Roddinglaw Road, Edinburgh, EH12 9FJ, UK

[Year of Pulses]< http://www.fao.org/pulses-2016/en/ >

SASA is a Division of the Scottish Government Agriculture, Food and Rural Communities Directorate

Disclaimer

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Groningen ESEB BiologicalClocks Aug20-25

ESEB Symposium on "EVOLUTIONARY SIGNIFICANCE OF BIOLOGICAL CLOCKS"

Dear Colleagues,

we would like to invite you to attend or contribute to the ESEB symposium

[S6] Evolutionary significance of biological clocks at the 16th Congress of the European Society for Evolutionary Biology (ESEB), in Groningen, Netherlands, 20-25 August 2017.

INVITED SPEAKERS: Steven Reppert (University of Massachusetts) Takashi Yoshimura (Nagoya University)

SYMPOSIUM DESCRIPTION: Biological clocks are found in almost all organisms and have evolved independently many times, suggesting they must convey considerable adaptive value. The adaptive value may lie in (1) optimizing energy expenditure in a world full of regular environmental changes, such as seasons, night and day and tides, (2) synchronizing reproduction within populations or with suitable environmental conditions or (3) escaping predation. In surprisingly few cases the adaptive value of biological clocks has been demonstrated experimentally. However, there are a number of examples where local adaptation of biological clocks to environmental clines (e.g. latitudinal temperature clines) gives indirect evidence for the adaptive value of biological clocks. These cases often also allow to study the evolutionary forces shaping biological clocks and their target clock molecules. Our symposium will be open to all evolutionary aspects of biological timekeeping - from seasonal over diel to tidal and lunar rhythms. We would like to showcase demonstrations of adaptive values of biological clocks, but also offer a platform for all other topics at the intersection of evolution and biological timekeeping. We aim to initiate discussion among evolutionary biologists and chronobiologists, in order increase mutual understanding and to foster the thinking about biological clocks in evolutionary terms.

Organizers: Roelof Hut (University of Groningen) Tobias Kaiser (MPI Evolutionary Biology, Plon)

The deadline for abstract submission is 10 January 2017.

Abstracts can be submitted online here: http://www.eseb2017.nl/call-for-abstracts/ Looking forward to seeing you in Groningen! Roelof and Tobias

Dr. Tobias Kaiser

Max Planck Research Group “Biological Clocks” Max Planck Institute for Evolutionary Biology August-Thienemann-Str. 2 | 24306 Plon | Germany Phone +49-4522-763-224 Homepage

Tobias Kaiser <kaiser@evolbio.mpg.de>

Groningen ESEB CoevolAntagonisticEcoInteractions Aug20-25

ESEB Symposium on “ Coevolution in antagonistic ecological interactions ”

Dear Colleagues,

Please be invited to the ESEB symposium

[S32] Coevolution in antagonistic ecological interactions at the 16th Congress of the European Society for Evolutionary Biology in Groningen, Netherlands, 20-25 August 2017, http://www.eseb2017.nl/ . INVITED SPEAKERS: Minus van Baalen (École Normale Supérieure, Paris) Candace Low (San Francisco State University) ABSTRACT SUBMISSION DEADLINE: The deadline for abstract submission is 10 January 2017. Submit abstracts online at http://www.eseb2017.nl/call-for-abstracts/ SYMPOSIUM DESCRIPTION: Exploitation strategies are at the core of consumer-resource interactions: herbivores exploit plants, predators exploit prey, and parasites exploit their hosts. Most theory on the evolution of exploitation strategies has concentrated on host-parasite interactions, modelling for example the virulence-transmission trade-off or within-host competition between strains with different exploitation strategies. However, this theory has rarely been applied to other antagonistic interactions, such as plant-herbivore or predator-prey interactions.

Recently, empirical work has made important progress in identifying exploitation strategies outside host-parasite systems. Herbivores, for example, not only express resistance to plant defence, but have now been shown to exploit their host through suppression of defence in many systems. Within a community context, these exploitation strategies have profoundly different consequences: resistance affects competition with other herbivores and apparent competition through natural enemies, but suppression and induction of plant defences directly affect food quality for others, such as kin, competitors and even natural enemies. Given that suppression of plant defences also benefits other community members, how could this exploitation strategy evolve? This symposium aims to bring together empiricists and theoreticians working on antagonistic coevolution in parasite-host, predator-prey and plant-herbivore systems, addressing the evolution of exploitation strategies in antagonistic ecological interactions.

SYMPOSIUM ORGANIZERS: Bram Knegt (University of Amsterdam) Felipe Lemos (University of Amsterdam, Federal University of Viçosa)

Looking forward to seeing you in Groningen!

Bram and Felipe

bramknegt@gmail.com

Groningen ESEB CoevolutionHostsMicrobiome Aug20-25

Dear All,

Abstract submission is open for our symposium: "[S22] Coevolution of hosts and their microbiome" planned for the *European Society for Evolutionary Biology meeting in Groningen, Netherlands, 20-25th August 2017.*

Deadline for abstract submission : 10th January 2017.

http://www.eseb2017.nl/call-for-abstracts/abstract-guidelines-/ Abstract:

The evolution of life-history traits in plants and animals has taken place in the midst of complex microbial communities. Biology is undergoing a fundamental reshaping where the phenotypic expression of individuals needs to be considered as the combined expression of the host and its associated microbial genomes, defined as the "holobiont" (i.e. the host and its microbiota). These concepts have wide ranging implications and have led to the realization that multicellular organisms coevolve with their microbial symbionts. Although host-microbe interactions can be understood by ecological processes, much less is known about the significance of evolutionary and eco-evolutionary processes. Given its complex structure, understanding the specific roles, adaptability, and functions provided by the microbiome is a new scientific frontier. Recent developments in molecular and statistical techniques have given holobiont studies new impetus by allowing researchers to address novel questions. We aim to discuss theoretical concepts and empirical evidences on the role of the microbiota in holobiont evolution. Specifically: 1) How do microbiota shape the holobiont phenotypic traits and their plasticity? 2) Do we have evidence for coevolutionary processes shaping the evolution of holobionts? 3) How can selection shape the evolution of the collective genomes of a holobiont (the "hologenome")?

Invited speakers: Seth Bordenstein, Nancy Moran, Philippe Vandenkoornhuys

Organizers:

Antton Alberdi, University of Copenhagen

Philipp Heeb, University of Toulouse-CNRS

Alexandre Jousset, Utrecht University

Morten Limborg University of Copenhagen

Irene B. Tieleman University of Groningen

Friman Ville, University of York

Zhong Wei, Nanjing Agricultural University

Philipp Heeb <philipp.heeb@univ-tlse3.fr>

Groningen ESEB EcoEvoDynamics Aug20-25

Dear Colleagues,

We are excited to invite you to submit abstracts and attend our upcoming symposium on

"Eco-evolutionary dynamics"

which will be part of the 2017 Congress of the European Society for Evolutionary Biology (ESEB). The conference will be taking place from August 20th - August 25th, 2017 in Groningen, the Netherlands. http://www.eseb2017.nl/home/ We are looking forward to many exciting contributions and to a stimulating discussion with you!

The deadline for ABSTRACT SUBMISSION is January 10, 2017.

To submit abstracts online, please go to: http://www.eseb2017.nl/call-for-abstracts/ Invited speakers:

Jonathan Pruitt (UC Santa Barbara)

Jen Schweitzer (University of Tennessee)

Isabel Smallegange (University of Amsterdam)

Andrew Hendry (McGill University)

Symposium description

[S24] Eco-evolutionary dynamics

In recent years, the scientific community has embraced the fact that evolutionary change can occur at ecological time scales and thereby interact with ongoing ecological dynamics. While theoreticians are exploring new ways to simultaneously account for ecological and evolutionary dynamics (e.g. demographic models, fast-slow dynamics), empiricists are investigating the drivers of eco-evolutionary feedbacks (e.g. environmental variation, evolutionary history, phenotypic plasticity, and community structure). To advance this "newest synthesis", we bring together theoreticians and empiricists focusing on the eco-evolutionary dynamics of biological interactions across three levels of biological organization: 1) interactions among coexisting individuals with alternative life-history strategies, including personalities and tactics; 2) interspecific interactions, including host-parasite, prey-predator and symbiotic interactions; and 3) interactions between phenotypic variation and community or ecosystem characteristics. We invite contributions on eco-(co)evolutionary dynamics providing mechanistic, empirical and theoretical insights into eco-evolutionary feedback loops. In this way, the symposium will aim to advance conceptual understanding of eco-evolutionary dynamics in coevolution, speciation and life-history evolution. In addition to the invited speakers (Jen Schweitzer and Jonathan Pruitt), we have also invited Isabel Smallegange and Andrew Hendry to contribute to the symposium.

We hope to see you in Groningen next summer!

Best wishes from the organizers,

Franziska Brunner, University of Liverpool

Jacques Deere, University of Amsterdam

Martijn Egas, University of Amsterdam

Christophe Eizaguirre, Queen Mary University of London

Joost Raeymaekers, Centre for Biodiversity Dynamics, Norwegian University of Science and Technology

If you have any further questions, please don't hesitate to contact

Martijn Egas (egas@uva.nl) or Franziska Brunner (franziska.brunner@liverpool.ac.uk)

–

Dr Franziska Brunner PDRA

Insitute of Integrative Biology University of Liverpool Biosciences Building, Crown Street L69 7ZB Liverpool

Franziska.Brunner@liverpool.ac.uk https://fsbrunner.wordpress.com Franziska Brunner <Franziska.Brunner@liverpool.ac.uk>

Groningen ESEB EvolutionaryNetworks Aug20-25

Abstract submission is open for our symposium: "*S3: **Network-based approaches in evolutionary biology and medicine*" planned for the *European Society for Evolutionary Biology meeting in Groningen, Netherlands, 20-25th August, 2017. *

http://www.eseb2017.nl/call-for-abstracts/abstract-guidelines-/ *Symposium information*: Network theory, with a long history in mathematics and computer science, is starting to play an exciting role in evolutionary biology across multiple levels of biological organization, from cellular to ecological systems. Relevant and timely examples include: the study of diseases as perturbations in complex intracellular networks rather than single-gene abnormalities (Barabasi 2011), the spatial and functional interactions of microbial communities over time (Baldassano & Bassett, 2016), epidemic outbreaks in animal networks (Shrestha 2015, Lofgren 2014), and dynamic interactions between large-scale neural circuits (Shi Gu, 2015, Bassett 2011), to name only a few. This symposium will bring together scientists working at the interface of network science and evolutionary biology with two primary aims: (1) to highlight the empirical and theoretical advances made by applying network topology and dynamics theory to biological data and evolutionary questions, and (2) to discuss the design of new evolutionary network models and the integration of network theory with classic evolutionary models to answer fundamental questions in biology. As methodologies evolve, greater scientific interaction at the interface of network theory and biological systems will be essential for predicting temporal, spatially embedded, multi-scale networked evolutionary systems and establishing an integrative approach to evolutionary population dynamics and disease.

Organizers: Oana Carja, Nicole Creanza

Invited speakers: Danielle Bassett, Laura Hindersin

Please contact Oana Carja (ocarja@sas.upenn.edu) with further questions.

oana.carja@gmail.com

Groningen ESEB ExptEvolution Aug20-25

Dear Colleagues, We would like to invite you to symposium [S15] "Experimental evolution in complex environments" that will take place at the 16th Congress of the European Society for Evolutionary Biology (ESEB), in Groningen, Netherlands, 20-25 August 2017. Organisms live in complex communities in which they are influenced by the social connections to their peers, which shape their environment. Hence adaptation to an environment is highly influenced by the abiotic environment as well as the social interactions with community members. Experimental evolution provides a superb approach for studying how social as well as abiotic environmental interactions affect the adaptation to novel and heterogeneous environments. In addition, it aids our understanding of the intricate connection between the abiotic environment, the individual organisms and their communities that inhabit it. Importantly, the community structure significantly influences the evolution of social interactions that could resolve in cooperation, mutualistic division of labor or competition and conflict. Recent advances in experimental evolution revolutionized our understanding of the principles underlying population dynamics in heterogeneous environments. The aim of this symposium is to bring together empirical and theoretical contributions that aim to understand the impact of the environment-mediated selective forces driving the evolution of microbes and other model systems in the laboratory and under natural settings. Invited speakers: Michael Brockhurst (University of York), Ivana Gudelj (University of Exeter); Organizers: Akos Kovacs (Technical University of Denmark), Marjon de Vos (Wageningen University). The deadline for abstract submission is 10 January 2017. More information can be found at http://bit.ly/2ge3LOo .We look forward to receiving your intriguing story on this topic and to welcoming you at the conference and our symposium. Marjon de Vos and Akos Kovacs

Akos T Kovacs <akos.t.kovacs@gmail.com>

Groningen ESEB FitnessInSocialEnvironments Aug20-25

Dear colleagues,

We would like to invite contributions to our symposium at ESEB 2017: “Fitness and evolution in a social environment: from theory to reality”

at the 16th Congress of the European Society for Evolutionary Biology to be held in Groningen, The Netherlands 20-25 August 2017.

http://www.eseb2017.nl/ http://www.eseb2017.nl/-sub/s9-fitness-and-evolution-in-a-socia/ Symposium Summary

Summary: An individual’s fitness will be shaped by multiple aspects of social interactions, including effects of competitive interactions, parental care and parent-offspring conflict, cooperative breeding and inbreeding. Because variation in fitness is the raw ingredient that drives natural selection and consequent evolution, how best to measure it in social environments poses a critical challenge for evolutionary biology. This challenge has been approached differently by different fields. Social evolution theory has well-developed models of inclusive fitness, but these often assume simplified genetic underpinnings. Recent advances in quantitative genetics have explored indirect genetic effects of con-specifics on phenotypic diversity, but the implications of variation in inclusive fitness for evolutionary dynamics are unclear. Analyses of life-history trait variation reveal different selection pressures if fitness is assessed by contributions across multiple generations, again with complex implications. Wish this symposium we hope to encourage integrated conceptual and empirical means of estimating fitness that bring together currently disparate subfields.

The symposium will showcase recent advances in understanding variation in fitness, and resulting evolution, in social environments. Specifically we aim to: (1) stimulate discussion and communication between theoreticians and empiricists working on a diversity of systems; (2) evaluate alternative methods for measuring fitness; and (3) illustrate the causes and consequences of variation in fitness in social environments for evolutionary dynamics.

Invited Speakers: Piter Bijma, (Wageningen University) Florence Debarre (Centre for Interdisciplinary Research in Biology, Paris)

Organizers Loeske Kruuk (Australian National University) Jane Reid (University of Aberdeen)

We invite submissions for both oral presentations and posters. The deadline for abstract submission is 10 January 2017. http://www.eseb2017.nl/call-for-abstracts/ We hope to see you there!

Professor Loeske Kruuk Division of Evolution and Ecology Research School of Biology The Australian National University ACT 2601, Australia Phone: +61 2 6125 6931 Loeske.Kruuk@anu.edu.au www.biology.anu.edu.au/-Loeske_Kruuk loeske.kruuk@anu.edu.au

Groningen ESEB FitnessLandscapesPredictingEvolution Aug20-25

Dear evolDir community,

we would like to remind you that the deadline for abstract submission for the upcoming conference of the "European Society for Evolutionary Biology" (ESEB 2017) to be held in Groningen (Netherlands) from 20 to 25 August 2017 (for more details see http://www.eseb2017.nl/) is approaching soon (*January 10th 2017*).

In this context, we would like to invite you all to submit an abstract to our symposium on "Fitness landscapes, big data and the predictability of evolution" (http://www.eseb2017.nl/sub/s14-fitness-landscapes-big-data-an/). Abstracts can be submitted here: http://www.eseb2017.nl/call-for-abstracts/ [S14] Fitness landscapes, big data and the predictability of evolution

Evolutionary biology has become increasingly powerful in inferring past evolutionary processes from patterns in present-day genomes. However, forecasting evolution's future routes remains an exciting intellectual challenge with substantial implications for global health and species conservation. The concept of the fitness landscape has been central to recent studies of the predictability of evolution, and has inspired evolutionary biologists and mathematicians alike. Combining microbial experimental evolution with next-generation sequencing, efforts have now been made to rigorously test for the repeatability and dynamics of evolution. At the same time, theoretical studies try to provide the necessary navigational tools for exploring the terra incognita of molecular evolutionary biology. This symposium aims to identify the key issues and challenges – both methodological and theoretical - to advance our understanding of the predictability of evolution, particularly in the light of "big data". We anticipate that insights from our symposium will stimulate and direct future studies of the predictability of evolution. With next-generation sequencing on board, fitness landscapes are heading for new shores: It's now time to check whether "there be dragons"!

Organizers: Santiago Elena, Inês Fragata, Sebastian Matuszewski, Arjan de Visser

Invited speakers: Michael Lässig, Lilia Perfeito

Please feel free to contact sebastian.matuszewski[at]epfl.ch if you have any questions.

Looking forward to seeing you all in Groningen, Sebastian Matuszewski

"sebastian.matuszewski@epfl.ch"
<sebastian.matuszewski@epfl.ch>

Groningen ESEB GeneExpressionEvolution Aug20-25

Abstract submission is open for our symposium: '[S19] Evolution of gene expression regulation' planned for the *European Society for Evolutionary Biology meeting in Groningen, Netherlands, 20-25th August, 2017. *

http://www.eseb2017.nl/call-for-abstracts/abstract-guidelines-/ More than four decades have passed since it was first suggested that gene expression regulation variation could play a significant role in the phenotypic divergence between chimpanzees and humans. Ever since, there has been an impressive and fruitful effort to characterize the molecular basis of regulatory variation within and between species. However, until recently, 'regulatory variation' has been used synonymously with 'differences in mRNA levels'. In recent years, though, new high-throughput sequencing technologies have offered us a window into fundamental questions about the evolution of post-transcriptional dynamics. With the introduction of methods such as ribosome profiling (RiboSeq) and mass spectroscopy (mass-spec), we can now measure post-transcriptional regulation in a variety of different conditions. These technologies are now being used to study questions from how regulatory variation evolves within and between species. Moreover, there exist exciting avenues in applying these methods to microbial evolution experiments to study how gene expression regulation evolves during adaptation. Other examples include new methods and insights into the evolutionary role of non-coding RNAs, which have been uncovered as key regulators of gene expression at the post-transcriptional level, or the evolution of protein post-translational modifications that can influence their function, activity or stability. Together, these studies have given us unprecedented insight into the evolution of transcriptional and post-transcriptional regulation. This symposium will bring together researchers that develop and employ high-throughput, quantitative techniques to measure gene expression regulation with the goal of understanding the molecular landscape of complex phenotypes.

Organizers: Oana Carja, Joshua Plotkin, Premal Shah

Inivited speakers: Leonid Kruglyak, Judit Villen

Please contact Oana Carja (ocarja@sas.upenn.edu) with further questions.

oana.carja@gmail.com

Groningen ESEB GenomicsOfAdaptation Aug20-25

Dear All,

We would like to invite abstract submissions for our upcoming symposium on the Genomics of Adaptation that will take place as part of the 16th Congress of the European Society for Evolutionary Biology (ESEB). The conference will take place from August 20th - August 25th, 2017 in Groningen, the Netherlands.

SYMPOSIUM DESCRIPTION: Genomics of Adaptation [S16] Model organisms for life-history research are mainly studied in the lab where functional genetics is assessable. In general, however, knowledge about their eco-evolutionary dynamics, such as biotic interactions, is rare. By contrast, in organisms for which the ecology and adaptation strategies in the field are well known, we typically lack the appropriate genetic tools to investigate functionality. Advances in genomics and statistics as well as investments in evolutionary model organisms are now providing access to putatively adaptive genome-wide variation within species from across the tree of life. In this symposium, we focus on integrating life-history biology, genetics and evolutionary ecology in the genomics era. We wish to (1) highlight the role of genetic architecture of complex traits, such as adaptations to biotic interactions or life-history traits; (2) contrast this to morphological traits which are generally thought to have a less complex genetic architecture; and (3) discuss the opportunities and drawbacks of specific model systems.

INVITED SPEAKERS: Josephine Pemberton, University of Cambridge (http://pemberton.bio.ed.ac.uk) Peter Tiffin, University of Minnesota (http://cbs.umn.edu/tiffin-lab/)

ABSTRACT SUBMISSION The deadline for abstract submission is January 10, 2017. For more information and to submit abstracts online, please visit: http://www.eseb2017.nl/call-for-abstracts/ We look forward to an exciting symposium and seeing you all in Groningen!

Sincerely, Ben Blackman, UC Berkeley Maaike de Jong, University of Bristol Bart Pannebakker, Wageningen University Noah Whiteman, UC Berkeley Jelle Zandveld, Wageningen University

Benjamin Blackman Department of Plant and Microbial Biology University of California, Berkeley 361 Koshland Hall Berkeley, CA 94720

Phone: 510.664.7807 E-mail: bkblackman@berkeley.edu Web: http://nature.berkeley.edu/blackmanlab "bkblackman@berkeley.edu" <bkblackman@berkeley.edu>

Groningen ESEB MutualismParasitism Aug20-25

ESEB SYMPOSIUM ON THE MUTUALIST-PARASITE CONTINUUM

Dear colleagues:

We would like to invite you to contribute to and/or attend the ESEB symposium

“ Evolution across the mutualist-parasite continuum ” [S31]

which will take place at the 16th Congress of the European Society for Evolutionary Biology (ESEB), in Groningen, The Netherlands, 20-25 August 2017.

SYMPOSIUM DESCRIPTION:

Symbioses, and other close-knit species relationships, are ubiquitous and important across all ecosystems. Such species interactions vary widely, from costly relationships which drive rapid antagonistic coevolution, to beneficial relationships which facilitate functional diversification. Rather than two extremes however, these interactions should be viewed as a continuum between mutualism and parasitism. This conceptual framework unites researchers studying host-parasite and host-mutualist interactions and explores the potential for transitions along the continuum. Our topic is timely and relevant to the ESEB community. It has broad evolutionary relevance for which many new insights have been generated in the last few years. This symposium will bring together researchers studying the evolution of parasitism and mutualism to: 1) highlight the role of these species interactions in shaping an organism's evolutionary biology; 2) emphasize the importance of linking phenotypic and state-of-the-art genomics analysis in revealing these effects; 3) bring together experimental evolution and field-based approaches in studying evolution across the continuum and 4) assess the role of ecology in shaping the evolutionary stability of these systems. Many important concepts in evolutionary biology will be covered, from coevolution, genetic diversity, virulence, and sex, to ecological networks. Our invited speakers are at the forefront of research on both sides of the continuum and use natural systems while combining genomics and experimental evolution approaches.

http://www.eseb2017.nl/sub/s31-evolution-across-the-mutualist-/ INVITED SPEAKERS:

Hinrich Schulenberg (CAU Kiel, D)

2nd speaker TBA

ORGANIZERS:

Ana Duarte (University of Exeter, UK)

Francisco Encinas-Viso (CSIRO, AU)

Ellie Harrison (University of York, UK)

Aniek Ivens (The Rockefeller University, USA / Vrije Universiteit Amsterdam, NL)

Kayla King (University of Oxford, UK)

We invite submissions for oral and/or poster contributions; we are interested in both empirical and theoretical work covering the ecology and evolution of species interactions along the parasitism-mutualism continuum.

The deadline for abstract submission is 10 January 2017.

http://www.eseb2017.nl/call-for-abstracts/ We are very much looking forward to seeing you in Groningen!

Ana, Fran, Ellie, Kayla and Aniek

Aniek Ivens, PhD Laboratory of Social Evolution and Behavior The Rockefeller University New York, NY (t) +1-212-327-7852 (e) aivens@rockefeller.edu (w) www.aniek.nyc Aniek Ivens <aivens@mail.rockefeller.edu>

Groningen ESEB NonGeneticInheritance Aug20-25

Dear Colleagues:

We are pleased to invite you to submit abstracts and attend the ESEB symposium

"Evolutionary implications of transposable elements, epigenetics, and non-genetic inheritance" [S20]

that will take place at the 16th Congress of the European Society for Evolutionary Biology in Groningen, The Netherlands, 20-25th of August 2017.

INVITED SPEAKERS: Prof. Brandon Gaut (University of California, USA) Prof. Tobias Uller (Lund University, Sweden)

SYMPOSIUM DESCRIPTION: It is now well known that rapid evolution and adaptation to new environments is not solely driven by variation at chromosomal gene loci, but that it is also influenced by various cytonuclear factors and by non-genetic inheritance. Epigenetic modifications and cytoplasmic elements can directly affect morphological, physiological and behavioural phenotypic variation across generations. Also, transposable elements that are ubiquitous sequences in virtually all genomes may have a strong impact on host gene regulation, which could be mediated by epigenetic modifications. The interaction between transposable elements, epigenetics and the environment may considerably increase the degree of phenotypic variation in natural populations, thus allowing for rapid local adaptation. Yet, the mechanisms underlying non-genetic inheritance and the effects of epigenetic modifications by transposable elements remain unclear. This symposium will bring together theoreticians and empiricists who are interested in the interplay of environmental factors, transposable elements, cytoplasmic components and transgenerational epigenetic changes. The aim is to better understand the nature of transposable elements and non-genetic inheritance and their impact on evolutionary dynamics. http://www.eseb2017.nl/sub/s20-evolutionary-implications-of-tra/ SYMPOSIUM ORGANIZERS: Josefa Gonzalez (Institute of Evolutionary Biology, CSIC-UPF, Spain) Willian Silva (Uppsala University, Sweden) Foteini Spagopoulou (Uppsala University, Sweden) Cristina Vieira (University of Lyon, France)

We would like to invite abstract submissions of oral and/or poster presentations on both empirical and theoretical work focused on the interplay between environmental factors and transposable elements or heritable non-genetic components.

ABSTRACT SUBMISSION DEADLINE: The deadline for abstract submission is the 10th of January 2017. http://www.eseb2017.nl/call-for-abstracts/-abstract-guidelines-/ We are looking forward to receiving your submissions and to seeing you in Groningen!

Foteini, Willian, Cristina and Josefa

Foteini Spagopoulou PhD student at Maklakov Lab Animal Ecology Department of Ecology and Evolution Evolutionary Biology Centre Uppsala University Norbyvagen 18D SE-752 36 Uppsala Sweden

E-mail: Foteini.Spagopoulou@ebc.uu.se Office: +46 18-471 2930

Foteini Spagopoulou <foteini.spagopoulou@ebc.uu.se>

Groningen ESEB ParasiteEvolution Aug20-25

ESEB Symposium on “PARASITE EVOLUTION IN RESPONSE TO TREATMENT”

Dear Colleagues,

We would like to invite you to attend or contribute to the ESEB symposium [S1] Parasite evolution in response to treatment at the 16th Congress of the European Society for Evolutionary Biology in Groningen, The Netherlands, 20-25 August 2017.

INVITED SPEAKERS: Pleuni Pennings (San Francisco State University) Sebastian Bonhoeffer (ETH Zürich)

SYMPOSIUM DESCRIPTION: Parasites evolve in response to our attempts to control them. Drug resistance, vaccine-driven strain replacement, and parasite life-history shifts are all examples of evolutionary mechanisms by which the benefits of our interventions are reduced. Understanding the drivers and limits of parasite evolution in response to interventions is essential for predicting evolutionary consequences in advance and defining best practices for disease management. This symposium will highlight work that seeks to generate this understanding and offer new insight for the management of infectious diseases. In particular, we welcome submissions of novel theory and empirical work investigating the coupling between epidemiological and evolutionary dynamics, the consequences of different spatio-temporal treatment strategies, and the short- and long-term evolution of parasite traits.

SYMPOSIUM ORGANIZERS: Sébastien Lion (CÃFÃ, Montpellier, France) Nicole Mideo (University of Toronto)

ABSTRACT SUBMISSION DEADLINE: The deadline for abstract submission is 10 January 2017. Submit abstracts online at http://www.eseb2017.nl/call-for-abstracts/ Looking forward to seeing you in Groningen!

Seb & Nicole

Nicole Mideo Assistant Professor Department of Ecology & Evolutionary Biology University of Toronto 25 Willcocks St. Toronto, ON M5S 3B2

Tel: 416 978 1316

“nicole.mideo@utoronto.ca”
<nicole.mideo@utoronto.ca>

Groningen ESEB PhyloInferenceGenomicEra Aug20-25

Dear all,

We are excited to invite you to submit your abstract and attend the symposium:

“Phylogenetics in the Genomic Era”

to be held at the European Society for Evolutionary Biology meeting in Groningen, The Netherlands (20-25th August 2017).

http://www.eseb2017.nl/ http://www.eseb2017.nl/-sub/s30-phylogenetics-in-the-genomic-er/ INVITED SPEAKERS: Scott Edwards (Harvard University, USA) Ziheng Yang (University College London, UK)

ABSTRACT: Accurate inference of species relationships is crucial to address fundamental questions in evolutionary biology. Empiricists have greatly benefitted from the continual ease of generating sequence data for phylogenetic inference and can now employ genome-scale datasets to infer the evolutionary history of clades across the tree of life. However, the availability of large phylogenomic datasets are not a panacea for all phylogenetic issues and these large datasets often present new challenges. In particular, individual genetic markers can have discordant phylogenetic histories due to processes such as incomplete lineage sorting, introgression and selection, potentially clouding the inference of organismal relationships. Most contemporary species tree estimation methods aim to model observed incongruence using the multi-species coalescent but these approaches often assume incomplete lineage sorting as the single source of discord and are computationally exhaustive or rely on the precision of individual gene trees. The development of novel approaches to account for sources of phylogenetic incongruence therefore remains a thriving area of research. Given the vigorous state of the field, it is thus timely to discuss recent advances and remaining challenges of species tree estimation in a symposium where we invite both theoreticians and empiricists.

ORGANIZERS: Mozes Blom (Swedish Museum of Natural History, Sweden) Matthew Fujita (University of Texas at Arlington, USA)

ABSTRACT SUBMISSION DEADLINE: The deadline for abstract submission is the 10th of January 2017. http://www.eseb2017.nl/call-for-abstracts/-abstract-guidelines-/ Please contact Mozes Blom (mozes.blom@gmail.com) if you have any questions!

Best,

Matt and Mozes

mozes.blom@gmail.com

Groningen ESEB RapidEvol Aug20-25

Dear Colleagues,

We extend an invitation to our upcoming ESEB 2017 [S23] symposium entitled Rapid Evolution Revisited.

The symposium will take place at the 16th Congress of the European Society for Evolutionary Biology (ESEB), in Groningen, Netherlands, 20-25 August 2017.

The deadline for abstract submission is 10 January 2017.

SYMPOSIUM DESCRIPTION: Times are changing, and our studies in evolutionary biology must change along with it. Many studies now demonstrate that natural populations can evolve at ecological timescales (i.e. across a few generations), which is particularly evident in adaptation to environmental change. At the same time, some of the best model systems to study evolution in action have demonstrated that predicting the magnitude and direction of evolution from estimates of selection is less than straightforward. The increased availability of genomic and long-term data in non-model organisms, and novel advances in statistical and technological methods, can provide new solutions to this puzzle. These advances acknowledge that our ability to predict evolution in natural populations can be improved by considering determinants of the whole phenotype (from genetic and plastic to transgenerational and epigenetic effects), and also eco-evolutionary feedback processes. Yet in many systems these novel frameworks and tools remain under-used. The goal of this symposium is to synthesize these into a more integrative framework for the study of evolution in nature; a timely topic given the pressing challenge of predicting responses to global environmental change. .

Organizers: Organizers: Swanne Gordon (University of Jyvaskyla), Andres Lopez-Sepulcre (CNRS-Universite Pierre et Marie Curie), and Katja Rasanen (Eawag, Swiss Federal Institute of Aquatic Science and Technology)

The deadline for abstract submission is 10 January 2017.

Abstracts can be submitted online here: http://-www.eseb2017.nl/call-for-abstracts/ Please join us, Swanne, Andres and Katja

Andrés López-Sepulcre <lopezsepulcre@gmail.com>

Groningen ESEB Recombination Aug20-25

We invite you to submit an Abstract to our ESEB 2017 symposium exploring the causes and consequences of variation in recombination rate in sexually reproducing organisms.

[S17] Evolutionary causes and consequences of variation in recombination rate http://www.eseb2017.nl/-sub/s17-evolutionary-causes-and-consequ/ INVITED SPEAKERS: Abraham Korol, University of Haifa, Israel. (http://evolution.haifa.ac.il/index.php/people/-203-abraham-korol-ph-d) Irene Tiemann-Boege, Johannes Kelper University, Germany. (http://-www.jku.at/biophysics/content/e54633/e97350/)

SYMPOSIUM DESCRIPTION: Recombination is paradoxical, it can create novel genetic combinations that natural selection can act on, and thus facilitate adaptation, but it can also break apart favourable combinations of alleles. In addition, recombination can play a critical role during meiosis, with recombination events regulated to ensure accurate segregation of chromosomes. Thus, tight regulation of recombination is expected, but variable rates of recombination may be favoured in different environments or contexts. While the role of recombination in the evolution of sex has been the focus of much empirical and theoretical work, investigation on how conflicting selection pressures are resolved, how recombination rate evolves, and what impact this has on evolutionary processes within sexually reproducing organisms has received less attention. Recent advances in DNA sequencing and bioinformatics has provided unprecedented opportunities to characterise variation in recombination rate. Now is a pertinent time to highlight (i) rapidly developing approaches to estimate recombination rate in the genomics era and (ii) our growing understanding of the causes and consequences of variation in recombination rates; including how recombination rate variation responds to selection, how recombination varies between individuals, sexes, populations, species and in response to the environment, and how recombination influences the processes of speciation and adaptation.

ABSTRACT SUBMISSION DEADLINE: The deadline for abstract submission is 10 January 2017. Submit abstracts online at http://www.eseb2017.nl/call-for-abstracts/ SYMPOSIUM ORGANIZERS: Susan Johnston, University of Edinburgh (https://susanejohnston.wordpress.com/) Anna Santure, University of Aukland (https://unidirectory.auckland.ac.nz/profile/a-santure) Jessica Stapley, ETH Zurich (http://jessicastapley.com/)

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 28399

“jessica.stapley@env.ethz.ch”
<jessica.stapley@env.ethz.ch>

Groningen ESEB RecombRateVariation Aug20-25

Dear all,

we are delighted to invite submissions to our symposium “S17: Evolutionary causes and consequences of variation in recombination rate” to be held at the European Society for Evolutionary Biology meeting in Groningen, Netherlands from 20-25th August, 2017.

http://www.eseb2017.nl/

http://www.eseb2017.nl/sub/s17-evolutionary-causes-and-consequ/ Abstract: Recombination is paradoxical, it can create novel genetic combinations that natural selection can act on, and thus facilitate adaptation, but it can also break apart favourable combinations of alleles. In addition, recombination can play a critical role during meiosis, with recombination events regulated to ensure accurate segregation of chromosomes. Thus, tight regulation of recombination is expected, but variable rates of recombination may be favoured in different environments or contexts. While the role of recombination in the evolution of sex has been the focus of much empirical and theoretical work, investigation on how conflicting selection pressures are resolved, how recombination rate evolves, and what impact this has on evolutionary processes within sexually reproducing organisms has received less attention. Recent advances in DNA sequencing and bioinformatics has provided unprecedented opportunities to characterise variation in recombination rate. Now is a pertinent time to highlight (i) rapidly developing approaches to estimate recombination rate in the genomics era and (ii) our growing understanding of the causes and consequences of variation in recombination rates; including how recombination rate variation responds to selection, how recombination varies between individuals, sexes, populations, species and in response to the environment, and how recombination influences the processes of speciation and adaptation.

Organizers: Philine Feulner, Susan Johnston, Anna Santure, Carole Smadja and Jessica Stapley

Invited speakers: Abraham Korol (https://scholar.google.co.il/citations?hl=3Den&user=3Dfoio3YsAAAAJ&view_op=list_works&sortby=pubdate) and Irene Tiemann-Boege (https://scholar.google.co.il/citations?user=

3DO6lGxtUAAAAJ&hl=3Den)

Please contact Anna Santure (asanture@gmail.com) if you have any questions!

asanture@gmail.com

Groningen ESEB SpatialEvolution Aug20-25

ESEB Symposium on "Spatial Evolution"

Dear Colleagues,

We would like to invite you to submit an abstract to our symposium [S25] on 'Spatial Evolution' at the 16th Congress of the European Society for Evolutionary Biology in Groningen, Netherlands, 20-25 August 2017

http://www.eseb2017.nl/sub/s25-spatial-evolution-although-disp/ http://www.eseb2017.nl/ INVITED SPEAKERS:

Hanna Kokko (University of Zurich)

Stephane Joost (EPFL, Lausanne)

ABSTRACT SUBMISSION DEADLINE:

The deadline for abstract submission is 10 January 2017. Submit abstracts online at http://www.eseb2017.nl/-call-for-abstracts/ SYMPOSIUM DESCRIPTION:

Although dispersal is one of the four mechanisms of evolutionary change, the explicit spatial context in which evolution occurs is frequently ignored. In addition, the dynamics of dispersal are important as well, as the ability to disperse itself may rapidly evolve and is subject to eco-evolutionary feedbacks. A particularly potent tool for elucidating spatial evolution is genomic data, which can be used to accurately assess (fine-scale) spatial genetic variation. Together with an improved understanding of spatial evolution, this helps us better understand applied processes such as biogeography, climate-change related range shifts, biological invasions and the spread of disease. Our symposium provides a platform for biologists studying evolution in a spatial context. We invite contributions from theory, experiments and comparative work considering all levels of organization, from individuals to communities, and particularly encourage studies incorporating multiple approaches. We will showcase the diversity of approaches (statistical approaches, modelling, experimental evolution, genetics, spatially informed genomics) as well as model and non-model organisms used in the study of spatial evolution (from microbes to vertebrates and digital organisms). This inclusive approach is a major precondition for promoting interaction and reaching synthesis in this quickly advancing field and designing future research avenues.

SYMPOSIUM ORGANIZERS:

Emanuel Fronhofer (Eawag & University of Zurich)

Flora Jay (CNRS, Paris-Sud University)

Benjamin Peter (University of Chicago)

Marjo Saastamoinen (University Helsinki)

Looking forward to seeing you in Groningen!

Dr Marjo Saastamoinen

Academy Research Fellow

Centre of Excellence in Metapopulation Research

Department of Biosciences

PO Box 65 (Viikinkaari 1)

FI-00014 University of Helsinki

FINLAND

tel. + 358 (0)50 448 4471

http://www.mv.helsinki.fi/home/msaastam/ "Saastamoinen, Marjo A K" <marjo.saastamoinen@helsinki.fi>

Groningen EvolutionMedicineSociety Aug18-21

Abstract submission is now open for The International Society for Evolution, Medicine & Public Health Third Annual Meeting will be August 18-21, 2017 in Groningen, Netherlands, in conjunction with the European Society for Evolutionary Biology (ESEB) meeting August 21-25.

The deadline for abstract submissions is February 15. Registration for both meetings will open in February.

Keynote speakers include Svante Pääbo, Linda Partridge, Stephen Stearns, Marian Joels, Mervyn Singer, Sylvia Cremer, Francisco Ubeda, and Peer Bork. Details are at the ISEMPH Website.

Full information at https://evolutionarymedicine.org/-2017-isemph-meeting/ rmnesse@gmail.com

Hannover Germany EcoEvoDynamcis Oct9-13

Conference: Flexibility matters: Interplay between trait diversity and ecological dynamics using aquatic communities as model systems

The conference will address trait-based ecology with a focus on biomass-trait feedbacks and eco-evolutionary dynamics typically arising from trophic interactions. We aim to bridge between theoretically guided empirical field and laboratory studies and data-informed development of theory and modelling. The meeting will provide opportunities to exchange ideas and results with members of the DFG funded Priority Program DynaTrait and guests through a series of contributed and invited talks, poster sessions and small working groups. The meeting focuses on aquatic systems, but other systems are welcome as well if results are sufficiently generalizable. For more information and list of speakers see http://web.evolbio.mpg.de/dynatrait/-Site_2/DynaTrait_Meeting_2017.html . The meeting will take place 9th-13th October 2017 in Hannover, Germany. If you are interested in joining us, please contact Alice Boit (alice@boit.net) .

Organizers and Contact Ursula Gaedke (University Potsdam) & Lutz Becks (MPI Evolutionary Biology)

Lutz Becks <lbecks@evolbio.mpg.de>

Italy Speciation Feb19-24

The full program is now available for SPECIATION 2017, a Gordon Research Conference (GRC) dedicated exclusively to speciation research:

https://www.grc.org/programs.aspx?id=16903 The conference - the world's largest of its kind - will be held at the Renaissance Tuscany Il Ciocco Resort & Spa in Italy during the week of February 19-24, 2017. For the first time, the conference will be preceded by a two-day Gordon Research Seminar (GRS), co-chaired by Amanda Hund and Laurel Symes, which offers unique opportunities for graduate students and early-career scientists to learn and get involved at the forefronts of modern speciation research.

The GRC conferences on speciation raise to a trans-Atlantic level a tradition of international conferences on speciation research that was initiated by the European Research Networking Programme 'Frontiers of Speciation Research'. The three conferences held thus far, in 2010, 2013, and 2015, have helped facilitate bridge-building between disparate approaches to speciation research and have attracted hundreds of participants from all facets of speciation research.

Registration for SPECIATION 2017 will continue until the venue's capacity is filled. At the time of writing, we can make only a few additional acceptances before we have to waitlist applicants so please apply soon if you are hoping to join us.

With many thanks and best wishes,

Ãke Brännström & Rebecca Safran

rebecca.safran@colorado.edu

Karkow EvolutionaryMyrmecology Apr21-24

Dear All,

7th Central European Workshop of Myrmecology website is online, please visit: cewm-krakow.com

Meeting is to be held in Krakow, Poland, from April 21 to April 24, 2017. Our goal is to provide a forum for the exchange of ideas, methods, and results in all evolutionary and ecological aspects of myrmecology.

Krzysiek Miler, IES JU <krzysztof.miler@uj.edu.pl>

Krzysztof Miler <krzysztof.miler@uj.edu.pl>

LundU SwedishOikos2017 Feb7-9 AbstractsFinalReminder

Don't forget to register for the 2017 Oikos meeting in Lund! Registration without abstract submission is possible until January 16th, but the deadline for abstract submission is Monday December 12th - that's in just a few days! We hope to be able to accommodate all submissions as either talks or posters.

Register here: http://oikos2017.event.lu.se/registration The Swedish Oikos Congress 2017 will take place 7th - 9th February 2017 in Lund. Venue for the meeting will be Paleastra, in the heart of the city. A conference dinner will be held on the evening of February 8^th , and there will be pre-congress workshops on Monday February 6th. The meeting is open to all ecologists and evolutionary biologists regardless of subdiscipline, and we have a wide breadth of talks and plenaries!

– Dr. Jessica K. Abbott Senior University Lecturer Department of Biology Section for Evolutionary Ecology Lund University Sölvegatan 37 223 62 Lund, Sweden Phone: 046 222 9304 Website: http://-jessicakabbott.com "It is those who know little, and not those who know much, who so positively assert that this or that problem will never be solved by science." - Charles Darwin, Descent of Man

Jessica Abbott <jessica.abbott@biol.lu.se>

LundU SwedishOikos2017 Feb7-9 AbstractSubmission

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Dr. Jessica K. Abbott Senior University Lecturer Department of Biology Section for Evolutionary Ecology Lund University Solvegatan 37 223 62 Lund, Sweden Phone: 046 222 9304 Website: http://-jessicakabbott.com "It is those who know little, and not those who know much, who so positively assert that this or that problem will never be solved by science." - Charles Darwin, Descent of Man

"jessica.abbott@biol.lu.se" <jessica.abbott@biol.lu.se>

Marseilles 21stEvolutionaryBiology Sep26-29 Info

Dear All the information about the

21st evolutionary biology meeting at Marseilles can be found now on the aeeb web site :

aeeb.fr

Please note the early registration dead line

best regards

Pierre

Pierre Pontarotti DR CNRS EBM unité I2M 7373 AMU/CNRS

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

Mexico CavefishAdaptation Mar12-15

We are pleased to announce that the 5th Annual Astyanax International Meeting for Cavefish will be held March 12-15, 2017, in Santiago de Querétaro, Mexico.

The meeting will feature many great talks about cavefish and adaptation to novel and extreme environments in general. We are happy to announce that Katie Peichel will be our keynote speaker to present her work how sticklebacks adapt to their environment. The meetings are usually very informal with a limited number of participants and enough time for social interactions to give students the ability to interact with faculty and vice versa. Student prices are subsidized by the faculty rates and very affordable. Mexican resident students can even attend for free.

Our venue will be the lovely Hotel Misión Juriquilla Querétaro. This hotel offers first class accommodation in a renovated eighteenth century farmhouse north of the city of Queretaro, surrounded by gardens and buildings that evoke the colonial Mexico.

The meeting will be followed by an optional caving trip to the Sierra del Abra biosphere reserve, March 15-18, 2017 for a limited number of participants.

Please visit our website for more information. http://www.stowers.org/aim2017/home We hope to see you there! AIM 2017 Organizers cavefin@stowers.org

"Williams, Stacey" <snw@stowers.org>

PorquerollesIsle France MathEvolBiol Jun12-16

MCEB - Mathematical and Computational Evolutionary Biology 12-16 June 2017 - Porquerolles Island, South of France.

Webpage: http://www.lirmm.fr/mceb2017/ Pre-registration deadline: February 27th

Notification to applicants: March 17th

Final list of attendees: April 17th

Registation page : http://www.lirmm.fr/mceb2017/register.php Scope: Mathematical and computational tools and concepts form an essential basis for modern evolutionary studies. The goal of the MCEB conference (at its 9th edition) is to bring together scientists with diverse backgrounds to present recent advances and discuss open problems in the field of mathematical and computational evolutionary biology.

The theme of this year's edition will be "Methods for integrative evolutionary biology: various sources of data, various scales of evolution", which includes the analysis of heterogeneous data (molecular, phenotypic, ecological...), different time scales (from recent times to the origin of life), different spatial scales (from local to worldwide range), the combination of phylogenetics and population genetics, multidisciplinary approaches, etc.. General concepts, models, methods and algorithms will also be presented and discussed, just as during the previous conference editions.

Where and when: Porquerolles Island, near Hyeres, in the South of France, 12-16 June 2017.

Cost: Conference fees including accommodation for four nights, meals, coffee breaks, etc., will be around 450euro, all inclusive. PhD students and postdocs would benefit of financial support.

Keynote speakers:

Elizabeth Allman (Department of Mathematics and Statistics, University of Alaska Fairbanks) http://www.dms.uaf.edu/%7Eeallman/ Guy Baele (Rega Institute / KU Leuven - Evolutionary and Computational Virology Section) https://rega.kuleuven.be/cev/ecv/lab-members/GuyBaele.html Stephane Dray (Laboratoire de Biometrie et Biologie Evolutive (LBBE), Lyon) http://pbil.univ-lyon1.fr/members/dray/cv.php Barbara Holland (Theoretical Phylogenetics Group, School of Mathematics and Physics, University of Tasmania) http://www.maths.utas.edu.au/People/Holland/ Anna-Sapfo Malaspinas (Institute of Ecology and Evolution, University of Bern) http://www.cmpg.iee.unibe.ch/about_us/team/researchers/ass_prof_dr_malaspinas_anna_sapfo/index_eng.html Yun Song (Calabi-Simons Chair in Mathematics and Biology, Departments of Mathematics and Biology, University of Pennsylvania) http://www.sas.upenn.edu/ ˜ yss/ Marc Suchard (David Geffen School of Medicine at UCLA, Departments of Biomathematics, Biostatistics and Human Genetics) http://faculty.biomath.ucla.edu/msuchard/ For more information, visit the website at: http://www.lirmm.fr/mceb2017/ Please forward this announcement!

Olivier GASCUEL <olivier.gascuel@pasteur.fr>

Portugal AlCoB Jun5-7

4th INTERNATIONAL CONFERENCE ON ALGORITHMS FOR COMPUTATIONAL BIOLOGY AlCoB 2017 Aveiro, Portugal June 5-7, 2017 Organized by:

Center for Research & Development in Mathematics and Applications (CIDMA) Institute of Electronics and Informatics Engineering of Aveiro (IEETA) University of Aveiro

Research Group on Mathematical Linguistics (GRLMC) Rovira i Virgili University — http://grammars.grlmc.com/AlCoB2017/ — AIMS:

AlCoB aims at promoting and displaying excellent research using string and graph algorithms and combinatorial optimization to deal with problems in biological sequence analysis, genome rearrangement, evolutionary trees, and structure prediction.

Previous events were held in Tarragona, Mexico City, and Trujillo.

The conference will address several of the current challenges in computational biology by investigating algorithms aimed at:

1) assembling sequence reads into a complete genome, 2) identifying gene structures in the genome, 3) recognizing regulatory motifs, 4) aligning nucleotides and comparing genomes, 5) reconstructing regulatory networks of genes, and 6) inferring the evolutionary phylogeny of species. — Particular focus will be put on methodology and significant room will be reserved to young scholars at the beginning of their career.

VENUE: — AlCoB 2017 will take place in Aveiro, an industrial city with an important seaport on the Atlantic Ocean, and known as "the Portuguese Venice" due to its network of canals. The venue will be:

Department of Mathematics University of Aveiro Campus Universitário de Santiago 3810-193 Aveiro — SCOPE: — Topics of either theoretical or applied interest include, but are not limited to:

Exact sequence analysis Approximate sequence analysis Pairwise sequence alignment Multiple sequence alignment Sequence assembly Genome rearrangement Regulatory motif finding Phylogeny reconstruction Phylogeny comparison Structure prediction Compressive genomics Proteomics: molecular pathways, interaction networks Transcriptomics: splicing variants, isoform inference and quantification, differential analysis Next-generation sequencing: population genomics, metagenomics, metatranscriptomics Microbiome analysis Systems biology — STRUCTURE:

AlCoB 2017 will consist of: — invited lectures peer-reviewed contributions posters — INVITED SPEAKERS: — Michael Biehl (University of Groningen), Prototype-based Models for the Analysis of Biomedical Data

Benedict Paten (University of California, Santa Cruz), The Human Genome Variation Map Project

Marie-France Sagot (INRIA, Villeurbanne), Algorithmically Exploring and Exploiting Interspecific Interactions

PROGRAMME COMMITTEE: — Can Alkan (Bilkent University, Ankara, TR) Stephen Altschul (National Institutes of Health, Bethesda, US) Yurii Aulchenko (PolyOmica, Groningen, NL) Timothy L. Bailey (University of Nevada, Reno, US) Bonnie Berger (Massachusetts Institute of Technology, Cambridge, US) Ken Chen (University of Texas MD Anderson Cancer Center, Houston, US) Julio Collado-Vides (National Autonomous University of Mexico, Cuernavaca, MX) Eytan Domany (Weizmann Institute of Science, Rehovot, IL) Dmitrij Frishman (Technical University of Munich, DE) Terry Furey (University of North Carolina, Chapel Hill, US) Olivier Gascuel (Pasteur Institute, Paris, FR) Debashis Ghosh (University of Colorado, Denver, US) Susumu Goto (Kyoto University, JP) Osamu Gotoh (Institute of Advanced Industrial Science and Technology, Tokyo, JP) Artemis Hatzigeorgiou (University of Thessaly, Volos, GR) Javier Herrero (University College London, UK) Karsten Hokamp (Trinity College Dublin, IE) Fereydoun Hormozdiari (University of California, Davis, US) Kazutaka Katoh (Osaka University, JP) Lukasz Kurgan (Virginia Commonwealth University, Richmond, US) Gerton Lunter (University of Oxford, UK) Carlos Martín-Vide (Rovira i Virgili University, Tarragona, ES, chair) Zemin Ning (Wellcome Trust Sanger Institute, Hinxton, UK) William Stafford Noble (University of Washington, Seattle, US) Cedric Notredame (Center for Genomic Regulation, Barcelona, ES) Christos Ouzounis (Centre for Research & Technology Hellas, Thessaloniki, GR) Manuel C. Peitsch (Philip Morris International, Bern, CH) Matteo Pellegrini (University of California, Los Angeles, US) Graziano Pesole (University of Bari, IT) David Posada (University of Vigo, ES) Knut Reinert (Free University of Berlin, DE) Peter Robinson (The Jackson Laboratory, Farmington, US) Julio Rozas (University of Barcelona, ES) David Sankoff (University of Ottawa, CA) Alejandro Schäffer (National Institutes of Health, Bethesda, US) Xinghua Shi (University of North Carolina, Charlotte, US) Nicholas D. Socci (Memorial Sloan Kettering Cancer Center, New York, US) Alexandros Stamatakis (Heidelberg Institute for Theoretical Studies, DE) Granger Sutton (J. Craig Venter Institute, La Jolla, US)

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UCalifornia SanDiego ExperimentalEvolution Jan5-6

Dear All,

Many recent advances in evolutionary biology have been achieved through the development of experimental approaches in systems ranging from molecules to multicellular organisms. To discuss this topic, please join us on Jan 5 and 6, 2017, for a two-day Californian Experimental Evolution Symposium on UCSD campus in La Jolla, CA.

The list of speakers and a tentative schedule can be found here:

http://www.cees2017.org If you would like to attend, please contact Joanna Dunn (jfdunn@ucsd.edu).

Best regards,

Sergey Kryazhimskiy Justin Meyer

"skryazhi@ucsd.edu" <skryazhi@ucsd.edu>

UMichigan PhenotypicPlasticity Mar10-12

CALL FOR NOMINATIONS

13th ANNUAL EARLY CAREER SCIENTISTS SYMPOSIUM

Ecology and evolutionary biology of phenotypic plasticity

The Department of Ecology and Evolutionary Biology at the University of Michigan invites nominations of outstanding scientists early in their careers to participate in an exciting international symposium about the ecology and evolutionary biology of phenotypic plasticity. The symposium events will take place from 10-12th of March 2017, in Ann Arbor, Michigan.

Eight early career scientists, alongside a keynote speaker, will be selected to present their work and to participate in panel discussions. We welcome nominations of early career scientists who are studying topics in ecology and evolution related to phenotypic plasticity. This symposium will highlight the work of up-and-coming scientists whose research foci span a breadth of subfields and levels of organization. We champion diversity and encourage the nomination of members of groups underrepresented in science.

Early career scientists are considered senior graduate students (who stand to receive their Ph.D. within one year), postdoctoral researchers, and first- or second-year faculty. A colleague or advisor must provide the nomination.

The nomination consists of a brief letter of recommendation addressing the nominee's scientific promise and ability to give a compelling talk, the nominee's curriculum vitae, and a brief abstract of the proposed presentation (< 200 words, written by the nominee). Nominations may be sent electronically (in one file, please) to eeb-ecss-nomination@umich.edu using the nominee's name as the subject line (last name first). Information about Early Career Scientist Symposia held in past years can be found at http://sites.lsa.umich.edu/ecss/ . Review of nominations will begin on December 31, 2016.

Selected participants will be contacted in mid January and will have all expenses covered

(registration, travel and accommodation). An official announcement of the slate of speakers will be issued soon thereafter.

For more information, contact Carol Solomon at carollyn@umich.edu.

The 2017 Early Career Scientists Symposium scientific committee includes:

Wei-Chin Ho

Andrea Hodgins Davis (chair)

Jill Myers

Annette Ostling

Mary Rogalski

Sonal Singhal

Carol Solomon

Andrea Hodgins-Davis Wittkopp Lab Postdoc Department of EEB University of Michigan

Andrea Hodgins-Davis <andreahd@umich.edu>

Vienna EvolutionaryEpigenetics Sep12-15

Dear all

Registration has opened for the 40th New Phytologist symposium on the topic "Plant epigenetics: from mechanisms to ecological relevance" to be held in Vienna, Austria, 12-15 Sept 2017.

Plant epigenetics has recently become a compelling research field. For an efficient integration of epigenetics in ecological and biodiversity research, an interdisciplinary and continuous flux of information is necessary, together with close cooperation between related disciplines. To this end, this symposium focuses on interdisciplinary discussion and aims to foster cooperation among research groups.

The symposium format will include six non-concurrent sessions on the following topics: Session 1: Population epigenomics in natural systems Session 2: Epigenetic regulation of plant phenotypes Session 3: Transgenerational inheritance of epigenetic patterns Session 4: Epigenetic regulation as a response to changes in environmental conditions Session 5: Epigenetic regulation of biotic interactions Session 6: Bioinformatic analysis for plant epigenetics

Twenty-five leading scientists are invited to speak at the symposium. We hope that this will stimulate focused discussion and the exchange of ideas at what will be a relatively small (around 120 delegates) and informal meeting. There will be also several selected talks and poster sessions. As the symposium benefits from generous support from New Phytologist and the symposium venue is provided by the University of Vienna, registration rates are low (120 for students and 240 for regular registration) and include lunches, coffee breaks, evening receptions, conference dinner, a tour of the Botanical Garden and a nostalgic tram tour through Vienna.

Places are limited, so please register early to avoid disappointment. The registration will close as soon as the maximum number of participants is reached. Abstract submission will remain open to 13 July 2017. For full details and to register, please visit https://www.newphytologist.org/symposia/40 Dr Ovidiu Paun Department for Botany and Biodiversity Research University of Vienna http://plantgenomics.univie.ac.at ovidiu.paun@univie.ac.at

GradStudentPositions

Austria BulbophyllumTraitEvolution

THREE-YEAR PHD POSITION IN PLANT EVOLUTIONARY BIOLOGY

A Ph.D. position in Plant Evolutionary Biology is available at the Dept. of Ecology and Evolution, Division of Plant Ecology, Diversity & Evolution, University of Salzburg, Austria, with Prof. Hans Peter Comes and Dr. Alexander Gamisch to study the tempo and mode of trait evolution and lineage diversification in a species-rich orchid (Bulbophyllum) clade endemic to Madagascar and adjacent islands.

The overall aim of this research project is to investigate the temporal stages of evolution in various trait complexes that likely had a major role in the group's radiation. Specifically, this involves (1) the completion of a time-calibrated and well-sampled multi-gene phylogeny of Madagascan Bulbophyllum: (2) the gathering of new datasets comprising variation in four suites of traits (i.e. macro- ecological habitat, photosynthetic pathway, flower morphology/shape and floral scent); and (3) the fitting of various macro-evolutionary models of lineage diversification, trait evolution, and trait-dependent diversification to the trait data and/or the molecular phylogeny.

The successful candidate will closely co-operate with the project postdoc (Dr. Gamisch) and will be mostly responsible for (1) gathering and analysing data of the orchids' three-dimensional (3D) flower morphology, using X-ray micro-computed tomography and landmark-based geometric morphometrics (in co-operation with Prof. Dr. Jürg Schönenberger/Vienna); and (2) collecting and analysing floral scent samples by means of gas chromatography/mass spectroscopy (in co-operation with Prof. Dr. Stefan Dötterl/Salzburg). The candidate is further expected to assist in routine molecular work and in the comparative phylogenetic analyses, and also has the opportunity to participate in field work in Madagascar.

The ideal applicant has a genuine interest in plant evolution and a strong background in at least one of the following fields of research: a) floral morphometrics; b) chemical ecology/analytical chemistry; and/or c) molecular phylogenetics. Apart from short research stays at the University of Vienna, fieldwork in remote places of Madagascar is required. Accordingly, the successful candidate should be willing to travel and have physical fitness to perform field research under tropical rainforest conditions. An MSc, diploma degree or equivalent in Botany, Ecology, Genetics or Evolutionary Biology is required. Fluent English is a must and French as second language would be an advantage. German is not mandatory. The position is starting April 1, 2017, with funding for three years by the Austrian Science Fund (FWF). The monthly gross salary is c. 2045 EUR paid 14 times a year. The University of Salzburg (http://www.uni-salzburg.at/) offers excellent facilities, and a very pleasant working and living environment in one of the m ost beautiful landscapes in Austria.

Please send (if possible via email) a letter of application together with a full CV, a copy of your master/diploma certificate, and the addresses of two referee s (all merged into a single pdf) to: Prof. Hans Peter Comes

Department of Ecology and Evolution

Division of Plant Ecology, Diversity & Evolution

Paris-Lodron-University Salzburg

Hellbrunnerstr. 34, A-5022 Salzburg

Austria

Tel.: ++ 43 (0) 662 8044-5505

Fax: ++43 (0) 8044-142 Email: peter.comes@sbg.ac.at

The position will be filled as soon as a suitable applicant is found.

Alexander Gamisch <AlexanderGamisch@gmx.at>

BaylorU SpeciationBehaviorGenetics

TheDanley Lab at Baylor University (http://sites.baylor.edu/danleylab/graduate-student-postions/) seeks two Ph.D. students broadly interested in evolutionary biology using East African cichlid fish as a model system. The exact nature of the research will be developed by the student in collaboration with Pat Danley though it should relate to the lab's previous research on sexual selection (mate choice, aggression), phylogeography, and speciation.

Applicantswith a background in behavioral, phylogenetic, and genomic methods are encouraged to apply. Applicants experienced with R and Python are a plus. Applicants should possess an M.S. degree or substantial undergraduate research experience, GRE Verbal and Quantitative Reasoning scores at or above the 70th percentile, GRE Analytical Writing score of 4.5 or greater, and undergraduate and graduate (if applicable) GPA of 3.5 or higher. Please review additional departmental admission guidelines (http://www.baylor.edu/biology/index.php?id=68418). Applicants must be able to begin by the fall of 2016.

Thesuccessful applicant will be admitted to the Department of Biology's Ph.D. program which provides 5 years of 12 month stipend ($22,500, plus possible enhancements for outstanding students of up to $8000/year). Admission also includes full tuition remission (up to a 20 credits per year), health insurance benefits (80% of cost of premium covered; cost to student ~$450/y in 2015), and additional funding opportunities for travel to professional meetings, books and fees.

TheBaylor's Department of Biology has an active graduate community of over 50 students and possesses strengthens in the areas of integrative organismal biology and aquatic ecology. Waco, home of Baylor University, is conveniently located 90 minutes from both Dallas and Austin and was recently ranked as one of America's Awesomest (sic) Cheap Cities making it a perfect home for would be graduate students. http://www.wisebread.com/10-of-americas-awesomest-cheap-cities Toapply, please send an email describing your background and interests to Dr. Patrick Danley (patrick_danley@baylor.edu). No application will be considered without previous interaction by email and telephone/skype with Dr. Danley. Complete applications need to be submitted to the Graduate School by January 25, 2017 to be eligible for all-expenses paid campus visit for the most qualified applicants. Applications will not be considered after February 15, 2017.

Patrick_Danley@baylor.edu

BrighamYoungU EvolutionaryBiology

The Department of Biology at Brigham Young University (BYU) welcomes applications from highly motivated students interested in joining our MS or PhD programs in the Fall of 2017. Housed in a new, state of the art building, the Department (http://biology.byu.edu) comprises a large and dynamic faculty spanning a diverse array of research areas including informal and collaborative research groups in Ecology, Evolutionary Ecology, Molecular Systematics, Bioinformatics, Conservation Biology, and Biological Science Education.

The Ecology and Evolutionary Ecology group is a diverse set of faculty working on plants, fungi, animals, and microbes in the areas of evolutionary ecology, conservation biology, biogeography, phylogeography, population and community ecology, biogeochemistry, environmental monitoring, evolutionary and ecological stoichiometry, and ecosystem ecology. There is a focus on integrating modeling, theory, and experimentation.

The Molecular Systematics group features faculty working in both model and non-model systems in experimental laboratory and field applications. Specific areas of research include genomics (experimental and computational), molecular evolution, population genetics, quantitative genetics, biogeography, phylogeography, and the evolution of genetic and infectious diseases.

Faculty in the Bioinformatics group maintain research programs in the genetics of human disease, molecular evolution, and computational biology, including solutions for next generation sequencing applications.

The Biological Science Education group involves research at all levels of education, focusing on inquiry teaching, learning theory, and assessment of science pedagogy. Faculty in this focal group also use this platform for various outreach activities, including K-12 collaborative projects with the State Office of Education.

Each of the focal groups in our department maintain strong collaborative ties with each other, as well as other departments on campus, including Plant and Wildlife Sciences, Microbiology and Molecular Biology, Physiology and Developmental Biology, Statistics, Computer Science, and the McKay School of Education.

Exceptional facilities and resources for carrying out research are available through the Monte L. Bean Life Science Museum (http://mlbean.byu.edu), Lytle Ranch Preserve (http://mlbean.byu.edu/lytle), the DNA Sequencing Center (http://dnasc.byu.edu), the Research Instrumentation Core Facility (http://ricfacility.byu.edu), the Microscopy Lab (http://microscopy.byu.edu) and the Fulton Supercomputing Lab (https://marylou.byu.edu).

BYU is located in Provo, Utah, where opportunities for world-class skiing, fly-fishing, kayaking, hiking, mountain biking, and many other outdoor recreational activities are less than 20 minutes from the lab. Salt Lake City is only 45 minutes travel by car or commuter rail.

For full consideration, complete applications should be received by January 15, 2017. We strongly encourage prospective applicants to contact faculty members as soon as possible to discuss their research interests. Financial support for graduate students is competitive and comes from a variety of sources, including teaching assistantships, research assistantships, fellowships, and external research funds. Faculty Profiles can be accessed here: http://biology.byu.edu/Connect/FacultyandStaff Byron Adams, Coordinator, Graduate Programs

Byron Adams <byron_adams@byu.edu>

BrighamYoungU PlantGenomeEvolution

Multiple graduate student positions (MS and PhD) in the evolution of plant genomes are available beginning Fall 2016 in the Department of Plant and Wildlife Science, Brigham Young University. Research focus of these assistantships center on the genome evolution of polyploid plants (*e.g.* cotton; see http://udall-lab.byu.edu). During their thesis work, students will employ molecular, structural, and genetic approaches to address basic questions in the evolution of plant domestication and genetic diversity of cotton. Specific technologies employed in the approaches include BioNano optical mapping, PacBio and Illumina DNA sequencing, and computational biology.

Successful applicants must be highly motivated, willing to work hard, and hopefully they are not too distracted by living in the most beautiful place in the world. Ideally, applicants should have a solid, but not necessarily deep, understanding of bioinformatics and an interest in genomics. Actual wet-lab experience with basic molecular biology techniques is a plus (PCR,cloning, sequence analysis, etc.).

Funding for this position is through a combination of Teaching and Research Assistantships from the National Science Foundation and Cotton Incorporated. This means students will be paid a stipend while they earn their graduate degree! In addition to the stipends, tuition and health insurance will also be provided for the accepted students. Interested students from other Universities than BYU could receive up to $30K per year through the HIDRA < https://graduatestudies.byu.edu/content/hidra > program (for off-campus applicant to BYU) or through the University Graduate Research Award (after first year of studies).

Interested applicants should send a CV, transcripts, GRE scores (if available) and a statement of research interests to Joshua Udall (jaudall@byu.edu). Applications will be considered until to February 1st, 2016. International students with strong credentials are welcome and encouraged to apply.

– Joshua Udall (4105 LSB) Brigham Young University 701 E. University Parkway Plant and Wildlife Science Depart. Provo, UT 84602

Office: 801-422-9307

jaudall1@gmail.com

BrookesU GeneDuplicateEvolution

Title of the project: Early Evolution of Gene Duplicates

Key words: gene duplication, gene dosage, gene regulation, CRISPR/Cas9, 4C-seq

Gene duplication is a major evolutionary mechanism leading to novel gene function and phenotypic diversity. However, very little is known about the period shortly after the duplication event. Molecular evolution studies suggest that gene dosage is an important contributory factor in determining whether new duplicates become fixed or not. However, in metazoans this evidence is largely based on statistical inference based on extant population data.

In this project, we aim to test the effect of gene dosage on the fate of new gene duplicates in an experimental framework using Drosophila melanogaster. The research project student will generate tandem gene duplications, deletions and non-functional mutants using the CRISPR/Cas9 system and other transgenic tools to target both genes likely to result in genes with dosage-sensitive functions as well as genes that are expected to display less sensitivity to dosage. The effect of the newly generated transgenic alleles will be measured by conducting fitness assays and functional genomics to quantify transcription (qPCR, RNAseq) and enhancer interactions (4C-seq).

Please follow the link for further details and how to apply: https://www.findaphd.com/search/ProjectDetails.aspx?PJID=79657 Note competitive fund is only available for UK/EU residents.

Contact details for informal enquiries:

Dr. Saad Arif

sarif@brookes.ac.uk

Dr. Maria Daniela Santos Nunes

msantos-nunes@brookes.ac.uk

Brussels MolecularEvolSeaStars

PhD position (4 years)

or

Post-doc position (2 years)

in molecular ecology at the Vrije Universiteit Brussel (VUB) < http://www.vub.ac.be/en/ >, Department of Biology < http://we.vub.ac.be/en/biology-department >, Marine Biology Lab < http://we.vub.ac.be/en/marc-kochzius >, Belgium.

We are searching for a highly motivated scientist that will work on *evolution, population genetics and connectivity in Antarctic sea stars* utilising a *genomics* approach (DNA barcoding, microsatellites and next generation sequencing) in the framework of the interdisciplinary project

Refugia and Ecosystem Tolerance in the Southern Ocean (RECTO).

Because of its long history and geographic isolation, the Southern Ocean (SO) provides a natural laboratory for research on evolution and biodiversity. Confronted with fast-paced environmental changes, biota in Antarctic ecosystems are strongly challenged and face three possible outcomes: adaptation, migration or extinction. Past glaciation periods have already forced marine zoobenthos of the SO into refugia, being either ice-free continental shelf areas, the deep sea or sub- or peri-Antarctic regions, followed by recolonization when the ice retreated. In a multidisciplinary approach and involving all major Belgian research groups studying evolution and diversity of SO faunas, RECTO will strive at understanding how such past events have driven diversification and adaptation in different animal groups and how these can be applied as proxies to understand the contemporary situation and predict future scenarios.

The Marine Biology Lab at the VUB specialises in research on molecular ecology of marine fauna from the poles to the tropics and from invertebrates to fishes. In the new collaborative research project RECTO the evolutionary history of Antarctic sea stars will be studied.

Profile of the candidate:

§MSc / PhD in (marine) biology with excellent study results

§Experience in genomics (lab work and bioinformatics)

§Interest in the ecology and evolution of Antarctic sea stars

§Excellent oral and written English skills (for minimum requirements see http://www.vub.ac.be/en/studying-at-the-vub/language-requirements)

§Willingness to participate in long sampling campaigns under extreme conditions in the Southern Ocean

§PhD student: obligation to finalise a doctoral thesis within 4 years

The marine biology lab offers excellent coaching in an inspiring research environment with up-to-date research facilities in the international and multilingual capital of Europe.

Interested candidates are requested to submit their application (motivation letter, two reference letters, summary of MSc / PhD thesis, MSc certificate with grades / PhD certificate, proof of proficiency in English and curriculum vitae) with the *subject line “RECTO PhD application” or “RECTO post-doc application”* to the head of the Marine Biology Lab, Prof. Dr. Marc Kochzius (marc.kochzius@vub.ac.be). Targeted start of the position is the first quarter of 2017. Applications will be considered until the position is filled.

Prof. Dr. Marc Kochzius

Department of Biology

Ecology and Biodiversity

Marine Biology Lab

Office 8F12

Vrije Universiteit Brussel

Pleinlaan 2

1050 Brussels

Belgium

Email: marc.kochzius@vub.ac.be

Phone: +32 2 629 3406

Fax: +32 2 629 3408

www.researchgate.net/profile/Marc_Kochzius http://we.vub.ac.be/en/marc-kochzius Secretary Biology Department

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www.we.vub.ac.be/en/biology-department Secretary Oceans & Lakes

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www.oceansandlakes.be

CharlesU Prague PDF PhD SexChromosomeEvol

CharlesU_Prague.PhD&MSc.SexChromosomeEvolution

PhD and MSc position in Evolution of sex chromosomes in squamate reptiles

Two positions for a PhD and a MSc candidate is currently open in the research team of Dr. Lukas Kratochvil, Department of Ecology, Charles University, Czech Republic. The successful candidates will join our current projects on the study of the evolution of sex chromosomes in squamate reptiles with molecular and cytogenetic methods.

Project description: The aim of the project is to examine the evolution of sex chromosomes and their homology based on gene content in selected lineages of squamate reptiles (eg. lizards and snakes). Squamate reptiles possess lineages with either XX/XY, ZZ/ZW or temperature-dependent sex determination. Despite the recent advances in the field, our knowledge about their sex determination systems and sex chromosome homology is limited only to few groups of reptiles (eg. iguanas, advanced snakes), while the majority of reptilian lineages remain unstudied. The successful candidate will collaborate with the other team members and will study the evolution of sex chromosomes in a multidirectional approach, involving cytogenetics (eg. FISH, chromosome painting), molecular genetics (eg. qPCR) and bioinformatics (eg. transcriptomics). More information about our current research activity can be found in the following publications:

https://www.ncbi.nlm.nih.gov/pubmed/27037610
http://www.ncbi.nlm.nih.gov/pubmed/26702042
http://www.ncbi.nlm.nih.gov/pubmed/24433436
Qualifications: For PhD candidates, the applicant should possess Master degree (or equivalent title) and has a proven expertise in a related field of biology: evolutionary biology, cytogenetics, phylogenetics, genomics and/or bioinformatics. Previous experience in herpetology is not necessary. The ideal candidate should be scientifically motivated, able to work both

independently and as a part of the team. High standard of spoken and written English is required. For Master students, the applicant should possess a degree in Biology (or relative subject) and a proven experimental expertise (eg. diploma thesis) in zoology, genetics and/or molecular biology.

Application: The applicant should send a short letter explaining his/her background and motivation, full CV and contact information for two references to both Dr. Michail Rovatsos (michail.rovatsos@natur.cuni.cz) and Dr. Lukas Kratochvil (lukas.kratochvil@natur.cuni.cz).

The successful candidate will be financially supported, with a salary sufficient for a comfortable living in Prague, Czech Republic, relevant to qualifications, which will be further increased based on performance.

Prague is often included in the top lists for best cities, considering safety, culture, popular travel destinations and quality of living. Some useful links:

Charles University website: http://www.cuni.cz/UKEN-1.html Faculty of Science, Charles University: www.natur.cuni.cz/en Student life in Prague: http://studyinprague.cz/about-prague/student-life-in-prague/ Cost of living: http://www.studyin.cz/living-costs/ Tourism guide: http://www.myczechrepublic.com/prague/ The position is valid until suitable candidates are selected and the starting date is flexible, with closest date 1/1/2017. Suitable candidates will be interviewed until January 31th. For any additional information, do not hesitate to write an email.

Michail Rovatsos

Researcher Department of Ecology Faculty of Science Charles University Vinicna 7, 128 43 Praha 2 Czech Republic

"Michail Rovatsos, Ph.D." <michail.rovatsos@natur.cuni.cz>

ClemsonU FacialEvoDevo

The Powder Lab at Clemson University is recruiting graduate students to study the genetic and developmental basis of craniofacial evolution of cichlid fishes (Evo-Devo). 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.

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 .Deadline for application is Jan 5, 2017.

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.

Please contact Kara Powder at kpowder@clemson.edu for more information

Kara E. Powder Assistant Professor of Biological Sciences Clemson University

"kpowder@clemson.edu" <kpowder@clemson.edu>

CUNewYork ComparativePopgenPhylogeo

NSF supported PhD position starting Fall 2017; Multitaxa population genetics; Application due Jan 1st https://hickerlab.wordpress.com/ Details:

The Hickerson lab at the City University of New York has an opening for a PhD student who is interested in community-level population genetics and comparative phylogeography. We are focusing on developing and implementing methods for bridging community ecology with population genetics and phylogeography to reconstruct the evolutionary and demographic histories of co-distributed species assemblages.

The ideal candidate will have a strong interest and aptitude in quantitative biology, modeling, and programming as well as an interest in evolutionary genetics and biogeography. The lab welcomes qualified applicants with diverse backgrounds, including biology, anthropology, mathematics, physics, computer science, and related fields.

Our lab is located in Manhattan and locally we have tight collaborations with the lab groups of Ana Carnaval (CUNY), Kyle McDonald (CUNY), Frank Burbrink (AMNH), and Brian Smith (AMNH), as well as international collaborations with Konrad Lohse (U. of Edinburgh, UK), and Brent Emerson (IPNA, Canary Islands, Spain). CUNY has a large and thriving community of faculty, students, and post-docs studying ecology, evolution, and behavior and we benefit from the academic environment in New York City that allows us to have close ties to the AMNH, the New York Botanical Gardens as well as other local universities, including Rutgers, Columbia, Fordham, Rockefeller, NYU and Stony Brook.

The position would start in the Fall of 2017. Contact mhickerson 'at' ccny cuny.edu if there is interest. Note that applications for Fall 2017 to the CUNY EEB subprogram must be received before January 1rst of 2017.

For more information visit: http://hickerlab.wordpress.com/ Michael J Hickerson Associate Professor City College of New York - Biology Department; City University of New York Ecology, Evolution and Behavior Sub-Program 160 Convent Ave New York, NY 10031 lab 212-650-3457

Ecology Evolution, and Behavior subprograms (EEB) City University of New York and the Graduate Center 365 Fifth Avenue New York, NY 10016-4309

Research Associate - Division of Invertebrate Zoology American Museum of Natural History http://hickerlab.wordpress.com/ "mhickerson@ccny.cuny.edu" <mhickerson@ccny.cuny.edu>

CWilliamMary PlantEvolutionaryGenomics

Graduate Position: Monarch Butterfly and Milkweed Conservation The Puzey lab at the College of William and Mary is recruiting graduate students (M.S) interested understanding the evolutionary history of Monarch-Milkweed interactions. More information about my lab can be found here: http://puzeylab.weebly.com . Positions for MS program start Fall 2017. Please contact Josh Puzey (jrpuzey@wm.edu) for more information.

The successful applicant will be passionate about evolution, interested in plant and insect interactions, and keen to use genomic techniques to address their research questions. Students working the Puzey lab get exposure to a wide range of analyses and techniques including next-generation sequencing (DNA, RNA, smRNA), population genomic analyses, and molecular ecology.

Details about the M.S. program in Biology at W&M can be found here (http://www.wm.edu/as/biology/graduate/). Full-time students are supported by teaching assistantships and full tuition waivers. Most students complete their master's degree in two years and go on to pursue either a Ph.D. or M.D. degree. Our program also provides the training required to enter technical positions in industry and government. Recent grads are pursuing Ph.D.s at Duke, UC Davis, Johns Hopkins, and University of Toronto; others are following career paths in biotech, pharmaceuticals, resource management, and environmental consulting.

Joshua Puzey <jrpuzey@gmail.com>

CzechRepublic 3 EvolutionaryParasitology

3 PhD student positions in molecular parasitology available at the Life Science Research Centre, University of Ostrava, Ostrava Czech Republic from September 1^st, 2017 in the laboratory of Molecular protozoology (Dr. Vyacheslav Yurchenko, http://www1.osu.cz/~yurchenko/)

1. To study the limits of trypanosomatids' biodiversity using molecular phylogenetic and phylogenomic methods.

Requirements: fluent English, knowledge of molecular phylogenetic principles and approaches. Basic biocomputing (e.g. genome and transcriptome analysis) and statistics experience are advantageous.

Recent publications:

Kostygov, A., Dobakova, E., Grybchuk-Ieremenko, A., Vahala, D., Maslov, D., Votypka, J., Lukes, J., Yurchenko, V. Novel trypanosomatid -bacterium association: evolution of endosymbiosis in action. mBio, 2016, 7(2): e01985-15. PMID: 26980834.

Votypka, J., d'Avila-Levy, C., Grellier, P., Maslov, D., Lukes, J., Yurchenko, V. New approaches to systematics of Trypanosomatidae: criteria for taxonomic (re)description. Trends Parasitol., 2015, 31: 460-469. PMID: 26433249.

2. To study the molecular mechanisms governing translation in Blastocrithidia sp.

Requirement: fluent English, advanced molecular biology skills (DNA, RNA, protein analyses, genome manipulations). Basic bio-computing experience (e.g. genome and transcriptome analysis) is advantageous.

Recent publication:

Zahonova, K., Kostygov, A., S evcikova, T., Yurchenko, V., Elias, M. An unprecedented non-canonical nuclear genetic code with all three termination codons reassigned as sense codons. Curr. Biol., 2016, 26(17): 2364-2369. PMID: 27593378.

3. To study novel virulence factors in Leishmania infection

Requirements: fluent English, advanced molecular biology skills (DNA, RNA, protein analyses, genome manipulations). Basic bio-computing experience (e.g. genome and transcriptome analysis) is advantageous.

Recent publications:

Flegontov, P., Butenko, A., Firsov. S., Kraeva, N., Elias, M., Field, M., Filatov, D., Flegontova, O., Gerasimov, E., Hlavacova, J., Ishemgulova, A., Jackson, A., Kelly, S., Kostygov. A., Logacheva, M., Maslov, D., Opperdoes, F., O'Reilly, A., Sadlova, J., S evcikova, T., Venkatesh, D., Vlcek, c., Volf, P., Votypka, J., Zahonova, K., Yurchenko, V., Lukes, J. Genome of Leptomonas pyrrhocoris: a high-quality reference for monoxenous trypanosomatids and new insights into evolution of Leishmania. Sci. Rep., 2016, 6: 23704. PMID: 27021793.

Kraeva, N., Butenko, A., Hlavacova, J., Kostygov, A., Myskova, J., Grybchuk, D., Lestinova, T., Votypka, J., Volf, P., Opperdoes, F., Flegontov, P., Lukes, J., Yurchenko, V. Leptomonas seymouri: adaptations to the dixenous life cycle analyzed by genome sequencing, transcriptome profiling and co-infection with Leishmania donovani. PLOS Path., 2015, 11(8): e1005127. PMID: 226317207.

Kraeva, N., Ishemgulova, A, Lukes, J., Yurchenko, V. Tetracycline-inducible gene expression system in Leishmania mexicana. Mol. Biochem. Parasitol., 2014, 198: 11-13. PMID: 25461484.

How to apply:

Please send your Resume and Cover/motivation letter to Dr. Vyacheslav Yurchenko by January 31, 2017. Do not forget to indicate position you are applying for. E-mail: vyacheslav.yurchenko@osu.cz

Laboratory of Molecular protozoology is a part of the Life Science Research Centre at the Faculty of Science, University of Ostrava focused on biological and biomedical research in the areas of functional genomics and bioinformatics. For more information, visit the lab web page at www1.osu.cz/~yurchenko/

Alexei Kostygov <kostygov@gmail.com>

CzechRepublic PlantCytogenetics

For the project "Repeatome dynamics in the earliest evolutionary stages of apomictic plants", funded by the Czech Science Foundation, we seek to the earliest possible date a highly motivated

PhD student in Cytogenetics

The project (duration 3 years) is aimed at a better understanding of mechanisms underlying the transition from sexual to apomictic reproduction. Apomixis is tightly connected with hybridization and polyploidization. Despite a great potential in agriculture, the genetic mechanisms of apomixis are still poorly understood. Hybridization causes genetic instability including a restructuring of the repeatome, the fastest evolving part of plant genomes. Bursts of transposable elements due to hybridization-induced genomic shock may trigger a switch to apomixis. In the project, sexual and apomictic Hieracium species will be investigated in an extensive breeding program, comparing artificial hybrids with natural apomicts of the same parentage as a model of hybrid speciation that may lead to the formation of apomictic lineages.

An interdisciplinary and international team of researchers from the Institute of Botany (www.ibot.cas.cz/en/) of the Czech Academy of Sciences and the Department of Botany of the Charles University in Prague (www.cuni.cz/UKEN-1.html) will tackle this complex biological question from various angles (cytogenetics, genomics, embryology, reproductive biology).

Responsibilities of the PhD candidate include karyotyping of plants, in situ hybridization (FISH, GISH) with a main focus on the localization of parental-specific repetitive elements using probes derived from NGS data as cytogenetic markers to investigate genome repatterning following hybridization. Further tasks include data processing and interpretation, presentations at international conferences and publications in IF journals.

Experience with karyological and cytological techniques, preferably in plants, is desired. The candidate should have an excellent command of English. Personal features should include reliability, patience, technical accuracy, flexibility, good social skills and the readiness to learn.

We offer creative work, the chance for personal development, a pleasant working atmosphere in a marvellous environment (Pruhonice Park, UNESCO World Heritage Site, www.pruhonickypark.cz/en/the-pruhonice-park/), and an excellent infrastructure at the Laboratory of Molecular Cytogenetics and Karyology (http://www.ibot.cas.cz/en/scientific-groups-and-laboratories/laboratory-of-molecular-cytogenetics-and-karyology/) under the leading of Dr. Alexander Belyayev. The PhD candidate will be enroled at Charles University in Prague, one of the oldest universities in Europe.

For more information, please contact Dr. Judith Fehrer (fehrer@ibot.cas.cz). Applications containing a motivation letter, a short CV and two references should be sent until 22. January to ibot@ibot.cas.cz.

Dr. Judith Fehrer Institute of Botany Czech Academy of Sciences Zámek 1 25243 Pruhonice near Prague Czech Republic

phone +420 271015415 fax +420 267750031 fehrer@ibot.cas.cz

Fehrer Judith <Judith.Fehrer@ibot.cas.cz>

DeakinU LifeHistoryStress

Ph.D. scholarship available Deakin University; Centre for Integrative Ecology, Geelong, Vic Australia Stress, song and transgenerational epigenetic inheritance

Although the transgenerational effects of early life stress have been well documented in a variety of non model organisms, the underlying mechanisms are unclear. The PhD student will join a supervisory team of Australian Research Council Future Fellow Professor Kate Buchanan, Professor Andy TD Bennett & Dr Ondi Crino, who are seeking an outstanding, highly motivated PhD candidate. Previous work has demonstrated the fundamental impact of early life stressors on vocal learning in songbirds. The aim of this PhD research is to assess the extent to which such effects occur across generations and test the possible mechanisms for transgenerational effects using Zebra Finches as a model systems. The PhD student will work with experimentally bred generation of wild-derived zebra finches in captivity, but opportunities for field work on wild populations of zebra finches in arid Australia are also available.

The PhD student will be in a vibrant and productive research team. They will test the role of early developmental stress for song learning, neural development and behaviour. They will conduct behavioural tests, bioacoustics analyses, neural sectioning and image brain sections for gene expression. Fundamentally the student will test whether early developmental conditions impose inherited influence on cognition, by assessing vocal learning in birds arising from control and developmentally stressed parents.

Start date: from March 2017 onwards Stipend: AUD$26,000 p.a. (tax exempt) for 3 years (for non-Australian/NZ citizens waivers to overseas tuition fee are potentially available)

It will build on our recent research, featured in the international leading journal Science, (and reported widely including The ABC Science Show, BBC, Smithsonian, New York Times) which showed transgenerational effects in zebra finches of singing to eggs. Check out https://www.youtube.com/watch?v=fDg67kUPAc PhD Project content: The student will join a productive ARC-funded team testing the effect of early life stress on vocal learning, neural development and behaviour. The student will have responsibility for carrying out behavioural playback experiments, recording and analysing avian song, collecting neural tissue and imaging the brain for gene expression. They will receive training in all these aspects, and as the research will involve collaboration with the Max Planck Institute for Ornithology in Germany, travel there may be possible. Although the project has clear aims to meet the project objectives, we seek a student who is keen to develop their own interests and so find their own individual niche within the project.

For further description of the research groups see the following sites: http://www.deakin.edu.au/profiles/kate-buchanan http://www.deakin.edu.au/profiles/andy-bennett http://cie-deakin.com/ Recent relevant publications by the group include: . Mariette M.M. & Buchanan K.L. (2016) Prenatal acoustic communication programs offspring for high posthatching temperatures in a songbird. Science 353: 812-814 DOI: 10.1126/science.aaf7049 . Buchanan, KL, J. Grindstaff and V.V. Pravosudov (2013) Condition- dependence, developmental plasticity and cognition: implications for ecology and evolution. Trends in Ecology and Evolution 28, 290-296. . Crino, O.L., K. L Buchanan, L.A Trompf, M. C Mainwaring, S. C Griffith (2016) Stress reactivity, condition, and foraging behavior in zebra finches: effects on boldness, exploration, and sociality. General and Comparative Endocrinology doi 10.1016/j.ygcen.2016.01.014. . Woodgate, J.L, K.L. Buchanan, A.T.D. Bennett, C.K .Catchpole, R. Brighton & S. Leitner. (2013) Environmental and genetic control of brain and song structure in the zebra finch. Evolution 68, 230- 240.

The Research Environment: The PhD student will be based in the Centre for Integrative Ecology (CIE) at Deakin University's Geelong campus. This is 50 minutes from the Melbourne CBD and 20 minutes from Bells Beach and the Great Ocean Road. Deakin hosts one of the largest ornithological research groups in the southern hemisphere, and in the recent ARC Research Assessment exercise received the highest possible rating (of 5) in Zoology. Excellent facilities are available including a 300m2 new aviary, modern lab and offices, well equipped 4WDs for fieldwork, excellent statistical support and established sites for fieldwork on zebra finches. The CIE has over 60 postdoctoral researchers and PhD students,

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DurhamU 3 EvolutionaryGenetics

Three competitive PhD studentship opportunities are available in evolutionary and ecological 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) Reconstructing the evolutionary history of ecological dynamics and extinction risk in seabirds

During their evolutionary history, birds have only rarely colonized the open oceans beyond the continental shelves. The Procellariiformes (albatrosses, shearwaters, storm-petrels, etc.) are by far the largest and most diverse group of oceanic birds, but their molecular phylogeny is poorly known. As part of an international collaboration, the student will use capture enrichment and next generation sequencing methods to collect a rich genomic dataset and resolve the phylogeny of all extant and recently extinct Procellariiformes, at and below the species level. This will advance our understanding of the evolution of oceanic avian predators, allow exploration of the role of ecology in the process of diversification, and inform conservation management of this globally-threatened group. Beyond this, the theory, methods, and skills learned while completing this project will be widely applicable and prepare the student for future success in academic, research, and non-governmental positions.

Eligibility: All nationalities Letters of interest should be received by 2 January 2017 If invited, full applications (including 2 reference letters) are due 9 January 2017

2) Using ancient DNA to uncover historical disease dynamics in North American and British deer

Diseases can have dramatic impacts by limiting population growth rates, producing strong selection pressures, and potentially leading to adaptive responses. While not infective to humans, chronic wasting disease (CWD) is a fatal disease in cervids (deer, elk, and moose). Analyses of the underlying Prnp gene suggest that particular alleles may influence susceptibility through decreased infection rates and/or slower disease progression. We will use ancient DNA techniques to examine changes in the frequencies of Prnp alleles through time in two deer species, European red deer (Cervus elaphus) and closely related North American elk (Cervus canadensis). For work on elk, the student will travel to the US and be hosted in the lab of our collaborator for three moths to study both infected and non-infected populations. While CWD is not currently present in the UK, evidence suggests that similar diseases may have influenced populations of red deer in the past, and investigation of contemporary populations will provide insights into current susceptibility, should CWD spread to the UK. Thus the student will have multiple opportunities to interface with UK governmental agencies working to prevent the spread of CWD to Britain.

Eligibility: UK citizens and EU citizens who have resided in the UK >3 years Letters of interest should be received by 9 January 2017 If invited, full applications (including 2 reference letters) are due 16 January 2017

3) Evolutionary insights for engineering improved globin

oxygen carriers

Around 2 million red blood cell units at a cost of 120 GBP per unit are transfused annually in England alone. These costs, together with a shortage of donors and inherent infection risks have led to the drive for the development of artificial, haem-based oxygen carriers. Our previous research has identified diving mammals as a natural model system for the study of biochemical/biophysical factors that allow greatly increased expression yields of the oxygen-binding protein myoglobin, a prototype for the development of haem-based oxygen carriers. This large-scale evolutionary, bioinformatics and phylogenetic analysis has revealed multiple convergent pathways to increased protein expression capacity by an order of magnitude in several mammalian lineages. These were associated with distinct increases in myoglobin net surface charge that presumably inhibit protein aggregation by electrostatic repulsion. We have since identified multiple convergent increases in myoglobin folding stability as another correlate of

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DurhamU UngulatePhylogeography

NERC PhD studentship available at Durham University (in collaboration with the British Geological Survey and the Natural History Museum) - full funding for UK nationals only:

Phylogeography of European ungulates from the last interglacial period and their subsequent evolution.

This project will involve ancient DNA and next generation sequencing to explore the genetic diversity of deer and other ungulates from the Eemian interglacial period, ~120,000 years ago. A key aspect of the study will be the integration of environmental data (including stable isotope analyses in collaboration with the British Geological Survey), so that any changes in demography or distribution can be interpreted in the context of changing environments. The studentship competition is through the NERC IAPETUS DTP. A detailed flyer describing the project is available at http://www.iapetus.ac.uk/ Application materials should include a c.v., academic records and at least two letters of reference sent to a.r.hoelzel@dur.ac.uk. Advisory team: Rus Hoelzel, Melanie Leng, Darren Grocke and Adrian Lister. Deadline is 20 January 2017

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

EastCarolinaU EvolutionaryGenetics

Graduate position: Evolutionary genetics at East Carolina University

Pending approval of funding, I will be recruiting a doctoral student to carry out research associated with a project focused on the genetic underpinnings of color pattern evolution in a mimetic radiation of poison frogs in Peru (see abstract below). The position would formally begin in the fall of 2017, but the student could potentially participate in fieldwork for the project in Peru in the summer of 2017 before starting in the doctoral program. Desirable qualifications for this position include relevant coursework or experience with modern approaches in evolutionary genetics and genomics, such as RNA and DNA extraction, RNA and DNA library preps, Next-generation sequencing (especially on the Illumina platform), exome capture sequencing, analysis of Next-Gen datasets including data clean-up, transcriptome assembly, differential expression analyses, population genomic analyses of genomic reduced representation (e.g. exome capture) datasets, and association analyses using multi-generational pedigrees. Experience working with amphibian breeding programs and/or fieldwork in Latin America would also be a plus. I encourage applications from minorities and under-represented groups of all kinds. Please send a letter detailing your relevant experience and explaining your interest in the position, as well as a current CV (including a summary of academic coursework, grades and achievements) and GRE scores (if available) to Kyle Summers (summersk@ecu.edu).

Information about evolutionary biology at East Carolina University The Department of Biology at East Carolina University has a strong commitment to research in evolutionary biology in general and evolutionary genetics in particular, with multiple faculty doing related research. Faculty with related interests include Chris Balakrishnan (avian evolutionary genomics), Michael Brewer (evolutionary genomics of arthropods), Jeff McKinnon (evolutionary ecology and genetics of sticklebacks), Susan McRae (avian evolutionary genetics and behavior), Trip Lamb (phylogeography of reptiles, amphibians and insects), April Blakeslee (evolutionary genetics of marine invertebrates), Carol Goodwillie (evolutionary ecology and genetics of plants), John Stiller (plant evolutionary genomics), Michael McCoy (theoretical ecology and evolution), Krista McCoy (ecological physiology), Jinling Huang (evolutionary genomics and horizontal gene transfer), and Ariane Peralta (Microbial ecological genomics). Information on applying for admission to the doctoral program at ECU can be found at: http://www.ecu.edu/cs-cas/idpbs/ . Abstract of proposed research The evolution of color pattern diversity in the context of mimicry has been a focus of theoretical and empirical attention, yet knowledge of the genetic basis of this diversity remains limited. Most work on this topic has focused on a small number of systems (e.g. Heliconius butterflies), limiting the generality of inferences. This project combines three research groups with complementary skills and realms of expertise to investigate the genetic basis and population genomic processes underlying color pattern divergence in the context of mimicry in the Peruvian mimic poison frog, Ranitomeya imitator: Dr. Kyle Summers (East Carolina University), Dr. Rasmus Nielsen (UC Berkeley) and Dr. Matthew MacManes (University of New Hampshire). The project focuses on four specific aims: 1. Identify key genetic factors involved in color pattern development in R. imitator by investigating differential gene expression across developmental stages and color pattern morphs. Next generation sequencing will be used to produce developmental stage-specific transcriptomes for each morph, which will be assembled and used to investigate patterns of differential gene expression. 2.Identify the causal gene(s) underlying differences in color pattern between morphs using genome-wide marker arrays (exome capture sequences) to screen transition zone samples and enable admixture mapping. We have identified three admixture zones in the mimetic radiation that will be appropriate for these analyses. 3. Test the association of specific candidate loci with color pattern using pedigree analyses of candidate genes identified from Aims 1 and 2, using a multigenerational pedigree. 4. Test specific hypotheses regarding selection and demographic processes in the transition zones and between mimics and models. These analyses will involve the development of new analytical tools for analyzing selection in admixture zones and targeted sequencing of model species. Together these complementary, reciprocally illuminating approaches will begin to reveal the genetic underpinnings and population genomics of color pattern diversity in this mimetic radiation of poison frogs.

Kyle Summers Dept. of Biology East Carolina University Greenville, NC 27858 252-328-6304

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ETH Zurich BacterialPhylodynamics

The Computational Evolution group led by Prof. Tanja Stadler at the Department of Biosystems Science and Engineering in Basel, ETH Zurich, invites applications for a

PhD position in bacterial phylodynamics: towards understanding the evolution and spread of antibiotic resistance.

All further information about the position and how to apply are available on https://apply.refline.ch/845721/5065/pub/1/index.html Tanja Stadler ETH Zürich Department of Biosystems Science & Engineering (D-BSSE) Mattenstrasse 26 4058 Basel Switzerland

Email: tanja.stadler@bsse.ethz.ch Phone: +41 61 38 73410 Office: 7.54

https://www.bsse.ethz.ch/cevo
tanja.stadler@bsse.ethz.ch

GriffithU PopulationGenomics

A Ph.D. scholarship in Bioinformatics/Population Genomics is available at Griffith University, Nathan, Australia. We have a world class Genomics laboratory and have sequenced the genomes of penguins, humans and canines. We are looking for an enthusiastic student with immense interest in the bioinformatics analysis of next generation sequence data. The prospective student will be working on a project to analyse genome data (to be generated in this lab as well as those available in the databanks) to examine the patterns deleterious mutations in human populations.

An honors or master's degree in biological, physical or computational science is required. Persons with a non-biology degree should have some basic understanding of genetics, evolution and molecular biology.

Essential skills include: [We wouldn't expect a starting PhD student to have many of these skills, but an ability and desire to learn them is obviously essential]

Scripting: Perl/Python Unix command line (particularly to use parallel computing clusters) Programming: Java/C/C++ (OOPS concept) Database: maintenance and design; MySQL/PosgreSQL/SQLite or similar Familiarity with sequence databases and genome browsers (eg. NCBI/EMBL/DDBJ, UCSC) Familiarity with the following software is desirable: Read mapping: BWA; Bowtie; GSMapper (454); SOAP De novo assembly: Velvet; SOAP de novo; Assembly summary: Samtools; GATK Population genetic software: PLINK; EIGENSOFT

English language requirements: A minimum overall band score of 6.5 on IELTS (Academic) with no subscore of less than 6.0 or A minimum score of 575 of TOEFL (Paper) or A TOEFL iBT score of 79 (no score less than 19)

For further details please contact Sankar Subramanian (s.subramanian@griffith.edu.au)

Regards Sankar

Sankar Subramanian Research Fellow Research Centre for Human Evolution Griffith University Nathan QLD 4111 Australia

Email: s.subramanian@griffith.edu.au Ph: 61-7-37357495 Fax: 61-7-37357459

Sankar Sankarasubramanian <s.subramanian@griffith.edu.au>

IGB Berlin HostParasiteCoevol ChineseCandidates

Open PhD position for Chinese candidates WolinskaÂs Lab is seeking an outstanding PhD Candidate for applying to a PhD program at the Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB) located in Berlin, Germany (affiliated with the Free University Berlin).

The candidate will apply for a PhD stipend with China Scholarship Council. The application deadline (i.e. first step) is 04.01.2017. For more information about the FUB-CSC funding program, please check: http://www.fu-berlin.de/en/sites/-china/foerdermoeglichkeiten/fuer_chinesen/csc/ For application procedure, please check: http://www.fu-berlin.de/en/sites/china/foerdermoeglichkeiten/-fuer_chinesen/csc/PhD_Offer_2017/index.html PhD Project description http://www.fu-berlin.de/en/-sites/china/foerdermoeglichkeiten/fuer_chinesen/-csc/PhD-Positions-2017/PhD-Wolinska-Evolutionary-Ecology.pdf Project title: Role of parasitic chytrids in regulating cyanobacterial blooms Project description: Parasitic fungi of the order Chytridiales (i.e. Chytrids) are able to infect a wide number of phytoplankton species. Although overlooked for a long time, chytrids are an important factor driving the dynamics of phytoplankton. For example, Chytrids seem to be involved in the decline of toxic cyanobacteria blooms, by inducing direct mortality of parasitized cells and indirectly by the mechanistic fragmentation which weakens the resistance to grazing. On the other hand, selection on host populations exerted by Chytrids is also thought to be responsible for maintaining high host diversity in nature. The candidate will use a novel host-parasite system (based on a cyanobacterial host and its chytrid parasite) for advancing in the field of parasitism in phytoplankton. The scope of the project will address different questions related to the physiology, molecular genetics and genomics (including next-generation-sequencing) of the interactions and their ecological and evolutionary implications.

Language requirements: excellent English skills (fluent conversation and good writing skills)

Academic requirements: Master degree in biology or bioinformatics. Solid background in ecology, evolution and/or molecular biology.

Information about Wolinska's lab: We are a group of evolutionary ecologists who study how rapid evolutionary changes are being influenced by environmental challenges. We have a long-standing experience working with the Cladoceran model system: Daphnia and its microparasites. Recently, we also employ a Cyanobacteria-Chytrid system to explore a number of ecological and evolutionary questions. http://www.igb-berlin.de/en/-profile/justyna-wolinska-0 http://www.igb-berlin.de/-en/disease-evolutionary-ecology Justyna Wolinska

Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) Department II (Ecosystem Research) Mueggelseedamm 301 12587 Berlin, Germany

Group Leader at the IGB & Professor for Aquatic Evolutionary Ecology at the Free University of Berlin

email: wolinska@igb-berlin.de

http://www.igb-berlin.de/en/profile/justyna-wolinska-0

Google Scholar: https://scholar.google.com/-citations?user=80WCzk8AAAAJ&hl=en Justyna Wolinska <wolinska@igb-berlin.de>

ImperialC London 12 Evolution

The Quantitative and Modelling Skills in Ecology and Evolution (QMEE) CDT is pleased to announce 8 NERC-funded PhD studentships plus 4 institutional PhDs starting in October 2017.

The QMEE CDT will train a cohort of researchers in Ecology and Evolution with the quantitative and modelling skills to solve real-world problems by connecting theory, data, and practice. To view example projects, instructions on how to apply and information on eligibility please visit our website.

The deadline for applications is 19th January 2017.

For any questions, please contact Ibi Wallbank, Departmental Manager, at qmee.cdt@imperial.ac.uk

Please help disseminate this opportunity to anyone you think may be interested.

QMEE CDT <qmee.cdt@imperial.ac.uk>

ImperialC London EcoGeneticSpeciation

PhD on 'The ecological and genetic determinants of speciation'

Department of Life Sciences, Imperial College London (Silwood Park Campus), UK

Competition-funded as part of the NERC Doctoral Training Partnership in Science and Solutions for a Changing Planet (SSCP).

Supervisor: Prof Tim Barraclough

Key words: speciation, evolution, adaptation, animals, plants, theory, models, phylogenetics, genomics, experimental evolution

Why does life diversify into multiple species? Why do some taxa diversify into clearly distinct species whereas others have blurred species boundaries? Does selection favour complete speciation or porous species boundaries? Or are species instead an incidental consequence of long-term isolation of populations?

Answering these questions requires knowledge of the rates and determinants of the multiple steps by which speciation occurs. First, an existing species must encounter conditions that favour divergence into separate species. Second, it must respond to those conditions and evolve population differences and restrictions to gene flow. Third, the descendant species must coexist and persist. Fourth, some of the descendant species must encounter new conditions that favour further diversification, for example by expanding their ranges.

We currently have good understanding of some parts (e.g. genetics of speciation, diversity patterns), but poor knowledge of others - especially how ecological conditions influence each step of diversification. Experiments that quantify key processes over multiple generations have been lacking - much of our understanding comes from observational evidence. In short, we lack the kind of robust theory and evidence that is available for other ecological and evolutionary processes.

The goal of this PhD is to build synthetic understanding of speciation by assembling information on the multiple steps in the process. The student will use several approaches to tackle the problem including 2 or more of the following:

1) Mathematical or computational modelling, combining macroevolutionary and population genetic approaches to model speciation dynamics

2) Comparative population genetics to quantify the nature of species boundaries and estimate the rates of different stages in speciation. An existing system that could be adopted is the flowering plants of the Cape region of South Africa

3) 'Speciation in action' in the laboratory - using experimental evolution to determine the conditions affecting selection on species boundaries. Existing systems that could be adopted include wild yeasts or tree-hole bacteria.

4) Meta-analyses of published data from a range of animal, plant and/or microbial groups, including the analysis of emerging whole genome data.

The balance of approaches will be flexible based on the student's interests and would be developed in discussion to address current gaps in understanding. If you have strong interests in evolutionary biology and you are keen to develop theoretical, molecular, experimental, field and/or molecular skills, then this is the PhD for you! Motivation to develop your own ideas is more important than existing experience in the above areas, which can be learned during the PhD.

For more information on topics and approaches currently used in the group, visit barralab.ic.ac.uk.

To apply:

Please send a covering letter explaining your interests and experience, your CV and names of 2 referees to Tim Barraclough at t.barraclough@imperial.ac.uk before the 16th January 2017.

Eligibility:

Applicants will have, or be about to obtain, a Masters qualification and a 2.1 or higher undergraduate degree. Exceptional students at Bachelors level without a Masters will also be considered. Relevant post-graduate experience will also be taken into account.

NERC-funded studentships are subject to RCUK eligibility requirements, which are outlined under "Student eligibility" and "Residence Requirements" on the RCUK website. In short you should be a citizen of the UK or other EU country and have been residing in the UK for the last 3 years (apart from temporary or occasional absences). More information at http://www.imperial.ac.uk/qmee-cdt/how-to-apply/ I am happy to discuss other scholarship options with students not meeting these criteria.

"Barraclough, Tim G" <t.barraclough@imperial.ac.uk>

ImperialC London EvolutionMicrobialCommunities

PhD on 'The evolutionary dynamics of microbial communities'

Departments of Life Sciences and Mathematics, Imperial College London, based at Silwood Park Campus, UK.

Competition-funded as part of the NERC Centre for Doctoral Training in Quantitative and Modelling Skills in Ecology and Evolution (QMEE).

Supervisors: Prof Tim Barraclough (Life Sciences) and Prof Mauricio Barahona (Mathematics)

Microbial communities underpin many ecosystem services that human populations depend upon. Nutrient cycling, waste-water treatment and the digestive systems of animals all depend on the combined actions of hundreds or thousands of interacting species. Understanding of microbial diversity has been revolutionised by metagenomics. Yet, it remains extremely hard to predict microbial dynamics in response to changing conditions, such as climate change, pollution or a change in diet. General theory for the dynamics of bacteria embedded in diverse systems is lacking.

Current models of microbial ecosystem functions often treat the community as a black-box - ignoring the fact that responses will depend on how metabolic functions and traits are packaged among interacting species. Critically, models and data are needed that incorporate evolution, since microbes can rapidly adapt to new conditions. Ecological interactions alter evolutionary responses and vice versa, but tracking evolution in diverse microbial assemblages is hard. Models are needed to shape predictions and to develop new methods for statistical inference from metagenome data.

In this PhD, you will develop new theory for predicting evolutionary and functional dynamics of microbial communities facing changing conditions. Over-arching questions include: how predictable are evolutionary dynamics in systems with hundreds of species, does evolution of constituent species promote or disrupt ecosystem functioning and stability and can we use evolutionary theory to guide human interventions in microbial communities, for example creating designer microbiomes?

The building blocks will be models that predict bacterial growth (and consequently species interactions) from their use of metabolites. In a decomposer community, input resources are broken down successively by different populations of bacteria into a set of output resources. Depending on context, we might want to optimise the breakdown of inputs (e.g. wood pulp waste), or production of intermediates (e.g. short-chain fatty acids in the human gut) or end-products (e.g. methane in biofuels).

You will develop mechanistic models of microbial communities to predict dynamics and devise statistical methods for detecting evolutionary dynamics from omic data, for example using network modelling (2). Interaction networks can be extracted from data using graph-theoretical methods for geometric dimensionality reduction as well as sparsification techniques from statistics. Predictions and statistical methods will be tested on real data - either from the literature or evolution experiments (3), depending on your interests. Validated models will then be used to identify conditions that promote particular dynamic outcomes and to design evolutionary strategies for improving functioning of microbiomes that humans rely on. The project will combine microbial ecology and evolution with mathematics and statistics.

To apply:

Please send a covering letter explaining your interests and experience, your CV and names of 2 referees to Tim Barraclough at t.barraclough@imperial.ac.uk before the 19th January 2017.

Eligibility:

Applicants will have, or be about to obtain, a Masters qualification and a 2.1 or higher undergraduate degree. Exceptional students at Bachelors level without a Masters will also be considered. Relevant post-graduate experience will also be taken into account.

NERC-funded studentships are subject to RCUK eligibility requirements, which are outlined under "Student eligibility" and "Residence Requirements" on the RCUK website. In short you should be a citizen of the UK or other EU country and have been residing in the UK for the last 3 years (apart from temporary or occasional absences). More information at http://www.imperial.ac.uk/qmee-cdt/how-to-apply/ A limited number of studentships might also be available to students not meeting the UK residency requirements.

References:

(1) Barraclough, TG 2015 How do species interactions affect evolutionary dynamics across whole communities? Ann Rev Ecol Evol Syst 46:25-48 (2) Bacik KA, Schaub MT, Beguerisse-Díaz M, Billeh YN, Barahona M 2016 Flow-based network analysis of the Caenorhabditis elegans connectome. PLoS Comput Biol 12: e1005055 (3) Lawrence, D, Fiegna F, Behrends, V, Bundy, JG, Phillimore, AB, Bell, T and Barraclough TG 2012. Species interactions alter evolutionary responses to a novel environment. PLoS Biology 10: e1001330.

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ImperialC London EvolutionSexualBehaviours

The evolution of sexual behaviours: developing and testing biological models of non-reproductive sex, including homosexuality

SUITABLE FOR STUDENT WITH EITHER MATHEMATICAL OR BIOLOGICAL STUDY BACKGROUND

Supervisor:

Professor Vincent Savolainen; Imperial College London, Life Sciences

Co-supervised by: Dr Richard Everitt (University of Reading; Mathematics and Statistics); Dr Jason Hodgson and Professor Emeritus Russ Lande FRS, Imperial College; in collaboration with Dr Emily Bethell (Liverpool John Moores University)

Project summary:

Sexual behaviour takes multiple forms across organisms, and although it has evolved for reproduction, it also serves other social purposes. Across species, males usually have sex with females (heterosexuality), however this is not always the case, and there are numerous possible variations. For example, homosexual behaviour is common throughout the animal world, and has often been considered an evolutionary paradox. The existence of the supposed paradox is likely a confluence of the assumption that those who engage in homosexuality fail to reproduce, coupled with cultural disapproval of homosexual behaviour. Some of this confusion may also stem from the fact that most researchers have considered sexuality to be a binary trait with either homosexual or heterosexual trait states. If sexual preference is a continuous trait influenced by many different genes of small effect, or some epigenetic marks canalizing a 'mosaic' development, then the persistence of homosexual behaviour is not particularly surprising. The seeming Darwinian paradox of homosexual behaviour has led to the development of several biological models to explain its prevalence. Most models fall into two broad categories: genetic and epigenetic models. Genetic models typically explain the persistence of a hypothetical homosexual gene variant (allele) through some indirect evolutionary advantage for that variant (e.g. see Savolainen & Lehmann, Nature 445:158, 2007). Epigenetic models explain homosexual behaviour as a result of heritable changes in gene expression patterns due to chemical modifications that occur to the DNA of developing organisms (Rice et al., Quarterly Review of Biology 87:343, 2012). These models each make clear predictions, however, there is only limited support for any of them. Also, these models may be too simplistic to account for the complexity of behaviours found in the wild. Furthermore, Savolainen & Hodgson (Encyclopaedia of Evolutionary Psychology, in press) have proposed an alternative model, the bisexual advantage model, whereby homosexuality is a quantitative trait controlled by many loci. This bisexual advantage model is perhaps the most conservative genetic explanation for the persistence of homosexual behaviour because sexuality would then follow the pattern of the vast majority of quantitative traits where intermediate phenotypes are favoured (Lande, Genetics Research 26:221, 1976). It may be the case that some degree of bisexuality is actually an evolutionary optimum phenotype in many species, including humans. The student will formalize mathematically models for the evolution of non-reproductive sexual behaviours depending on the ecology of species, and also including the bisexual advantage model proposed above. The student will make predictions using mathematical genetics, computer simulations and computing tools such as machine deep learning. S/he will also use and/or collect behavioural data in a well-established field system to test these predictions. This project will integrate approaches from evolutionary biology, animal behaviour, genetics and mathematical biology to disentangle the evolutionary ecology of sexual behaviours in natural environments, while addressing a problem with large social implications in human societies.

HOW TO APPLY:

You should send to v.savolainen@imperial.ac.uk: (1) an extended CV detailing your academic credentials and research experience; (2) a covering letter explaining in details how your would fit and why you are interested in (3) the Centre for Doctoral Training in Quantitative and Modelling Skills in Ecology & Evolution (http://www.imperial.ac.uk/qmee-cdt/) and (4) that project; (5) the names and e-mail addresses of two academic referees (at least one of them should have supervised you on a previous research project).

SUITABLE FOR STUDENT WITH EITHER MATHEMATICAL OR BIOLOGICAL STUDY BACKGROUND

DEADLINE 19 JANUARY 2017

Note that you should meet the UK NERC eligibility criteria (i.e. be a resident in the UK)

Prof. Vincent Savolainen Professor of Organismic Biology Department of Life Sciences Imperial College London, Silwood Park Campus Buckhurst Road, SL5 7PY Ascot, Berks, UK Tel: +44 (0)20 7594 2374 Fax: +44 (0)20 7594 2339 v.savolainen@imperial.ac.uk skype vincent.savolainen1 www3.imperial.ac.uk/people/v.savolainen

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ImperialC London PopGenomicsChytrid

Population genetics of amphibian-killing fungi: from big genomic data to big ecological insights

SUPERVISORS:

Dr Matteo Fumagalli (Imperial College London, Life Sciences), Professor Matthew Fisher (Imperial College London, Infectious Disease Epidemiology), Dr Richard Everitt (University of Reading, Mathematics and Statistics)

PROJECT SUMMARY:

The amphibian chytrid fungus Batrachochytrium dendrobatidis (Bd) is responsible for hundreds of species' extinctions (Fisher et al. Nature. 2012). The genetic mechanisms that underpin Bd's virulence are not known yet, although extreme chromosomal plasticity has been suggested to play a role (Farrer et al. PLoS Genet. 2013). 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.

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/). Informal inquiries can be addressed to m.fumagalli@imperial.ac.uk

DEADLINE 19 JANUARY 2017

Matteo Fumagalli 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
m.fumagalli@imperial.ac.uk

LMU Munich Paleobiology

Applications invited for the Master's program "Geobiology and Paleobiology" (MGAP) at the Ludwig-Maximilians-Universität (LMU) Munich (Germany) for international students until 31 Jan 2017

The Master's program "Geobiology and Paleobiology" (MGAP) is a consecutive, research-focussed, two-year Master of Science program at the Faculty of Geosciences of the Ludwig-Maximilians-Universität (LMU) Munich, in collaboration with researchers of the Bavarian Natural History Collections and the GeoBio-Center @ LMU. MGAP aims to provide students with a comprehensive introduction into the interdisciplinary research fields of geobiology and paleobiology to prepare them for careers in science and beyond.

The MGAP program is based on interdisciplinary, research-oriented courses in geo- and biosciences that address patterns and processes of the evolution of life and its habitats on our planet. Principal topics are evolutionary and environmental geobiology and paleobiology, supported by courses in complementary areas e.g., bioinformatics and statistics.

The module-based curriculum provides an integrative approach facilitated by experts in different areas of expertise. Students will learn and acquire routines with a wide range of scientific methods such as modern techniques in molecular biology, fieldwork, collection management, comparative morphology & phylogeny, bioinformatics, statistics and (paleo-) biodiversity assessments. Students will learn independent scientific work in individual and intensively supervised research projects at early stages of the curriculum.

MGAP in brief

- International Master's program in Geobiology and Paleobiology (Master of Science, M.Sc.) at the LMU Munich
- 2 years, 4 semesters, start in October (winter semester)
- All courses taught in English
- Courses are combined in Modules
- Course total: 120 credit points (ECTS)

More information is available on the program's website: < http://www.mgap.geo.uni-muenchen.de >

For the winter semester 2017-2018 (courses start mid-October), application deadlines are as follows:

1. January 31, 2017 for international students (non-EU students and EU students (non-German)), applications are possible now: < http://www.mgap.geo.uni-muenchen.de/admission >

2. February 15 to May 31, 2017 for German and EU students.

All applications have to be submitted via an online submission portal:

< https://www.efv.verwaltung.uni-muenchen.de/-mageopal> The Department of Earth- and Environmental Sciences (Division of Palaeontology & Geobiology) of the Ludwig-Maximilians-Universität Munich offers an excellent multidisciplinary research and learning environment, one of its particular strength being the close interaction between Geosciences, the Biological Faculty, and the Bavarian Natural History collections (< http://www.snsb.de >) in the framework of the GeoBioCenter@ LMU (< http://www.geobio-center.uni-muenchen.de >).

The LMU Munich is the leading research university in Germany, with a more than 500-year-long tradition, and builds upon its success in the Excellence Initiative, a Germany-wide competition promoting top-level university research. LMU Munich also has been successful in the "Qualitätspakt Lehre" initiative by the German Federal Ministry of Education and Research (BMBF) to promote innovative teaching and learning. Munich has also been repeatedly voted Germany's most liveable city.

Oliver Voigt <oliver.voigt@lmu.de>

MississippiStateU EvoDevo

Research in the Range lab deals with fundamental questions in animal evolution and development - how signal transduction interactions control the gene regulatory networks that establish specific territories along the major axes during early embryogenesis. Most of our research focuses on understanding how a network of three different Wnt signaling branches (Wnt/Beta-catenin, Wnt/JNK, and Wnt/Ca2+) coordinate the regulatory networks that establish territories along the anterior-posterior axis in sea urchin embryos. Remarkably, functional and expression studies in other metazoans (vertebrates, urochordates, hemichordates, echinoderms and cnidarians) suggest that many aspects of this Wnt network governing AP axis specification in the sea urchin might have existed in the common ancestor of bilaterians and cnidarians.

We are recruiting a talented PhD student to work on a NIH funded project beginning in the Fall of 2017. The project will focus on the role of the Wnt/JNK pathway and the gene regulatory network it activates during AP axis specification and patterning in sea urchin embryos. A secondary focus will be on the conservation of this mechanism during hemichordate AP axis specification and patterning. The position offers training in a combination of molecular manipulations, high-throughput genome-wide assays and bioinformatics, gene regulatory network analysis as well as classical embryology.

Interested applicants should contact Dr. Ryan Range at range@biology.msstate.edu. With your inquiry, please include a CV, unofficial transcript, and unofficial copy of your GRE scores if available.

Mississippi State University is situated in the quintessential college town of Starkville and is located close to several major cities (e.g. New Orleans, Memphis, Birmingham) as well as the beaches along the Gulf of Mexico. You can learn more about the Department of Biological Sciences at Mississippi State University at http://biology.msstate.edu . Applications for the fall are accepted until June 1st, 2017. Please contact Dr. Range if you would like to be considered for recruitment day in late February/early March 2017.

Recent publications related to the position:

Integration of canonical and non-canonical Wnt signaling pathways patterns the neuroectoderm along the anterior-posterior axis of sea urchin embryos. Range RC, Angerer RC, Angerer LM. PLoS Biol. 2013;11(1):e1001467. doi: 10.1371/journal.pbio.1001467. PMID: 23335859

Specification and positioning of the anterior neuroectoderm in deuterostome embryos. Range R. Genesis. 2014 Mar;52(3):222-34. doi: 10.1002/dvg.22759. Review. PMID: 24549984

An anterior signaling center patterns and sizes the anterior neuroectoderm of the sea urchin embryo. Range RC, Wei Z. Development. 2016 May 1;143(9):1523-33. doi: 10.1242/dev.128165. PMID: 26952978

Ryan C. Range Assistant Professor Dept. of Biological Sciences Mississippi State University P.O. Box GY, 295 E. Lee Blvd Mississippi State, MS 39762

E-mail: range@biology.msstate.edu Phone: 662-325-7569

"Range, Ryan" <range@biology.msstate.edu>

MonashU MarineEvolEcol

Two PhD positions available: the evolutionary ecology of marine heterotrophs. by dustinmeeg

Two fully-funded PhD stipends are available to students interested in working on the evolutionary ecology of marine heterotrophs in the Centre for Geometric Biology (https://cgb.org.au). Prof Dustin Marshall is the director of the Centre and Prof Craig White is deputy-director, however the specifics of the project and the most appropriate supervisors from the CGB will depend on the interests of the successful students and collaboration between student and supervisor.

The stipends include all course fees plus ~$26,288 AUD per annum tax-free with no teaching requirements for 3.5 years (the length of a PhD in Australia). Domestic students (Australian and New Zealand) will be eligible for 'top up funding' to a total stipend of $30,000. Guaranteed funding of project costs and research support, including the costs of attending at least one conference per year, is included

Project start dates to be in the first half of 2017.

To be eligible, applicants must have completed at least one year of post-graduate research in ecology and/or evolution.

Successful applicants will hold a BSc H1 or equivalent (first class honours degree) or a Masters by research degree and preference will be given to those with strong quantitative skills and publications in international journals.

Any offers made by the CGB are subject to acceptance by Monash University.

Interested students should send a CV, brief statement of interests and contact details of two referees to Liz.Morris@monash.edu Application closing date January 22^nd 2017.

Dr. Liz Morris Administration Manager Centre for Geometric Biology School of Biological Sciences Monash University Clayton, Vic 3800 Australia Mob: +61 3 404 069 210 Email: Liz.Morris@monash.edu

Liz Morris <liz.morris@monash.edu>

RiceU EvolutionaryBiol

Graduate Coordinator | BioSciences at Rice University | marya@rice.edu |

W131 George R. Brown Hall - MS 140 | 713-348-4230 (phone) / 713-348-4790 (fax)

The Graduate Program in Ecology and Evolutionary Biology in the Department of BioSciences at Rice University invites applications for admission into our PhD program. The department is home to a vibrant community of faculty, postdoctoral, graduate, and undergraduate scholars in ecology and evolution. Our program has particular strengths in population and community ecology, behavioral ecology, conservation biology, evolutionary ecology, speciation, and evolutionary genetics and genomics.

We are located in Houston, Texas, an exciting, diverse, and affordable city with world-class opportunities for dining, arts, and entertainment and access to diverse terrestrial and aquatic environments. Rice is located beside one of the country's largest medical research centers, providing additional opportunities in bioinformatics, genomics, and translational research.

Completed applications should be received by December 31 to ensure full consideration. There is no application fee for US citizens and permanent residents. Prospective applicants are encouraged to contact potential faculty advisors before applying. Complete information about the graduate program, including application instructions, may be found at https://biosciences.rice.edu
Mary Aycock <marya@rice.edu>

RiceU:PopGenConservation

The Egan Lab at Rice University is looking for a prospective PhD student to participate in a set of grant-funded projects linking population genetics, conservation biology, and biodiversity monitoring.

Our lab is broadly interested in integrative evolutionary biology, including studies of ecology, evolution, and population genetics. Primary work in the lab focuses on the evolution of ecological specialization, the evolution of new species, and applied projects dealing with conservation and/or the genetic detection of rare species (invasive, endangered, or dangerous). Current funding the lab supports two projects: (1.) linking population genetics with environmental monitoring of rare species and (2.) genetic biodiversity monitoring of entire aquatic communities. Students with experience in molecular genetics and bioinformatics are strongly encouraged to apply.

The Department of BioSciences at Rice University is home to a vibrant community of faculty, postdoctoral, graduate, and undergraduate scholars in Ecology and Evolution, Biochemistry, Cell Biology, Genetics and Neuroscience. Our EEB program has particular strengths in species interactions, animal behavior, population and community ecology, conservation biology, evolutionary ecology, and evolutionary genetics and genomics.

Completed applications should be received by December 31 to ensure full consideration. There is no application fee for US citizens and permanent residents. Prospective applicants are strongly encouraged to contact the Egan Lab before applying. Complete information about the graduate program, including application instructions, may be found at http://biosciences.rice.edu . For more information, please contact Scott Egan and include a CV, GPA, and GRE scores.

Scott P. Egan, Assistant Professor of Ecology and Evolutionary Biology, Department of BioSciences, Rice University, Houston, TX

Email: scott.p.egan@rice.edu; Website: https://sites.google.com/site/scottpegan/
"scott.p.egan@rice.edu" <scott.p.egan@rice.edu>

StellenboschU LizardColourEvolution

PhD opportunity (2017-2019)

Project title: The thermal properties of lizard coloured integument: mechanisms and evolution

Project summary: Colouration in animals can be shaped by a multitude of factors, from chemical and physical properties of the skin to higher-level drivers of colour variation such as natural and sexual selection. While a lot of the focus has been directed to the role of colour in signalling and camouflage, much less has been devoted to the potential role that colour plays in thermal relations and its adaptive significance. Using a combination of techniques, this project aims to investigate the thermal effects of coloured integumentary tissue in lizards from both a proximate and ultimate perspective by 1) characterizing thermal properties of differently-coloured integument, 2) elucidating form-function relationships for different colour production mechanisms (including iridescence) through optical and heat-transfer models and 3) explore the role of thermal effects in the evolution of animal coloration.

This project is part of a collaboration between Prof. Matthew Shawkey (Dept. of Biology, Ghent University, Belgium, http://users.ugent.be/~mshawkey/Shawkeys_Lab/Home.html) and Prof. Susana Clusella-Trullas (CL*I*M*E Lab, Dept. Botany and Zoology, Stellenbosch University, South Africa, http://www.clusellatrullas.blogspot.co.za/).

The student will be based at Stellenbosch University, will perform field work in South Africa and will receive training in histological methods and heat-exchange modeling approaches at the University of Ghent. Applicants must be highly motivated and committed, independent, have an excellent academic track record and preferably have a good publication record and advanced analytical skills. All project running costs have been secured and the selected applicant will be able to start immediately (2017).

To apply, please send a CV with contact information of 3 academic referees, academic transcripts and a personal statement describing your research interests and past experience (max. 500 words) to sct333@sun.ac.za. Review of applications will begin from the 16th of January 2017 and short-listed candidates will be contacted to set up interviews by phone or skype.

Susana Clusella-Trullas Associate Professor - Physiological Ecology Department of Botany and Zoology & Centre for Invasion Biology Stellenbosch University Private Bag X1 - Stellenbosch 7602 South Africa Tel: +27 21 808 3974

http://clusellatrullas.blogspot.co.za/ "Clusella-Trullas, S, Prof <sct333@sun.ac.za>" <sct333@sun.ac.za>

StonyBrookU NY AnthropologicalGenomics

The Veeramah Lab (*http://life.bio.sunysb.edu/ee/veeramahlab/index.html*) is looking to recruit two PhD Students to begin in Fall 2017. The primary focus of the lab is examining genetic diversity in human and non-human primates. The lab currently has ongoing projects examining primate evolution through genomic scale data, as well as a variety of paleogenomic projects involving European human and non-human populations. The exact research project topics for potential students are flexible, but those individuals looking to perform research within the general research themes of the lab will be preferred. Applicants must hold a university degree.

Please note that while interested applicants are encouraged to contact Krishna Veeramah before applying, students wishing to join the lab must ultimately apply to the Stony Brook Interdepartmental Doctoral Program in Anthropological Sciences (IDPAS). All relevant information for this program can be found at the website (http://www.stonybrook.edu/commcms/idpas/applying.html) and a link to the application can be found at https://app.applyyourself.com/AYApplicantLogin/fl_ApplicantLogin.asp?id=sunysb-gs .Please note that the deadline for receipt of all Ph.D. application materials is January 15th, 2017. Earlier submissions are encouraged, particularly for those wishing to be considered for Campus wide Graduate Council Fellowships and W. Burghardt Turner Fellowships.

Prospective students are encouraged to address specific questions to the IDPAS Program Coordinator (IDPAS_Director@stonybrook.edu) or to Krishna Veeramah (*krishna.veeramah@stonybrook.edu*).

Krishna Veeramah <krishna.veeramah@stonybrook.edu>

TexasAMU 2 SocialInsectPhylogenomics

Openings for two PhD positions are anticipated to study molecular ecology and phylogenomics of social insects and possibly other urban arthropod pests in the laboratory of Ed Vargo in the Department of Entomology at Texas A&M University. The Vargo lab (http://urbanentomology.tamu.edu/) is a dynamic research group housed in the Rollins Urban and Structural Facility, a state of the art research and training facility. Our research focuses on population genetics and colony breeding structure of urban insect pests, primarily termites and ants. Research topics in the lab include the invasion biology of termites, ants, bed bugs and cockroaches using phylogenomic approaches, causes and consequences of colony breeding structure in ants and termites, the genetic and behavioral basis of disease immunity in social insects, and management of urban pests.

Students will develop specific research projects based on their interests and aptitudes that fit within the research areas explored by the lab.

Candidates should have some background in molecular ecology and/or entomology with an interest in one or more of the following areas: population genetics, genomics/bioinformatics, invasion biology and behavioral ecology.

The Department of Entomology at Texas A&M University (http://entomology.tamu.edu/) is one of the leading entomology departments in the U.S. and offers outstanding graduate training, excellent facilities and competitive stipends. In addition Ed Vargo is a faculty member in the Ecology and Evolutionary Biology interdisciplinary doctoral program (http://eeb.tamu.edu/) consisting of faculty across campus. Pursuing a degree in the EEB program is an option. Texas A&M University is located in College Station, a small but vibrant college town located near other major cities in Texas (Houston, Austin, San Antonio) offering an abundance of cultural attractions.

Interested applicants should send a C.V., a brief statement about research interests, (unofficial) transcripts, GRE scores and contact information for three references to ed.vargo@tamu.edu. Starting date is Summer 2017.

– Ed Vargo Professor and Endowed Chair in Urban and Structural Entomology Department of Entomology 2556 F&B Rd., Building 1804 2143 TAMU Texas A&M University College Station, TX 77843-2143, U.S.A.

Email: ed.vargo@tamu.edu Tel.: 979-845-5855 Fax.: 979-845-5926 Skype: ed.vargo Web page: http://urbanentomology.tamu.edu/ "Vargo, Edward L" <ed.vargo@tamu.edu>

TexasAMU Evolution

The Ecology and Evolutionary Biology Doctoral Program at Texas A&M is pleased to announce the availability of travel grants for prospective PhD students. These travel grants, which will be awarded on a competitive basis, will cover the costs of a domestic flight to and from College Station, hotel accommodations while in College Station, plus a per diem for meals. The aim of the travel grant is to provide prospective PhD students the opportunity to:

-Interview with faculty and meet current graduate students -Tour the department and campus to learn about available resources and facilities -Explore College Station and its surrounding areas

Travel grants will be awarded in January with travel scheduled for February 5-7, 2016. Travel grant awardees will spend time together during their visit, thus gaining immediate insights into their future cohort.

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 fellowships. Texas A&M University is positioned in Blackland Prairie and Post Oak Savannah habitat, which supports great species diversity and a wealth of research opportunities with great year-round climate. 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? To be considered for a travel grant, prospective PhD students first need to contact Jason Martina, the EEB Program Coordinator (email: jpmartina@tamu.edu; phone: 979 845-2114). To receive a travel grant, an official Graduate Application package must be submitted to the EEB Program. For additional information about the EEB Program and the graduate application process please visit: http://eeb.tamu.edu For consideration for merit fellowships, your application needs to be received by January 1, 2017

– Jessica E. Light Associate Professor and Curator of Mammals Department of Wildlife and Fisheries Sciences Biodiversity Research and Teaching Collections Texas A&M University College Station, TX 77843 Phone: 979-458-4357 http://www.jessicalight.org/ "jlight2@tamu.edu" <jlight2@tamu.edu>

TrentU WildlifeDiseaseGenomicsBats

PhD Opportunity in Wildlife Disease Genetics - Trent University/Ontario Ministry of Natural Resources and Forestry

We are seeking a graduate student (preferably a Ph.D candidate) to perform research in the realm of bat genomics in relation to rapid changes in selective pressures from disease.

Infectious diseases are critically important in species adaptation, evolution, and persistence. However, climatic changes are altering disease dynamics many systems by promoting the invasion of novel diseases and disease vectors. We intend to investigate the capacity of bats to adapt to rapid changes in pathogen-mediated selection, and thus assess threats to their persistence. One approach for understanding adaptation to disease is to examine the correlation between the geographic distribution of host immunogenetic variation and of disease variants, with these correlations interpreted relative to demographic parameters that also influence the distribution of adaptive and non-adaptive genetic variation. We are seeking a student to take an adaptive landscape genomics approach to investigate contemporary evolution and demographic constraints on local adaptation among coevolved and naïve disease vectors. This work will take place within a collaborative group of Trent University and Ontario Ministry of Natural Resources and Forestry (OMNRF) researchers investigating bat declines and White Nose fugus.

The successful candidate will also be encouraged to develop/explore independent research within the framework of existing funding. This research will be conducted within the Natural Resources DNA Profiling and Forensic Centre (www.nrdpfc.ca). Applicants would ideally hold a MSc in Landscape/Population Genetics or Bioinformatics, and have experience processing large data sets from massively parallel sequencing platforms. There may also be an opportunity to participate in field work. Previous experience working with bats is preferred but not required. Candidates must be willing to be vaccinated against rabies. All candidates should submit a letter of application and research interest, curriculum vitae, and names and contact information for three referees to Drs. Kyle and Davy. The position will commence as soon as possible but no later than September 2017. Applications will be accepted until a suitable candidate has been found.

Dr. C. J. Kyle, Associate Professor Forensic Science Department, DNA Building, Trent University christopherkyle@trentu.ca

Dr. C. Davy, Research Scientist Ontario Ministry of Natural Resources and Forestry Christina.davy@ontario.ca

Additional Information: The Natural Resources DNA Profiling and Forensic Centre (NRDPFC) is located within the new DNA building of Trent University (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, including the rabies virus.

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>

TulaneU RainforestEvolutionaryEcol

Subject Line: PhD Opportunity in Evolutionary Ecology Message:

The Karubian Lab (http://karubian.tulane.edu) is seeking applications from prospective PhD students interested in tropical rainforest evolutionary ecology and conservation, with a focus on palm trees in Ecuador.

Students will be encouraged to develop independent research that combines fieldwork on ecological processes (e.g., dispersal, competition, survival) with laboratory-based analyses (e.g., genomics, transcriptomics) to better understand the forces that regulate patterns of diversity within and among species. In doing so, students will build upon previous and ongoing NSF-funded work in the Karubian lab 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/-publications/ and http://karubian.tulane.edu/research/-

plant-animal-interactions/ for more information.

The Karubian lab has a strong commitment to linking our research to real world conservation outcomes via meaningful engagement with local communities in the areas where we work. Incoming students are encouraged to participate in and contribute to this effort. Please see http://karubian.tulane.edu/engagement/overview/ for more information.

The Karubian lab is based at the Department of Ecology and Evolutionary Biology at Tulane University, in New Orleans LA. We have an outstanding and supportive group of students and faculty. Ph.D. students in good standing receive TA-ships that cover stipend and tuition costs during their time at Tulane. Competitive fellowships and in-house research support are also available.

The deadline for applying is January 15, 2017. Please see http://www2.tulane.edu/sse/eebio/academics/graduate/apply.cfm for more information. Prior to applying, interested students should contact Dr. Jordan Karubian (jk@tulane.edu) with a statement of interest and CV. Students from Latin America and from under-represented groups in ecology and evolution are particularly encouraged to apply.

– Jordan Karubian Associate Professor Ecology & Evolutionary Biology Tulane University (504) 865-5549 jk@tulane.edu karubian.tulane.edu

Jordan Karubian <jk@tulane.edu>

UAkron EvolutionPlantMatingSystems

A PhD assistantship is available for Fall 2017, in Randy Mitchell's laboratory at The University of Akron. A portion of the student's research must focus on empirical exploration of the effects of ecological context (pollinator sharing) on pollination biology and mating system of Mimulus ringens in Ohio and Wisconsin. Beyond that requirement, there is substantial freedom to develop and explore many aspects of the general topics of pollination, and mating systems. The student's research will be part of a joint project coordinated with Jeff Karron at the University of Wisconsin-Milwaukee), Dorset Trapnell (University of Georgia), Emmanuelle Porcher (Muséum National d'Histoire Naturelle) and Celine Devaux (Université de Montpellier). This collaborative research will use empirical and theoretical investigations to test the hypothesis that interactions with co-flowering species alter the evolutionary tradeoff between outcross siring and selfing. This position includes TA support, and, pending funding, two years of RA support and summer stipend.

The Integrated Biosciences PhD program at the University of Akron is a unique interdisciplinary PhD program where biology is at the interface of research that cuts across traditional departmental boundaries. IB PhD students take a synthetic approach in their research and education, and gain skills and training in how to work across fields of study. For this project, interdisciplinary connections to mathematics, geography, or statistics are promising possibilities. Learn more about the Integrated Biosciences program at https://www.uakron.edu/ib/ . And learn more about the Department of Biology at https://www.uakron.edu/biology/ .

The University of Akron is a state university located in the heart of Akron, Ohio, near the scenic Cuyahoga Valley National Park (CVNP). The Biology Department emphasizes collaborative and integrative research, including the PhD program in Integrated Bioscience, and a MS program in Biology. Facilities include a 400+ acre field station, greenhouse, and live animal research center. We have excellent relations with the CVNP and local metroparks, which provide access to over 40,000 acres of potential field sites within 40 miles. Our graduate students have been successful in finding employment in their specialties, including work as professors, consultants, field technicians, government agents (e.g., EPA, Department of Natural Resources), park naturalists, and so forth.

The Biology Department has a strong program in Ecology and Evolutionary Biology. Areas of interest for graduate research include: life history evolution, mating systems, aquatic ecology, pollination biology, wetland ecology, physiological ecology, isotope ecology, behavioral evolution, spider biology, and evolutionary biomechanics.

For more information, contact Randy Mitchell (rjm2@uakron.edu), and visit https://blogs.uakron.edu/mitchell/ "Mitchell,Randall J" <rjm2@uakron.edu>

UAlberta ConvservationGenetics

Graduate Student Opportunity in Molecular Ecology at the University of Alberta.

I am seeking highly motivated students interested in pursuing graduate study at either the MSc or Phd level in molecular ecology, conservation genetics or ecological genomics to join my research group in the Department of Biological Sciences at the University of Alberta (http://www.biology.ualberta.ca) to start in Sept 2017. The Department of Biological Sciences offers a vibrant research environment and outstanding research infrastructure including next-generation sequencing platforms http://www.biology.ualberta.ca/facilities/. All students admitted to our graduate program have secured financial support for the first 2 years of a M.Sc. program and the first 5 years of a Ph.D. program, at the minimum rate of approximately $24,000 (M.Sc.) and $24,500 (Ph.D.) CDN per year, subject to annual review of academic and teaching performance.

Projects

Research projects in my group involve the development and application of molecular markers to study a range of topics in the ecology and evolution of wildlife species (https://scholar.google.ca/-citations?user=3L1oVhgAAAAJ&hl=en). Projects often involve close collaboration with field biologists and ecologists. Some potential topics include 1) inbreeding dynamics and genomic heterozygosity-fitness correlations in red squirrels, 2) the genetic architecture of fitness-related traits in mountain sheep and goats, and 3) hybridization, prion gene variation and chronic wasting disease spread in wild deer. I am also open to ideas and encourage potential applicants to contact me directly to discuss their interests and suitability.

Application requirements

I am looking for students who have a strong demonstrated background (BSc or equivalent with minimum GPA 3.3 on a 4-point scale) in ecology and evolution, molecular biology or bioinformatics. Experience in the field research and/or with molecular techniques is preferred, and both numeracy and proficiency in English are required.

See details here https://www.ualberta.ca/biological-sciences/graduate-studies . Contact details

Dr. David W. Coltman (dcoltman@ualberta.ca)

Professor

Department of Biological Sciences

University of Alberta

Edmonton, Alberta

Canada T6G 2E9DA, T6G 2E9

"dcoltman@ualberta.ca" <dcoltman@ualberta.ca>

UBath DinosaurBirdEvolution

Dear colleagues,

Please see the following advertisement for a fully funded PhD position at the University of Bath, UK, entitled 'Anatomy, phylogeny, and biomechanics across a crucial interval during the dinosaur-bird transition'.

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=80679 Funding is available for UK and EU students; applications from overseas students with externally-sourced funding will be accepted year-round.

Please distribute the advertisement to suitable candidates who may be interested.

Best,

Daniel Field

– Daniel J. Field, PhD Yale University Department of Geology and Geophysics danieljfield.com

Daniel Field <daniel.field@yale.edu>

UBath GeneNetworkEvolution

== Adaptive and non-adaptive processes in gene regulatory network evolution

== Supervisor: Dr Tiffany Taylor < http://-www.bath.ac.uk/bio-sci/contacts/academics/-tiffany-taylor/ >; Co-superivsors:* Dr Nick reist < http://www.bath.ac.uk/bio-sci/contacts/academics/-nick_priest/ >; Prof Michael Tipping < http://-www.miketipping.com/ >

==roject Description: It is generally assumed that adaptation drives genome evolution. But, there has not been an experimental system to study the evolutionary significance of non-adaptive processes, such as genetic drift, mutation and recombination. Using a combination of experimental and computational methods, this PhD studentship will identify how adaptive and non-adaptive processes contribute to the evolution of gene regulatory networks. Employing our well-established Pseudomonas system, the project uses experimental evolution in conjunction with molecular biology and genomics to assess whether novel mutations affecting gene regulation are adaptive or non-adaptive. Employing the University's Balena system (a massively parallel architecture, high-performance computing platform), the experimental work will be complimented by simulations of gene regulatory network evolution to identify the processes driving non-adaptive evolutionary patterns. The computational biology component of the project may also stimulate the development of techniques in machine learning, to train computers to recognise patterns of gene networks which contribute to adaptive and non-adaptive processes in the context of network evolution.

== Location: This project will be conducted under the direct supervision of Dr Tiffany B. Taylor, and based within the Department of Biology and Biochemistry at the University of Bath (UK) in the new Milner Centre for Evolution (http://www.bath.ac.uk/groups/milner-centre-for-evolution/).

== Requirements: We are looking for a biology graduate who has a strong interest in genetics and gene networks, or a computer science graduate with interests in evolution and evolutionary theory. Some practical experience in microbiology and molecular techniques is highly desired but training will be provided to strengthen these areas. The successful candidate will be enthusiastic, highly motivated, independent, have experience in microbiology, molecular biology or evolutionary biology (or a combination), and have a relevant degree. The applicant must meet the standard University of Bath English language requirements. The applicant must be a UK citizen or an EU citizen who has been residing in the UK for 3 years prior to appointment.

== Training: The candidate will be trained to use the University's Balena system and have the opportunity to develop new approaches to machine learning to help solve biological problems. In this unique project the student will also develop laboratory skills in microbiology, molecular biology and genomics. To achieve this, the candidate will require access to the labs - laboratory training will be provided by Tiffany Taylor. They will also need access to the Balena HC cluster - training to be provided by Michael Tipping. And in order to effectively design a computational simulation that is relevant to biological systems, Nick Priest will offer training and guidance in theoretical evolution and mathematical modelling in ecology and evolution.

== lanned start date: 2 October 2017 (3.5 years funding)

== Contact: For informal enquiries please contact Tiffany Taylor T.B.Taylor@bath.ac.uk. More information can be found at https://www.findaphd.com/-search/rojectDetails.aspx?PJID=80595&LIDi == Funding Notes: UK and EU students applying for this project may be considered for a University Research Studentship which will cover Home/EU tuition fees, a training support fee of 1000 per annum and a tax-free maintenance allowance of 14,296 (2016/17 rate) for 3.5 years. This is a competitive funded hD project.

== References: 1. Taylor, T. B. et al. Science, 347 (6225), pp. 1014-1017; 2. Taylor, T. B. et al. 2015. Microbial Cell Factories, 2 (7), pp. 256-25Warning: base64 decoder saw premature EOF! 8; 3.

Wang, Y.et al. 2015. In: The 13th European Conference on Artificial Life, 2015-07-20 - 2015-07-24.; 4. Alsohim, A. S. et al. 2014. Environmental Microbiology, 16 (7), pp. 2267-2281; 5. Lynch, M. 2007. Nature Reviews Genetics, 8(10): 803-813.

Tiffany Taylor <t.b.taylor@bath.ac.uk>

T.B.Taylor@bath.ac.uk

UBath SpeciationGenetics

Genetics of speciation in house mice: Identifying molecular and developmental mechanisms of hybrid male sterility

Main supervisor: Dr Leslie Turner Second supervisor: Prof Jason Wolf

Linking genotype to phenotype and fitness in nature is the ultimate goal of most evolutionary genetics research, but is rarely accomplished in practice. The genes and molecular mechanisms underlying adaptation and speciation remain largely unknown. The goal of this project is to determine genetic and developmental causes of hybrid male sterility, a key reproductive barrier between house mice subspecies. This research builds on previous studies identifying genetic variants associated with reduced fertility in a laboratory cross and in hybrid zone mice. Characterizing the mechanisms of a single locus in natural or outbred populations is challenging due to genetic variability among individuals. To over-come this challenge, we will use a unique set of inbred mouse strains bred from wild-caught hybrid zone mice by Dr Turner over the last several years. Leveraging the power of inbred strains, we can compare nearly identical wild-derived genomes in multiple individuals and different developmental stages. This novel approach has great promise for identifying pathways, genes, and molecular mechanisms contributing to the evolution of a reproductive barrier in nature.

The student selected for this project will integrate approaches from evolutionary genomics and reproductive biology to (1) determine the nature and timing of defects during spermatogenesis, and (2) functionally evaluate candidate sterility genes. You will characterize defects in hybrid lines across a developmental time course. Next, to identify the most promising candidate genes, you will combine your results with population genomics and data mining of available 'omics and knockout data. Finally, you will evaluate candidate genes using in vitro and in vivo functional assays.

This project will be based within the Department of Biology and Biochemistry at the University of Bath (UK) in the new Milner Centre for Evolution (http://www.bath.ac.uk/groups/milner-centre-for-evolution/). The student will gain expertise in both experimental and bioinformatic approaches from genetics, evolutionary genomics and reproductive biology and have access to excellent research facilities (e.g., animal facility, histology, imaging).

Requirements: We are looking for a biology graduate with a strong background in genetics, evolutionary biology or reproductive biology. Experience in molecular techniques is highly desired. The successful candidate will be motivated, independent, and enthusiastic about learning diverse skills for interdisciplinary research.

UK and EU students applying for this project may be considered for a University Research Studentship which will cover Home/EU tuition fees, a training support fee of 1000 per annum and a tax-free maintenance allowance of 14,296 (2016/17 rate) for 3.5 years.

Note: ONLY UK and EU applicants are eligible for the studentship; unfortunately, applicants who are classed as Overseas for fee paying purposes are NOT eligible for funding. We welcome all-year round applications from self-funded candidates and candidates who can source their own funding.

Application deadline: January 31, 2017 Anticipated start date: October 2017

For details about the position/application process see: https://www.findaphd.com/search/ProjectDetails.aspx?PJID=80678 For additional information about research see http://leslieturner.net/ For informal enquiries contact Leslie Turner L.M.Turner@bath.ac.uk

Leslie M. Turner, Ph.D. Lecturer, Milner Centre for Evolution Department of Biology and Biochemistry University of Bath Claverton Down, Bath BA2 7AY, UK +44 (0)1225 385015 http://leslieturner.net "L.M.Turner@bath.ac.uk" <L.M.Turner@bath.ac.uk>

UCalifornia Riverside Macroevolution Reduviidae

Graduate position: UC_Riverside_Macroevolution_Reduviidae

The Heteropteran Systematics Lab @ UCR (http://heteroptera.ucr.edu/) is looking for a new PhD student (starting fall 2017) who would be part of a research team investigating the evolutionary history of Reduvioidea, the assassin bugs. Candidates with strong background in systematic entomology and phylogenetics are preferred. Please contact christiane.weirauch@ucr.edu for more information and check UCR Entomology for details on application procedures.

The project: an international research team led by the Heteropteran Systematics Lab @ UCR will shed light on the evolutionary history and diversification of a charismatic clade of predatory and hematophagous insects, the speciose Reduvioidea or assassin bugs (>6,822 described spp.). Existing phylogenies of Reduvioidea are inadequate to address many evolutionary questions, the paucity of well-described fossils has made it difficult to establish time-lines for events including the transition from predatory to hematophagous life style, and the classification of Reduvioidea is in disarray. We will: 1) test phylogenetic hypotheses with emphasis on the poorly resolved Higher Reduviidae and contentious relationships of the hematophagous Chagas disease vectors Triatominae, while maximizing taxonomic coverage and integrating transcriptomic, anchored hybrid enrichment, traditional molecular, and morphological datasets; 2) describe and redescribe fossil reduvioids to bridge taxonomic and geological gaps in the fossil record and test hypotheses on the timing of key biological events; 3) study diversification across Reduvioidea, focusing on hypotheses of diversification rate shifts and correlated key innovations, and morphological, physiological, and ecological traits involved in the transition between predation and hematophagy; 4) use the phylogenetic information generated during this project to propose a new classification of Reduvioidea.

Potential PhD projects: could focus on phylogenetic and phylogenomic approaches to unravelling relationships within Reduvioidea, comparative morphology and morphological character evolution across the group, key innovations in the evolution of hematophagy, or diversification analyses.

– Eric Gordon Ph.D. Candidate Department of Entomology University of California, Riverside 3401 Watkins Dr. Riverside, CA 92521 Email: egord003@ucr.edu

Eric Gordon <egord003@ucr.edu>

UCincinnati 2 JumpingSpiderColorEvolution

Hi all,

I am recruiting two PhD students to join my research group at the University of Cincinnati in the summer or fall of 2017. I am particularly interested in recruiting new students to join our research on the coevolution of jumping spider color vision and coloration.

One available PhD position, funded through an active NSF grant, will investigate the role of female visual attention/gaze in driving the evolution of complex male displays in the North American jumping spider genus Habronattus. This research project combines intensive field work with lab-based video characterization of male displays and eye-tracking of female gaze responses to video playback of displaying males (the latter in collaboration with Beth Jakob at the University of Massachusetts, Amherst).

The second doctoral position will support a new research initiative in my group to understand the repeated evolution of color vision across jumping spiders. Thus far, we have identified two independent and functionally distinct transitions from dichromacy to tri-/tetrachromacy in jumping spiders, which are tightly associated with subsequent rapid diversification of male color ornamentation. We are now interested in identifying any additional evolutionary transitions in color vision, characterizing when and why they occurred, and investigating their "downstream" consequences for biodiversity in this group of animals. This work will leverage international field work with molecular, microspectrophotometric, and hyperspectral imaging approaches.

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 my lab website: www.morehouselab.com . Students interested in joining the lab should contact me as soon as possible 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.

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) and an NSF-funded REU program in Sensory Ecology, UC provides a vibrant intellectual environment for research and student training. Plans are afoot for the development of a regional consortium of sensory biologists, including researchers at Purdue and Case Western. Matching research strengths in sensing and sensor technologies in UC's nationally-renowned College of Engineering offer a number of cross-disciplinary training opportunities. In addition, UC's strengths in design and the fine and performing arts provide exciting opportunities for my lab's ongoing involvement in art-science collaborations, including the College of Design, Architecture, Art, and Planning (ranked 3rd internationally) and the Cincinnati Conservatory of Music (ranked 6th nationally). The University of Cincinnati and my lab also 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 (https://grad.uc.edu/content/dam/grad/docs/awards/-Provost_Fellow_Program_Description_2017.pdf), which provides a 3 year $25,000 stipend plus tuition remission, and the Yates Fellowship, which awards grants to underrepresented minority candidates. Finally, Cincinnati is a culturally and economically vibrant city with a low cost of living, offering an unbeatable quality of life for our graduate students. Vogue just named Cincinnati as one of the "5 industrial cities making America's rust belt shine again": http://www.vogue.com/13506742/rust-belt-travel-guides-detroit-pittsburgh-chicago-cincinnati-covington-milwaukee/ Graduate applications are due January 1, 2017. More information on the graduate program at the University of Cincinnati and associated application materials can be found here: http://www.artsci.uc.edu/-departments/biology/graduate/future.html . All my best,

Nate

Nathan Morehouse

Assistant Professor Department of Biological Sciences University of Cincinnati 711H Rieveschl Hall Cincinnati, OH 45221-0006 Office: (513) 556-9700 colorevolution@uc.edu http://www.morehouselab.com

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UConnecticut SymbiontPhylogenomicsEvol

PhD student positions in phylogenomics, host-symbiont diversification in the Simon Lab (see also our postdoctoral ad)

The Simon lab at the University of Connecticut seeks creative and motivated PhD students and Postdoctoral candidates interested in phylogenetics, molecular phylogenomics, bioinformatics, and/or symbiont-host interactions (endosymbionts and/or microbiomes) to begin in the summer or fall of 2017. Experience in the preceding subjects preferred but not required.

Applicants will participate in an NSF sponsored project entitled: Exploring Symbiont Biodiversity and Complexity in the Family Cicadidae. The major goal of this proposal is to study the co-diversification 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? Similarly, we ask whether the changes in the gut microbiota affect primary endosymbionts (keeping in mind that gut microbiota are known to synthesize essential amino acids for some hosts). Other hypotheses concern changes in symbiont consortium membership related to changes in the biotic or abiotic external environment coincident with the invasion of new biogeographic areas characterized by different climates and host plants. Broader impacts will involve teaching collaborations with team members in the US, Brazil, China, India, NZ, and Fiji. Field trips to Brazil, Chile, Argentina, Fiji, and India are planned.

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), and 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. I recommend applying asap and prior to January 15th. 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 75 North Eagleville Road, University of Connecticut

Storrs, CT 06269-3043

Brood VI is emerging in May 2017 in western North and South Carolina. Report sightings to Magicicada.org

chris.simon@uconn.edu

Office (860) 486-4640; Lab (860) 486-3947; Fax (860) 486-6364, Office: Biopharm 305D, Lab: Biopharm 323,325

C. Simon Home page: http://hydrodictyon.eeb.uconn.edu/projects/cicada/simon_lab/member_pages/c_simon.php Simon Lab Home:

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UGroningen 12 Evolution

12 PhD Scholarship positions in Evolutionary Life Sciences

Host organization

The University of Groningen has an international reputation as a dynamic and innovative institution of higher education, offering high-quality teaching and research. Balanced study and career paths in a wide variety of disciplines encourage the 30,000 students and researchers to develop their own individual talents. The University of Groningen is proud to be among the global elite with a classification in the top 100 of the Shanghai ARWU, the QS World University Rankings, and the THE World University Rankings. It marks the 24th place in the global ranking of Best Places to Work in Academia, scoring 3rd best in Europe and 5th non-US university. Joining forces with prestigious partner universities and networks, the University of Groningen is truly an international place of knowledge.

The Groningen Institute for Evolutionary Life Sciences (GELIFES)

GELIFES, the largest institute of the Faculty of Mathematics and Natural Sciences (FMNS) fills a special niche in the life sciences by covering and integrating mechanistic, evolutionary and ecological approaches, aiming to understand adaptation on all levels of biological organisation. Researchers pursue fundamental questions while collaborating with partners from industry, medicine and other realms of society. For its new research programme, called Adaptive Life, which is one of the four focus themes of the FMNS, the institute received a large university grant.

Our research fields include behavioural biology, chronobiology, ecology, evolutionary biology, genetics and genomics, neurobiology, physiology and theoretical modelling, using a wide array of research tools. Research levels range from molecular and organismal to population and community, performed under laboratory, semi-natural and field conditions. Studying mechanisms within the framework of evolutionary adaptation allows for a large diversity of model organisms, for which we have extensive facilities. A wide array of species are studied, from microbes, algae, plants and insects to vertebrates such as fish, birds, rodents, marine mammals and humans. We are currently searching for candidates to fill a substantial number of open PhD positions within our Adaptive Life programme.

PhD project description

GELIFES offers 12 four-year scholarship PhD positions for the most talented and motivated national and international students, starting between May and September 2017. All PhD positions are integrative by nature, spanning across different expertise groups and being strengthened by complementary PhD projects already in progress and in preparation.

PhD candidates are invited to approach potential supervisors (PIs; 2 minimum) within GELIFES (a 3rd supervisor may be attracted externally) with a draft research proposal (500 words) within the scope of the integrative topics listed below and submit their personal files. PI teams will select three candidates at most based on their information and research plans and invite them to write a full research proposal. All final proposals will be reviewed by an external committee and ranked according to scientific quality, feasibility as well as fit to the adaptive Life programme and integrative potential. Only the 12 highest ranking proposals will be eligible for funding.

Upon selection, PhD candidates will receive expert supervision and mentoring, and excellent training through cutting-edge research projects, advanced courses and training opportunities, complemented by workshops on generic research, transferable skills and teaching. The home base for GELIFES' research is the new spectacular Linnaeusborg at Zernike Campus. Research is performed with state of the art equipment and in well-equipped facilities.

As a PhD candidate, you are committed to conduct independent and original scientific research, to report on this research in international publications and presentations, and to present the results of the research in a PhD dissertation, to be completed within four years. After thesis completion, many of GELIFES' PhD students move on to top positions in academia or industry.

Integrative topics

PhD candidates are invited to develop their own research proposal within the frame work of one of four integrative topics of the Adaptive Life Programme listed below, or more specifically within a proposed research theme as indicated on our Adaptive Life vacancy website: http://www.rug.nl/research/fmns/-themes/adaptive-life/research/vacancies 1. Causes and consequences of consistent individual differences

GELIFES is renowned for its research on 'animal personalities', i.e., systematic individual differences in physiology or behaviour that are stable in time and consistent across contexts. The study of such individual differences is currently a hot topic in the animal and human behavioural

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UHalle Germany BeeVirusCoevolution

3 year PhD on host-parasite coevolution: bumble bees and their viruses

A PhD position is available for a newly funded project on the evolutionary ecology of viruses in bees, funded by iDiv (www.idiv.de) and within Robert Paxton's lab at the University of Halle, Germany.

The overarching goal of the research is to understand the role of viral evolutionary change for pathogen emergence and host switching as well as host evolutionary response, with a conservation focus on rare and declining species of bumble bee. Research will involve lab and field-based experiments (in Germany) as well as molecular genetic analysis of viruses and their hosts. We seek a highly motivated individual with an interest in host-parasite coevolution and skills or a background in bioinformatics, entomological experimentation, or molecular genetic techniques. Two pre-requisites are a valid driving licence and the ability or willingness to work with bees.

The candidate will be part of iDiv's comprehensive graduate school yDiv (https://www.idiv.de/ydiv.html). The position is available for 3 years commencing April 2017 or soon thereafter. The working language of the lab is English. The neighboring group of Robin Mortiz makes for a strong profile in bee biology and genetics at the University of Halle. Halle is a delightful, historical city approximately 1.5 hours SW of Berlin and 45 minutes from Leipzig, iDiv's seat, to which Halle is connected by several trains per hour. The salary is on the standard German PhD scale of 65% E13, which translates to ca. Euro 30 K per annum.

Further details of the project can be obtained from Robert Paxton (robert.paxton@zoologie-uni-halle.de) and iDiv (https://www.idiv.de/the_centre/-career/flexpool_positions.html#c4681). Applications should be sent on-line to iDiv (apply.idiv.de) by 1 January 2017. Interviews are planned for early February 2017.

Robert Paxton <robert.paxton@zoologie.uni-halle.de>

UHelsinki HostPathogenCoevol

FOUR-YEAR PHD STUDENT POSITION in HOST-PATHOGEN COEVOLUTION

Applications are invited for a four year PhD student position in the research group of Professor Anna-Liisa Laine. The successful applicant will join the Centre of Excellence in Metapopulation Research at the University of Helsinki.

The project is focused on the interplay between ecology, genetics and evolution shaping the interaction between host plant Plantago lanceolata and its pathogens. Host plant P. lanceolata and its specialist fungal pathogen Podosphaera plantaginis have been intensively studied in the Ãland Islands. With 16 years of epidemiological data from over 4000 host populations and solid experimental protocols, this system offers unique opportunities for testing classic hypotheses regarding host-pathogen co-evolution with direct links to epidemiological dynamics.

In practice, you will carry out field work in the Ãland Islands archipelago (SW Finland) and conduct experimental work in the laboratory and under semi natural field conditions. There is also potential to develop and use genomic tools to identify genes involved in disease resistance and infectivity. The work may involve extended periods in the field sites in Ãland and working with international collaborators abroad. You are expected to present your findings in scientific meetings and workshops, as well as prepare publications for international scientific journals.

Motivated students with a MSc degree in ecology, evolutionary biology or molecular biology (or other related fields) are encouraged to apply. Prior expertise in experimental design, statistical analysis, bioinformatics or molecular laboratory work are a bonus but your most important assets are enthusiasm for research, motivation to learn new things, and ability to work independently while being an active member of a research team.

Please send your application to biotiede-mrg@helsinki.fi by 22 January 2017 with title PhD COEVOLUTION. Attach a CV (with possible publications included), a copy of your transcript records (= printout of the courses you've completed during your MSc), contact details of two references (e.g. MSc thesis supervisor), and a letter (MAX 1 page) with a description of your researcher interests and why you would be a suitable candidate for the project.

The work is scheduled to start in Winter/Spring 2017. For more information, please contact Anna-Liisa Laine (anna-liisa.laine@helsinki.fi) and visit the website at http://allaine.it.helsinki.fi/ For information on the University of Helsinki, please visit: http://www.helsinki.fi/-university/index.html Professor Anna-Liisa Laine

Center-of-Excellence in Metapopulation Biology

Department of Biosciences

PO Box 65 (Viikinkaari 1)

FI-00014 University of Helsinki, Finland

allaine.it.helsinki.fi

helsinki.fi/science/metapop/

twitter: @annaliisalaine

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

UHongKong TreeConservationGenetics

A fully funded PhD studentship is available for the study of population genetics and conservation biology of the endangered tree Aquilaria sinensis at the University of Hong Kong, in collaboration with Kadoorie Farm and Botanic Garden, Hong Kong.

Aquilaria sinensis, also known as incense tree or agarwood tree, is one of the most famous medicinal plants in Hong Kong and China. However, due to the rising demands for agarwood, this species is threatened by illegal felling throughout the region. To conserve and maintain healthy incense tree populations in Hong Kong, there is an urgent need to study the conservation genetics of this species. We now seek a high calibre student to (1) study the genetic diversity of Aquilaria sinensis in Hong Kong and understand how the genetic diversity is affected by illegal felling; (2) understand the genetic variation of Aquilaria sinensis at different age classes, and disentangle the gene flow patterns of this species. This work will contribute to the synthesis of a Species Action Plan and information gained from this project will be useful for conservation and restoration of this species in Hong Kong and throughout the region.

Prospective students with a background in conservation biology or population genetics are encouraged to apply. A strong academic record, evidence of excellent writing and analytical skills, as well as enthusiasm for field and laboratory research will be a plus.

The PhD studentship includes a postgraduate scholarship, travel insurance and research support for four years. To apply, please send application materials, including a cover letter and copies of academic transcripts, resume and contact information for 3 references to gfischer@kfbg.org or saunders@hku.hk. Review of applications will begin immediately and continue until the position is filled.

Huarong Zhang, Ph.D.

Senior conservation geneticist

Flora conservation department

Kadoorie Farm and Botanic Garden

Hong Kong

hzhang@kfbg.org

UKonstanz 15 Adaptation

The Research Training Group "R3 - Responses to biotic and abiotic changes, Resilience and Reversi-bility of lake ecosystems" funded by the Deutsche Forschungsgemeinschaft (DFG) and based at the University of Konstanz welcomes applications for up to 15 PhD Positions (Salary Scale 13 TV-L / 65 % - 75 %) for a three-year structured program. The RTG will start on 1 April 2017.

The scientific goal of this RTG is to study the mechanism resulting in the resilience of lake ecosystems to environmental change. Our approach is to study the response of a model system - Lake Constance - with a multitude of different approaches and from different viewpoints, i.e., combining classical and novel methods such as population genomics and metagenomics approaches, metabolic profiling, compound-specific stable-isotope analyses, comparative multi-species experiments, paleolimnological and resurrection ecology approaches, time-series analyses, and numerical simulation models. The RTG will use these methods to study lake responses in three tightly linked research areas: Response, resilience and reversibility of ecosystem structure, Response, resilience and reversibility of biotic interactions Response, resilience and reversibility of carbon and nutrient flows

We offer a structured doctoral qualification programme combining a mentoring program, specific lectures on research and applied questions in ecology and limnology, a seminar and visiting program among students, flexible one-week courses, transferable skills courses, visits by guest researchers, and annual retreats. Furthermore you can expect a highly stimulating research environment.

Further information about the Doctoral positions, and the scientists involved can be found at: http://www.rtg-resilience.uni-konstanz.de .

The University of Konstanz encourages disabled persons to apply. They will be given preference if appropriately qualified (contact + 49 7531 / 88 - 4016 und 88 - 2834).

The University of Konstanz is an equal opportunity employer that tries to increase the number of women in research and teaching.

The University of Konstanz has been certified as a family-friendly institution by the Hertie Foundation and is committed to further the compatibility of work and family life.

The University of Konstanz offers a "Dual Career Couples Program". Information can be obtained from: http://www.uni-konstanz.de/dcc .

Requirements: Excellent Master (or equivalent) in ecology, biology, physics, biology, microbiology, bioinformatics, mathematics depending on RTG project. We expect strong motivation, good communication skills and the ability for teamwork.

For application, please submit: - motivation letter, including interests, motivation to become part of the RTG, ranking of 3 preferred projects, specific qualifications for chosen projects, - curriculum vitae including degree certificates, - abstract of master thesis, - two letters of recommendation. Interested candidates should submit their application containing the above mentioned documents including reference number 2016 / 254 in one PDF file to the speaker of the RTG, Prof. Dr. Frank Peeters, RTG_resilience_joboffers@uni-konstanz.de .

Review of the applications will begin on 9 January 2017 and will continue until the positions have been filled. Selection of invited applicants will be done at a two-day workshop in the 2nd half of February 2017 at the University of Konstanz.

Mark van Kleunen <mark.vankleunen@uni-konstanz.de>

ULausanne BacterialCommunities

I am looking to recruit a motivated and curious PhD student to work on building mathematical and computational models of evolving multi-species bacterial communities at the Department of Fundamental Microbiology in the beautiful city of Lausanne in Switzerland. The position is fully funded with a generous salary, and can start any time after May, 2017 (exceptions can be made to start earlier).

The successful candidate will work within a multidisciplinary group to construct models that capture interactions between five bacterial species. These models will then be fit to data observed in the lab, and used to make predictions that can later be validated again in the laboratory. The work will include dynamical systems (differential equations), individual-based models, and possibly control theory. A background in any of these areas is not required but will be appreciated. A passion for the subject, programming skills and a good command of written and spoken English are required.

For more information on the type of work we do in the lab, please visit our website: unil.ch/mitrilab. Please send questions and applications (including a one-page motivation letter with your research interests, a CV and evidence of a Master's degree) to sara.mitri[at]unil.ch.

"sara.mitri@unil.ch" <sara.mitri@unil.ch>

ULeicester 3 GeneticEpidemiology

Deadline for application is approaching for three PhD positions in Genetic Epidemiology at University of Leicester.

1. MRC IMPACT studentship (3.5 years): Idiopathic Pulmonary Fibrosis: novel insights into the genetic basis of risk and survival times (Theme: Precision Medicine: Pathology to Population Health). MRC IMPACT studentships are for 3.5 years which includes an initial 13 week Cohort Training Programme with the PhD project commencing in January 2018.

For more information, please contact Louise Wain (louisewain@le.ac.uk) and visit http://www.birmingham.ac.uk/schools/mds-graduate-school/scholarships/mrc-impact/index.aspx (then click on "Precision Medicine: Pathology to Population Health") to apply. Deadline for applications is 16th January 2017! [Note the requirement for 2 referee statements].

Idiopathic pulmonary fibrosis: novel insights into the genetic basis of risk and survival times

Supervisor: Dr Louise Wain (University of Leicester) and Professor Gisli Jenkins (University of Nottingham)

Summary: Idiopathic Pulmonary Fibrosis (IPF) is a rare, chronic and progressive lung disease with a very poor prognosis (median survival 3 years) and limited treatment options and there is a need for new therapy and approaches to treatment. The primary aim of this project will be to discover novel genetic determinants of IPF risk and survival. These will further our understanding of the disease processes involved in IPF by identifying genes and pathways involved, and could lead to the development of new IPF drugs. In addition, inclusion of genetic predictors of risk and survival time in clinical prediction models could improve clinical care by facilitating approaches to stratify disease ("precision medicine"). The student will be based within an internationally-recognised respiratory genetic epidemiology group with close collaborations with leading IPF clinicians and researchers. A broad training in genetic epidemiology will equip the student for a career in the fast-moving and opportunity-rich field of human disease genetics. Applicants should have a background in bioinformatics, epidemiology, statistics or genetics (or similar) with an aptitude for computing (prior experience of programming is advantageous but not essential) and a keen interest in genetics and human disease.

2. Department funded studentship (3 years): The role of complex genetic variation of immune system genes in respiratory health and disease. Supervised by Dr Louise Wain and Dr Ed Hollox (Department of Genetics) The studentship is for 3 years and will commence in October 2017. The student will be based in the Department of Health Sciences.

Respiratory disease is major public health concern and the third leading cause of death globally. Genome-wide association studies (GWAS) have identified multiple regions of the genome associated with respiratory health and disease and amongst these, one of the strongest signals of association is in the Human Leukocyte Antigen (HLA) region gene cluster on chromosome 6 which encodes proteins with essential roles in the immune system. However, the HLA region is complex and understanding the mechanisms underlying the genetic signals of association in this region requires sophisticated analytical approaches. Bespoke computational methods which measure variation of the HLA region, and of other clusters of functionally-related genes, at both the genetic and protein level, have been developed. This project will involve applying these methods to large general population cohorts to explore both the direct and interactive effects of variation at immune gene clusters on respiratory traits and disease. The student will develop research skills at the interface of genetics, statistics and computer science which will equip them for a career in the exciting and fast-moving field of genetic epidemiology. A background in bioinformatics, genetics or statistics is preferred and a keen interest in developing further skills in all of those areas, and in the use of high performance computing to analyse very large data sets, is essential. Contact Louise Wain (louisewain@leicester.ac.uk) for further details. The deadline for applications for this studentship are likely to close ~9th January 2017. The advert, and details of how to apply, will become available shortly.

3. MRC IMPACT studentship (3.5 years): Towards precision medicine in primary care: genetic epidemiology of treatment failure in primary care (Theme: Precision Medicine: Pathology to Population Health). MRC IMPACT studentships are for 3.5 years which includes an initial 13 week Cohort Training Programme with the PhD project commencing in January 2018. Supervised by Professor Martin Tobin and Dr Louise Wain.

Many prescribed drugs lack efficacy or generate adverse effects. Central

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ULeicester KinshipDeductionForensicsGenealogy

Fully-funded BBSRC-iCASE PhD Project: Next-generation kinship deduction for forensic and genealogical analysis

University of registration: University of Leicester

Project supervisors: Professor Nuala Sheehan (Department of Health Sciences) & Professor Mark Jobling (Department of Genetics)

Non-Academic partner: Dr Martin Blythe - DNA Worldwide Group

Project outline:

The use of DNA analysis to determine familial relationships between human individuals is very well established. For close (first-degree) pairwise relationships as targeted in the paternity test, a small number of polymorphic markers (the short-tandem repeats [STRs] also used in forensic individual identification) is analysed, and probabilities of true paternity can be established with near certainty. However, there is also a need in some applications to estimate more distant kin relationships: in forensic casework 'familial searching' exploits the fact that a perpetrator and their relative(s) are expected to share 'similar' DNA profiles, which can provide investigative information when the relative(s) are in the National DNA Database but the perpetrator is not; in immigration cases a claim of relationship may need to be validated in order to allow entry; in genealogical research participants may have specific hypotheses about their relationships which they wish to support via DNA evidence. The kinship estimation problem is more difficult in these cases because with each additional generation that separates two individuals, the expected proportion of the genome shared identical by descent (IBD) halves. Additional power can be gained by increasing the number of DNA markers analysed, for example by using genome-wide SNP chips.

The project proposed here addresses these issues by exploring the potential of NGS forensic multiplexes and genome-wide SNP data in relationship estimation, using real-world data. Forensically-relevant data will be generated by typing either the Promega Powerseq or Illumina Forenseq multiplex on existing pedigree DNA collections. Anonymised genome-wide SNP data will be obtained from DNA Worldwide (consenting clients, and a dataset of 72 individuals from 9 pedigrees). Both the forensic multiplexes and the genome-wide data (based on the HumanOmniExpressExome-8 chip) include uniparentally-inherited markers (Y chromosome, mitochondrial DNA) as well as biparentally-inherited (autosomal) markers. A novel feature of this project is to investigate efficient incorporation of such data with SNP-based likelihood estimates by considering haplotype frequencies and possible pedigree structures including sex. A key issue will be to understand the sensitivity of relationship estimation to allele frequencies, and a number of approaches will be taken, including the use of internal frequencies from the data themselves, data from public resources such as HapMap, or our own datasets. Detailed sensitivity analyses will be carried out through extensive simulation studies.

In this industrially-sponsored iCASE project, the student will spend a total of at least 3 months during the PhD working at DNA Worldwide, in Frome, Somerset. Training will be given in the bioinformatic analysis pipelines and databasing used to process, categorize and manage the multitude of data generated through consumer genotyping, and in essential business skills involving public presentation, listening and communication, organisation, project management, marketing and finances.

Closing date for applications: 8th January 2017

For informal enquiries contact the supervisors: Nuala Sheehan < nas11@leicester.ac.uk> and Mark Jobling <maj4@le.ac.uk>

Find more information here: http://www2.le.ac.uk/colleges/medbiopsych/research/pg-research/mitbp-at-the-university-of-leicester Check eligibilty and apply here: https://www2.warwick.ac.uk/fac/cross_fac/mibtp/pgstudy/phd_opportunities/application/ Please note: iCASE students must fulfil the MIBTP entry requirements and will join the MIBTP cohort for the taught modules and masterclasses during the first term. iCASE students can then start their PhD project in Jan 2018 but must complete a 3-month miniproject (at a non-home institution) before the end of their first year. They will remain as an integral part of the MIBTP cohort and take part in the core networking activities and transferable skills training.

“maj4@leicester.ac.uk” <maj4@leicester.ac.uk>

ULeicester SexSelection

Sex, selection and differential gene expression: do changes in the mode of sexual reproduction influence the magnitude and extent of sex-biased gene expression?

Competition funded PhD studentship at the University of Leicester (UK) in collaboration with Africa Gomez at the University of Hull (UK)

For more details: rh225@le.ac.uk

Females and males have almost identical genomes but are exposed to conflicting selective pressures. It is hypothesised that these conflicting selective pressures - known as sexually antagonistic selection - are the explanation for multiple independent evolutions of sex-biased gene expression and also sex chromosomes [1]. However, empirically testing the role of sexually antagonistic selection has been hampered by the lack of suitable experimental systems as sex differences are often longstanding [2].

Using a model system we have developed [3-5] - the tadpole shrimp, Triops sp. - this project will test whether changes in the mode of sexual reproduction influences the magnitude and extent of sex-biased gene expression.

We have shown that tadpole shrimps (Triops) show multiple transitions between separate sexes (dioecy) and individuals with male and female function (hermaphrodites) [3, 6]. Importantly such changes alter the strength of sexually antagonistic selection [7]. We therefore have a system where sexually antagonistic selection differs so its role on sex-biased gene expression to be tested. Furthermore, we have shown that sex is genetic in Triops cancriformis and that sex chromosome regions are larger in dioecious populations than in hermaphrodite populations, a pattern consistent with a reduction in sexually antagonistic selection [5].

This PhD will investigate two species where hermaphroditism has evolved independently and there are both dioecious and hermaphrodite populations (Triops cancriformis and Triops longicaudatus).

The student will test whether: - genes with female biased expression in dioecious populations are less biased in hermaphrodites - genes with male biased expression in dioecious populations less biased in hermaphrodites - There is an effect of genome position (e.g. within or outside the sex chromosome region) of genes on the degree of change in expression bias. - There are convergent patterns of change in Triops cancriformis and Triops longicaudatus.

Objectives: 1. To develop sex-specific genetic markers for identification of males, females and hermaphrodites in T. cancriformis / longicaudatus. 2. To identify genes located within the sex specific region of males, females and hermaphrodites in T. cancriformis / longicaudatus. 3. To test for a reduction in the differential expression of sex- associated genes in the transition from dioecy to hermaphroditism in T. cancriformis / longicaudatus

The student will be based in the Department of Genetics at the University of Leicester and supervised by Rob Hammond (https://goo.gl/fhTYcg) in Leicester in collaboration with Africa Gomez and the University of Hull (https://goo.gl/Hfqgpn) and with Eamonn Mallon (https://goo.gl/oqoTgc) as the second supervisor in Leicester.

1. Vicoso B., Kaiser V.B., Bachtrog D. 2013 Sex-biased gene expression at homomorphic sex chromosomes in emus and its implication for sex chromosome evolution. Proceedings of the National Academy of Sciences 110(16), 6453-6458. (doi:10.1073/pnas.1217027110). 2. Wright A.E., Dean R., Zimmer F., Mank J.E. 2016 How to make a sex chromosome. Nat Commun 7. (doi:10.1038/ncomms12087). 3. Mathers T., Hammond R., Jenner R., Zierold T., Hanfling B., Gomez A. 2013 High lability of sexual system over 250 million years of evolution in morphologically conservative tadpole shrimps. BMC Evol Biol 13(1), 30. 4. Mathers T.C., Hammond R.L., Jenner R.A., Haenfling B., Gomez A. 2013 Multiple global radiations in tadpole shrimps challenge the concept of ’living fossils’. PeerJ 1. (doi:10.7717/peerj.62). 5. Mathers T.C., Hammond R.L., Jenner R.A., Hanfling B., Atkins J., Gomez A. 2015 Transition in sexual system and sex chromosome evolution in the tadpole shrimp Triops cancriformis. Heredity 115(1), 37-46. (doi:10.1038/hdy.2015.10). 6. Zierold T., Hanfling B., Gomez A. 2007 Recent evolution of alternative reproductive modes in the ’living fossil’ Triops cancriformis. BMC Evol Biol 7. (doi:10.1186/1471-2148-7-161). 7. Bedhomme S., Bernasconi G., Koene J.M., Lankinen A., Arathi H.S., Michiels N.K., Anthes N. 2009 How does breeding system variation modulate sexual antagonism? Biology Letters 5(5), 717- 720. (doi:10.1098/rsbl.2009.0401). 8. Harrison M.C., Hammond R.L., Mallon E.B. 2015 Reproductive

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ULeicester WildlifeConservationSequencing

A 4 year iCASE PhD studentship, fully funded for UK / EU students, is available at the University of Leicester, UK , in conjunction with Oxford Nanopore Technologies (ONT, UK) as part of the BBSRC Midlands Integrative Biosciences Training Partnership (MIBTP).

Subject: Nanopore DNA sequencing in forensics: wildlife crime and conservation

Supervisors: Dr Celia A May, Prof Mark A Jobling, Dr Jon H Wetton, MCSFS (University of Leicester) and Zoe McDougall (ONT, UK).

Informal enquiries to primary supervisor Dr Celia May (cam5@le.ac.uk).

Full details of the iCASE MIBTP programme, and how to apply can be found at the MIBTP website:

http://www2.le.ac.uk/colleges/medbiopsych/research/Postgraduate%20Opportunities/mitbp-at-the-university-of-leicester/icase Application Deadline: 8 January 2017 Interviews: 26 January 2017 Start Date: 25 September 2017

Project Description:

Nanopore sequencing has the potential to free DNA analysis from the specialist laboratory and enable tests to be performed at an affordable price when and where required. Hand portable third generation DNA sequencers such as the MinION developed by the industrial sponsor Oxford Nanopore Technologies are intended to make sequencing a commonplace activity by simplifying and automating as much of the process as possible with disposable microfluidic units ultimately performing the stages manually performed by laboratory personnel. â€We wish to explore the capabilities of nanopore sequencing for capacity building in countries that lack easy access to DNA analysis centres. A primary need for both the conservation geneticist and the wildlife protection agencies is the ability to analyse mitochondrial DNA which encompasses not only the highly conserved barcode genes, which vary characteristically between species allowing confident assignment to a taxonomic group, but also the hypervariable DNA regions. The latter can be used to discriminate between different maternal lineages within a population as a result of their very high mutation rate, whilst other regions of the mitochondrial genome with intermediate mutation rates offer information at the sub-specific and population level. â€

see also FindaPhD.com entry: https://www.findaphd.com/search/phd.aspx?keywords=Celia%20May Eligibility requirements: â€

1st or a 2.1 degree in a relevant field (a 2.2 plus Master's degree or 3+ years relevant post-graduate experience may be eligible). â€Evidence of quantitative training (AS or A level Maths, IB Standard or Higher Maths, or University maths/statistics course). Please note that EU applicants that have not been resident in the UK for the past 3 years will only be eligible for bench fees and the training grant, but not the stipend as stipulated by Research Council UK policy.

"May, Celia A. (Dr.)" <cam5@leicester.ac.uk>

ULinnaeus Sweden EvolutionaryEcolLepidoptera

PhD position: Ecology with emphasis in evolutionary ecology of butterflies and moths

The doctorate student will work within the research project 'Evolutionary ecology of butterflies and moths'. The aim of the project is to investigate the causes and consequences of genetic and phenotypic variation, using butterflies and moths as model systems. Part of the research will be conducted in within the framework of an ongoing project regarding the ecological consequences for populations and species of variation in functionally important traits, such as life-history characteristics and color patterns. For this, we have at our disposal ecological data for a large number of moth species that can be used for comparative analyses to evaluate hypotheses and test predictions. The research will also include initiating a new project. Field studies and laboratory work will be used to collect information on the distribution, dynamics, genetic structure and composition of natural (meta-) populations of selected moths and butterflies, likely on the island of Ãland. Data will be used to investigate how environmental heterogeneity impact on ecological and evolutionary processes and shape patterns of population-level diversity, and how population-level diversity in turn may feed-back on ecological and evolutionary processes. The successful applicant will be part of EEMiS, a multidisciplinary center of excellence within Linnaeus University.

Linnaeus University was established when Kalmar University and Växjö University merged. The Department of Biology and Environmental Science is part of the Faculty of Health and Life Sciences. The research activities within the Department of Biology and Environmental Science include the areas of aquatic ecology, cell and organism biology, evolutionary biology, microbiology, environmental science and environmental engineering as well as zoonotic ecology. For more information see: www.Lnu.se The PhD studies are limited to 4 years (100%) but may be extended to 5 years through teaching at the undergraduate level. Successful completion of the post-graduate studies will lead to a PhD in Ecology with emphasis in evolutionary ecology. The position is located in Kalmar, Sweden and will start from 1 February, 2017, or as soon as possible thereafter.

Closing date for application is January 26th, 2017.

Applications through https://lnu.se/en/meet-linnaeus-university/work-at-the-university/. Mark your application with reference number 2016/7072-2.2.1.

Further information: https://lnu.se/en/meet-linnaeus-university/work-at-the-university/?rmpage=-job&rmjob=2480&rmlang=UK Contacts: Project leader and principal supervisor: Professor Anders Forsman (anders.forsman@lnu.se), +46-(0)480-446173 Head of department: Per-Eric Betzholtz (per-eric.betzholtz@lnu.se), +46-(0)480-446238 Human resources consultant: Christian Andersson (christian.andersson@lnu.se>), +46-(0)470-448506 Union representatives may be contacted via the university switchboard at +46-772-288000

– Dr. Martin Wiemers Department of Community Ecology Helmholtz Centre for Environmental Research - UFZ Theodor-Lieser-Str. 4 06120 Halle Germany Tel. +49 345 558-5322 e-mail: martin.wiemers@ufz.de http://www.ufz.de/index.php?en=31235 private: Wielandstr. 8 06114 Halle Germany Tel. +49 345 27950187 Mobile +49 157 85401271 Fax +49 3212 6968883 e-mail: mwiemers@web.de

Martin Wiemers <martin.wiemers@ufz.de>

UManchester BirdSongEvolution

PhD Position: Understanding and controlling the evolution of reproductive behaviour during ex situ conservation

Main supervisor: Tucker Gilman (https://manchesterbehaviouralevolution.wordpress.com/people/) University of Manchester

Human appropriation of land and resources is reducing the habitat available to non-human species. As a result, many species are now being conserved ex situ. In such cases, natural phenotypes and diversity must be maintained in captive populations to allow for potential rewilding in the future. Much attention has been paid to the conservation of genotypes and genetic diversity, but heritable behaviours can also evolve in captivity, and the conservation of behaviours has received relatively little attention.

Birdsong is one behaviour that can evolve in captivity. For example, the Bengalese finch is a domesticated variant of the white-rumped munia, and during domestication its song has become more complex than that of its wild ancestor. Because of its role in mate recognition, birdsong is of particular importance to conservation practitioners. If the songs of captive and wild populations diverge until the animals cannot recognise each other as mates, it may be impossible to supplement wild populations with releases from captivity. In addition, if songs diverge among captive populations, it may be difficult to maintain genetic diversity by transferring animals among ex situ conservation facilities.

The Java sparrow is a congener of the Bengalese finch and is a species of conservation concern. A formal ex-situ conservation programme for the species is being developed. Despite its close relationship to the Bengalese finch, nothing is known about how captivity affects the song of the Java sparrow. Thus, population managers do not know whether they should be concerned about song conservation in this species. Moreover, if song conservation is important, practitioners lack evidence-based tools for achieving it.

In this project, we aim to i) understand how and why Bengalese finch song has evolved in captivity, ii) assess whether Java sparrow song is also affected by captivity, and iii) evaluate strategies for maintaining wild-type birdsong in captive populations. The student will:

1. Use molecular approaches to reconstruct the population history of the Bengalese finch in captivity. This will help us to understand when and how Benaglese finch song diverged from that of its wild ancestor.

2. Assess whether song has diverged among Bengalese finch populations in North America, Europe, and Asia. This will help us to understand whether songs have evolved due to drift, or whether similar selective pressures drive song evolution in different captive populations.

3. Use mate choice trials to determine whether divergence among Bengalese finch populations, and between Bengalese finch and white-rumped munia populations, is sufficient to inhibit mating and influence gene flow.

4. Assess whether song has diverged among native, captive, and introduced populations of Java sparrows. If divergence has occurred, assess whether this is sufficient to inhibit gene flow between populations.

5. Design and assess husbandry practices to slow or reverse song divergence in captive populations of estrildid finches.

The student in this project will receive training in modern molecular genetic approaches for analysing population history (e.g., whole mtDNA sequencing or haplotype sharing), statistical approaches for assessing similarity and divergence between birdsongs, mate choice trials and behavioural assays, and birdsong recording in the field and in the lab.

The project will be a CASE partnership with Chester Zoo. The supervisory team will include Tucker Gilman and Susanne Shutlz (University of Manchester), Leah Williams (Chester Zoo), and Jakob Bro-Jorgenson (University of Liverpool). For more information, email tucker.gilman@manchester.ac.uk. Apply at http://-tinyurl.com/java-sparrow-phd by 18 January 2017.

“tucker.gilman@manchester.ac.uk”
<tucker.gilman@manchester.ac.uk>

UmeaU FishSpeciation

PhD position in Ecology with a focus on ecological speciation and invasion history of freshwater fish

We are looking for a PhD student for studies of speciation and colonization history of freshwater fish, using ancient DNA in lake sediments. Last date of application: 2017-01-15. Project start: early 2017

Project description

The recent discovery that extracellular DNA can be detected in ancient lake sediments extends the time window through which we can observe evolution and community change from a few decades to more than 10 000 years. In this project we will use this novel tool to study ecological speciation and the colonization and extinction dynamics of fish in Scandinavian lakes. The project is financed by Biodiversa, Oskar and Lili Lamm's stiftelse and Umea University.

Admission requirements

For this position, we are seeking a candidate with relevant academic background in ecology, evolutionary biology, physical geography or similar subjects. Strong merits are knowledge of fish biology, speciation, sedimentology, and relevant molecular techniques. The successful applicant should have good ability to write and speak in English, be creative, take initiatives, be independent and collaborative. Evaluations will be based on the individual letter, results from university courses, quality of master's thesis and other publications, references, the interview, and, possibly, the candidate's performance in a writing test given after the interview.

Application The application should include:

- a short letter (max 2 pages) describing your research interests and why you are interested in the position

- CV, including academic achievments

- Digital copies of Bachelor/Master thesis

- Scientific publications, certificates from higher education and other documentation that supports your application

- Contact information to three reference persons.

Your application must be registered in Umea University's e-recruitment system MyNetwork Pro (at http:/-/www.umu.se/om-universitetet/lediga-jobb/) no later than January 15th 2016.

Starting date: By agreement

Further information: please contact Professor Goran Englund, who will act as PhD supervisor, +46-(0)70 245 1038, goran.englund@umu.se, or assistant supervisor Xiao-Ru Wang, xiao-ru.wang@umu.se, Rich Bindler, rich.bindler@umu.se, Folmer Bokma, folmer.bokma@umu.se.

The Department of Ecology and Environmental Science (EMG) at Umea University conducts research and offers postgraduate studies in Ecology, Environmental Sciences and Physical Geography. The department has about 160 employees, including about 30 PhD-students (for further information, see http://www.emg.umu.se/english/?languageId=1 . Link to ad: http://www.umu.se/english/about-umu/open-positions?languageId=1 Göran Englund <goran.englund@umu.se>

UMuenster 12 EvolutionaryAdaptation

12 PhD positions in the Research Training Group “Evolutionary Processes in Adaptation and Disease” (EvoPAD): PhD projects in Biology, Medicine, and Philosophy

Start: 1st April 2017. 3-year positions (TV-L E13 65 %).

The new DFG-funded Research Training Group “Evolutionary Processes in Adaptation and Disease” (EvoPAD, GRK 2220) unites biological, medical, and philosophical research at the University of Munster, Germany. The core idea is to use the theory of evolution to understand processes leading to adaptation and/or disease. 12 PhD students will work on advancing evolutionary theory, and in turn, apply modern evolutionary approaches to medical questions. EvoPAD doctoral researchers will perform cutting-edge research in an interdisciplinary environment. Our multidisciplinary qualification program is tailored to individual career tracks, and offers opportunities for international cooperation, summer schools, and courses covering evolutionary and population genetics, bioinformatics, experimental design, philosophy of science, and bioethics.

EvoPAD is coordinated within the stimulating city of Munster near Munster’s University Palace and offers a family friendly and international atmosphere.

For project descriptions please visit: www.uni-muenster.de/EvoPAD/application Requirements

- Outstanding Master’s or equivalent degree in Biology, Biomedicine, Bioinformatics, Biotechnology, Philosophy or related fields.

- Proven qualifications with particular relevance to EvoPAD (e.g., research experience in modern genomics or emerging infectious diseases).

- Capacity to formulate and solve research problems and effectively interpret research results.

- Willingness to interact with colleagues in an interdisciplinary setting.

- Motivation to manage a PhD project and to participate in our multidisciplinary qualification program.

- Fluency in written and spoken English.

How to apply

The application should include:

- CV including information about former academic education and degrees, professional experience, publications, fellowships/awards, conference contributions, languages, and further relevant skills and abilities.

- Cover letter stating the candidate’s expectation from EvoPAD and motivation to join the project.

- Master’s thesis abstract.

- Two letters of recommendation from former supervisors.

Applications from women are particularly encouraged. Disabled candidates with equivalent qualifications will be preferentially considered.

Applications should be sent by e-mail as one PDF file (max. 5 MB) to the EvoPAD Coordinator Dr. Vanessa Kloke (evopad@uni-muenster.de) by January 8th, 2017. Please indicate in the cover letter the project that you would like to apply for and also give a second choice (if wanted).

Shortlisted candidates will be interviewed by Skype between 17th - 20th January 2017. The most promising candidates will then be invited to Munster to take part in an admissions workshop on 2nd & 3rd February 2017 (travel costs and accommodation will be reimbursed).

—

Dr. Vanessa Kloke

Coordinator of the Munster Graduate School of Evolution

Westfalische Wilhelms-Universitat Munster

Hufferstr. 1a, D-48149 Munster, Germany

Phone: +49 251 83-21252

E-Mail: mgse@uni-muenster.de

Website: http://www.uni-muenster.de/Evolution/-mgse/ “Vanessa Kloke, MGSE” <mgse@uni-muenster.de>

UMuenster ExperimentalEvolution-PlasticityImmunePriming

Graduate position: UMuenster.ExperimentalEvolutionPlasticityImmunePriming

We invite applications for a PhD position in the group of Animal Evolutionary Ecology at the Institute for Evolution and Biodiversity, University of Muenster, Germany (http://www.uni-muenster.de/-Evolution/animalevolecol/).

We are seeking a highly motivated student, ideally with a background in evolutionary ecology. The successful candidate needs to have a Master or Diploma in Biology or related subjects. Experience with molecular or microbiological techniques is advantageous but not required. The successful candidate will work in the fields of experimental evolution and ecological immunology. The project aims at elucidating conditions for rapid adaptation by investigating a prime example of phenotypic plasticity, the invertebrate immune memory (i.e. 'priming'). This topic will be addressed with serial passage experiments of the entomopathogen Bacillus thuringiensis in the red flour beetle Tribolium castaneum and with experiments that focus on host experimental evolution in relation to immunological plasticity. In addition to these long-term experiments, and depending on the experience and interest of the candidate, analyses of transcriptomic data sets and/or further lab experiments on immune pr iming can be included.

Working language of the lab is English. PhD students can become member of the Muenster Graduate School of Evolution (MGSE, http://www.uni-muenster.de/-Evolution/mgse/). With its large university and vibrant city centre, Muenster is known as one of the most livable cities in Germany (see http://www.muenster.de/en/ and http://www.uni-muenster.de/en/ for further details).

The position is available for 3-years, starting March 1st, 2017. The salary will be 65% of a E13 TV-L position of the German tariff for public employees. The University of Muenster is an equal opportunity employer and is committed to increasing the proportion of women academics. We also welcome applications from candidates with severe disabilities. A German version of the job description can be found at https://www.uni-muenster.de/Rektorat/-Stellen/ausschreibungen/st_20152509_sk15.html . Interested candidates should send applications via email (please use the keyword 'rapid evolution' as the subject) as a single pdf (max. 5 MB) that is named with the family name of the applicant. The pdf should contain a CV, a list of publications (if available), a short statement of research interests and the addresses of two potential referees. Please send your application to:

Prof. Dr. Joachim Kurtz joachim.kurtz@uni-muenster.de

Closing date is December 30th, 2016.

Prof. Dr. Joachim Kurtz

University of Muenster Institute for Evolution and Biodiversity Animal Evolutionary Ecology Group Huefferstr. 1, 48149 Muenster, Germany

Phone (secretary): + 49 251 83 21638 / 21027 Phone (direct): + 49 251 83 24661 Fax: + 49 251 83 24668 Room: 109 joachim.kurtz@uni-muenster.de http://www.uni-muenster.de/Evolution/-animalevolecol/kurtz.shtml DFG SPP Host-Parasite Coevolution Münster Graduate School of Evolution (MGSE)

"joachim.kurtz@uni-muenster.de" <joachim.kurtz@uni-muenster.de>

UNamur Belgium EvolutionRotifers

A PhD position is available to study extreme stress responses inthe notorious bdelloid rotifers, UNamur, Belgium

A PhD position is available immediately to start working on the oxidative stress responses of bdelloid rotifers following desiccation and radiation within the group of Prof. Karine Van Doninck (Laboratory of Evolutionary Genetics and Ecology) and Dr. Florence Chainiaux at the University of Namur (Belgium).

While several metazoan asexual lineages exist, the most notorious and successful clade is the bdelloid rotifers containing at least 460 morphospecies that seems to have evolved for tens of millions of years without sexual reproduction (including fertilization and meiosis with pairing of homologous chromosomes). Besidestheir asexual mode of reproduction, they are also well-known for their extreme desiccation and radiation resistance. Entering a desiccated state is however harmful in most animals and is expected to be accompaniedby the generation of reactive oxygen species (ROS), known to induce damages at the DNA, protein and lipid level if not neutralized by antioxidants. This PhD project will study and characterize in detail the oxidative stress generated during desiccation and radiation in the model bdelloid species Adineta vaga and investigate their antioxidant responses. Being funded by the European Space Agency, this Phd will also investigate the impact of simulated micro gravity on oxidative stress responses and be involved in space mission preparation.

This PhD position is for 1 year and can start as soon as February 1^st 2017, being funded by two projects, ESA (European Space Agency) and ARC (Actions de Recherche Concertees). An extension of another 3 years ispossible but the candidate will be encouraged to apply for its own FRIA orFNRS Belgian PhD grant.

Prof. Karine Van Doninck recently acquired an ERC Consolidator Grant to study the mechanisms of genome evolutionin the absence of meiosis in bdelloid rotifers; this ERC CoG will start in 2017. This PhD will join a very dynamic research lab including nowadays 5 postdocs, 2 PhD students and 3 technicians at UNamur. We employ interdisciplinary approaches (cellular and molecular biology, comparative genomics, bioinformatics and community level) to study evolutionary processes in the absence of sex andthe mechanisms of extreme resistances. Our team obtained the first draft genome of the bdelloid rotifer A. vaga (Flot_etal_2013_Nature), we have optimized desiccation and radiation protocols (Hespeels_etal_2014_JEB) and recently we discovered horizontal gene transfer between A. vaga individuals sampled in the wild (Debortoli_etal_2016_Current Biology). Our laboratory works in close collaboration with Dr. F. Chainiaux at UNamur, studying ageing and oxidative stress in human, with Prof. S. Lucas at LARN (UNamur)for the radiation experiments, with Prof. B. Hallet at UCL (Belgium) specialized in DNA repair studies and with Dr. S. Baatout of the SCK-CEN radiobiology unit (Mol, Belgium) for the microgravity experiments.

Contacts: For more information contact Prof. Karine Van Doninck, karine.vandoninck@unamur.be or Dr. Boris Hespeels, boris.hespeels@unamur.be from the University of Namur, Laboratory of Evolutionary Genetics and Ecology http://www.lege-unamur.be Application: Applicants should have a Msc degree in Biology or Molecular Life Sciences or Medical Biology with a specialization in molecular biology, evolutionary genetics, biochemistry or similar. The successful candidate should be proficient in English and should demonstrate his motivation to do a Phd and work in a multidisciplinary research team with a highly collaborative spirit.

The closing date for applications is 9^th of January 2017.

Interested applicants should send a cover letter (briefly describingresearch experience, interests, and career goal), curriculum vitae (with list of publications if any), and the names of three references (including address, phone number and Email) to Karine VAN DONINCK (karine.vandoninck@unamur.be)

Karine VAN DONINCK Full Professor Department of Biology

T. +;32 (0)81 724 407 F. +32 (0)81 724 362 karine.vandoninck@unamur.be http://perso.fundp.ac.be/~kvandoni/ Universite de Namur ASBL Rue de Bruxelles 61 - 5000 Namur Belgique

Karine Van Doninck <karine.vandoninck@fundp.ac.be>

UNevada LasVegas HawaiianDrosophila

A PhD Assistantship position is available in the School of Life Sciences at the University of Nevada, Las Vegas (UNLV).

The successful student will be supported through a combination of RA and TA positions. The student will become part of a vibrant, interdisciplinary research team investigating the evolutionary genetics, ecology, and behavior of Hawaiian picture-winged *Drosophila* in Dr. Donald Price's laboratory (https://sites.google.com/a/unlv.edu/donald-price/). The student will enroll in the PhD program in Biological Sciences with a start date for the position of August 2017.

Project Summary - The spectacular diversity of the ca. 120 species of Hawaiian picture-wing *Drosophila* display highly divergent behavioral, ecological and morphological traits. The overarching goal of this project is to determine the functional genomics underlying adaptive radiation for three Hawaiian picture-wing *Drosophila *species. Recombinant inbred lines between *D. silvestris* and *D. heteroneura* and between *D. silvestris *and* D. planitibia* will be created and the genomes of each line sequenced. RNA-seq analysis will be conducted in targeted tissues to analyze the tissue-specific gene expression profiles and phenotypic traits will be measured that differ between species that play critical roles in adaptation, reproduction and reproductive isolation between species. The combined analysis of genome sequence analysis, RNA-seq profiling and phenotypic trait analysis in these recombinant lines will allow for an understanding of the role of structural genomic and gene expression in the development and expression of phenotypic traits important in adaptive divergence. The graduate student will be engaged in each phase of this project with a focus on analyzing the genomes and phenotypic traits in the recombinant lines. The graduate student will be expected to develop independent research projects.

The student must meet admission requirements to the PhD program of the School of Life Sciences (https://www.unlv.edu/lifesciences/admissions). Additionally, to be considered for this position, the student ideally will have: a) completed a master's degree or graduated by August 2017. Someone with a Bachelor's degree with extensive research experience may qualify; b) performed laboratory or field research in evolutionary or behavioral genetics as part of master's degree research; c) published (or in prep.) one or more manuscripts from a research project from master's degree research or other research. The student should be self-motivated, able to work in teams, and have an interest in working and living in southern Nevada and being part of UNLV graduate and research programs.

The School of Life Sciences is one of the largest academic units on the UNLV campus. It has 30 full-time faculty members, 10 adjunct and research faculty, approximately 2000 undergraduate majors and 50 graduate students. Further information on the program and university is accessible via the School of Life Sciences website (http://www.unlv.edu/lifesciences). UNLV is an urban university surrounded by extensive public land including Lake Mead National Recreation Area, Red Rock Canyon National Conservation Area, Desert National Wildlife Refuge, and the Spring Mountains National Recreation Area. Outdoor recreation opportunities abound year-round.

Interested candidates should email me (donald.price@unlv.edu) the following: (a) 1-page statement of interest outlining your background, coursework, research and publication experience including laboratory and fieldwork, research interests and career goals; (b) CV or resume including undergraduate and Master's degrees and GPA, list of relevant coursework, and employment and professional experience; (c) names and contact information of three academic or professional references. In your email, please use a subject line of: Hawaiian Drosophila UNLV PhD Position Application (your name). We will contact applicants directly for further consideration.

Donald K. Price, Ph.D. Director and Professor School of Life Sciences University of Nevada, Las Vegas 4505 S Maryland Pkwy Las Vegas, NV 89154 School of Life Sciences: Director Office: 702.895.2053 Office: 702.895.4456 Lab: 702.895.4457

donald.price@unlv.edu

https://www.unlv.edu/lifesciences https://sites.google.com/a/unlv.edu/donald-price/home
"donald.price@unlv.edu" <donald.price@unlv.edu>

UNevada Reno PlantPopGenetics

The Parchman lab at the University of Nevada, Reno is recruiting a PhD student to conduct population genetic and genomic analyses on a suite of native plants in the Great Basin Desert. The student would be advised by Dr. Thomas Parchman (Department of Biology) and co-advised by Dr. Elizabeth Leger (Department of Natural Resources and Environmental Sciences). This work, funded by a USDA NIFA grant, aims to determine the phenotypes and evolutionary histories that enhance seedling establishment and to analyze the genetic structure and diversity of native plant populations to inform restoration practices. Ideal applicants would have strong interest in plant evolutionary genetics and a combination of some or all of the following qualifications: 1) Molecular genetic laboratory experience, 2) Programming experience in R, Unix, and Perl (or Python), 3) Past experience or serious interest in the ecology and evolutionary biology of Great Basin native plants 4) Past experience or strong interest in restoration ecology and restoration genetics.

UNR has a strong interdisciplinary PhD program in Ecology, Evolution, and Conservation Biology (http://environment.unr.edu/eecb/). Graduate students accepted into the EECB program are guaranteed financial support through Teaching Assistantships (TAs), which includes health insurance and an out-of-state tuition waiver. For this position, funds are additionally available for a number of semesters will be available through Research Assistantships (RAs). The successful applicant will begin the PhD program in Summer or Fall 2017, with the possibility of joining the lab sooner as a technician.

University of Nevada, Reno (UNR) is a Tier I research university located in a spectacular environment at the confluence of the Great Basin and the Sierra Nevada Mountains. The faculty and graduate students at UNR are highly interactive and include an internationally known group of evolutionary biologists and ecologists. The Parchman lab has recently been renovated, and is equipped with ample (and new) molecular and computational resources for modern genome sequence analysis. We are also located in an ideal setting for field-based projects in the Great Basin and Sierra Nevada regions, allowing enviable access to spectacular montane and desert ecosystems. Reno is only 40 minutes from Lake Tahoe, offers a high quality of living, an excellent climate, and is a large enough city to offer diverse activities and amenities. World class rock climbing, skiing, and mountain biking opportunities are in extremely close proximity.

Interested applicants should send a CV, copies of transcripts, and a statement of research experience and interests to Tom Parchman (tparchman@unr.edu) and Elizabeth Leger (eleger@cabnr.unr.edu). Consideration will begin on January 30th, but will be open until filled.

Thomas L Parchman <tparchman@unr.edu>

UNewHampshire ComparativePhylogenomics

NSFfunded PhD position available at the University of New Hampshire!—

TheLesser, Plachetzki (http://www.unh.edu/plachetzki-lab/), and MacManes (http://genomebio.org) Labs at the University of New Hampshire are in search of a talented PhD student to work on a NSF-Dimensions of Biodiversity-funded project aimed at examining the relationships between marine sponges and their microbiomes.

Theproject will identify the phylogenetic, genetic, and functional biodiversity of coral reef sponges across the Caribbean basin. This work will combine cutting edge techniques in phylogenetic comparative methods and the analysis of high throughput Illumina sequencing data. Though this student will focus on phylogenetic comparative methods and genomics, there will be opportunities for field work in the Caribbean to learn techniques in marine and coral reef biology. We especially encourage students of diverse and non-traditional backgrounds to apply. The successful candidate may have an undergraduate degree in Biology, Computer Science, Statistics, Mathematics, or other disciplines.—

Applicationsare to be submitted to the UNH graduate school (http://www.gradschool.unh.edu/-apply.php, Deadline January 15). Interested students are strongly encouraged to contact us at matthew.macmanes@unh.edu and david.plachetzki@unh.edu. Please include a CV and statement of purpose with correspondence.—

MatthewMacManes @macmane

Matthew.Macmanes@unh.edu

UOklahoma EvolutionaryPhysioEcol

UOklahoma Graduateposition Evolutionary physiological ecology

I am recruiting graduate students to join me at the University of Oklahoma starting Fall 2017! My lab focuses on understanding the impacts of temporal variability in stress on ectotherms, and the evolution of these traits, and integrates tools from gene expression through to species distribution modeling at multiple levels of biological organization. While my past work focused on energetic and mechanistic effects of repeated freezing and cold events in insects, I'm broadening my scope in this new lab to include desiccation and heat tolerance. Upcoming studies include work on eastern spruce budworm and tropical dung beetles, with the potential for fieldwork in Arizona and Ecuador. I'm happy to accomodate individual students' research interests and keen to pursue evolutionary questions as they pertain to stress tolerance.

Prospective students can read more about my work here: http://www.ou.edu/content/cas/biology/people/-faculty/katie-marshall.html Geographical ecology is a significant core focus of the OU Department of Biology, where I am part of a Geographical Ecology cluster hire, together with Dan Allen (stream and riparian ecology) and Katie Marske (comparative phylogeography). Students will have the opportunity to interact with these and other talented faculty and students in the Geographical Ecology focus group and throughout the department.

http://www.ou.edu/content/cas/biology.html Lab resources include a wet lab for RNA sequencing preparation, physiological assays, and thermal performance measures, a separate microscope room, access to cloud computing resources, and an insectary for insect rearing. Other Biology facilities on campus include a new Biology Core Genomics lab, the Oklahoma Biological Survey and the Sam Noble Museum of Natural History. OU is also home to state-of-the-art climate and weather research, including the National Weather Center, the Oklahoma

Mesonet, the Oklahoma Climatological Survey, and the South Central Climate Science Center.

Funding for graduate students is currently available in the form of 10-month teaching assistantships with stipends, full tuition waivers and excellent health care coverage, and numerous scholarships are available to support graduate student research during the summer.

Interested students should get in touch (kemarshall@ou.edu) with a brief summary of your research interests and relevant experiences and attach a resume/CV. I will also be at SICB and would love to chat (please email first). Candidates from groups underrepresented in STEM are encouraged to apply.

Find out more here: http://www.ou.edu/content/cas/-biology/graduate-studies.html Dr. Katie Marshall

Assistant Professor Department of Biology, University of Oklahoma Norman, Oklahoma

kemarshall@ou.edu

"Marshall, Katie E." <kemarshall@ou.edu>

UOtago NewZealand PopGenTheory

PhD in Epigenetic Theory

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 in biology and/or mathematics (or a related field) that included a research component (e.g., a dissertation or a thesis). The degree (e.g., BSc(Hons), MSc) will have been awarded with first-class honours/distinction.

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.

For details about living in Dunedin, in the South Island of New Zealand, 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).

Applications will close on Wednesday, 18 January 2017.

Hamish Spencer <hamish.spencer@otago.ac.nz>

UQueensland MarsupialEvolution

University of Queensland, Marsupial evolution, focusing on short-term evolution of 3D shape variation

The Weisbecker Lab at the University of Queensland and the Phillips lab at Queensland University of Technology (Brisbane, Australia), are looking for a motivated PhD candidate to work on the short-term shape evolution in the skeleton of marsupial mammals.The candidate will be a central part of an Australian Discovery Project grant project. The work will contribute to the development of evolutionary baselines for morphological shape evolution in marsupial mammals, with particular focus on the question of how quickly morphological shape changes in the evolutionary short-term. Expected outcomes include improved understanding of short-term vs. long-term morphological evolution, and a novel statistical framework for analysing morphological data, which allows fossils to be merged into the tree of life.

Essential skills for this position are proficiency in R (particularly the phylogenetics and geometric morphometrics packages). Good spoken and written English is also essential. Experience in vertebrate morphology and virtual 3D visualization (e.g. using Meshlab, Mimics, or Avizo) is an advantage. Experience in the field of vertebrate evolution is also desirable but not essential.

Acceptance for this PhD is contingent on a successful application for PhD funding, with half the funding coming from the Weisbecker/Phillips labs and the other half from the School of Biological Sciences at the University of Queensland. OVERSEAS APPLICATIONS ARE ENCOURAGED. The next deadline for international scholarships is in on January the 27th for starting in June 2017; applicants with at least one publication have particularly good chances of being accepted. International applicants can apply before conferral of their degree if the degree is conferred soon (contact for details). Students within Australia can apply for an Australian Postgraduate Award. Note also that UK applicants need to have a Master's degree. For further information and conditions of employment, please visit http://www.biology.uq.edu.au/scholarships . Please send expressions of interest, along with a CV, to Vera Weisbecker: v.weisbecker@uq.edu.au

Dr Vera Weisbecker

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School of Biological Sciences

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Ph.: +61 7 336 57071

UQ ALLY :: Supporting the diversity of sexuality and gender identity at UQ.

www.weisbeckerlab.com.au Vera Weisbecker <v.weisbecker@uq.edu.au>

UReading EvolutionCancerDispersal

== QMEE CDT Project available at the University of Reading, UK, planned start date October 2017: http://www.imperial.ac.uk/qmee-cdt/ == Title: Evolution of dispersal and motility in cultured cell lines

== Main Supervisors: Dr Louise Johnson, University of Reading (https://www.reading.ac.uk/biologicalsciences/about/staff/l-j-johnson.aspx); Prof James Bullock, CEH (http://www.ceh.ac.uk/staff/james-bullock); Dr Cristina Lo Celso, Imperial College (https://www.imperial.ac.uk/people/c.lo-celso)

== Co-Supervisor: Dr Tiffany Taylor, University of Bath (http://www.bath.ac.uk/bio-sci/contacts/academics/tiffany-taylor/)

== Project description: Dispersal and its evolution are central to ecology, impacting processes such as speciation, the maintenance of genetic diversity, and adaptation to changing environments. Extensive theory supports this view, but robust empirical data is lacking, partly due to practical difficulties with current model organisms (Duputie & Massol, Interface Focus 3:0028, 2013). However, dispersal theories can be tested in the lab with microbial models (Kümmerli et al. Evolution 63:939-49, 2009; Taylor et al. J Evol Biol 26:2644-53, 2013). Key questions in dispersal depend on a) the genetic and epigenetic basis of dispersal phenotypes, and b) the connections between dispersal and normal movement patterns during an organism's life. We seek a student to address the evolution and genetics of dispersal using data from a novel model system: cultured cell lines derived from human cancers. Cell lines share advantages with microbes (Taylor et al. Evol. Appl. 6: 535-548, 2013): they are small, tractable, clonal, and can be frozen down. Lines are available with varying motility and hence dispersal phenotypes. However, unlike bacteria, cancer cells exhibit complex epigenetic control of phenotype, and appear to show plastic dispersal. Low nutrient environments can result in increased motility both in the short term, presumably due to plasticity, and longer term, which may be the result of selection (T. Taylor, unpublished data). By tracking cells and their descendants, we have found a high broad-sense heritability of motility within cancer cell populations in vitro (Wass et al. in prep.), showing that cell lines should rapidly respond to selection on motility. This offers an easily identifiable phenotype on which to track the evolution of dispersal traits. Cell motility is also a key component of metastasis, which has been analogised to dispersal, although there is debate over the extent to which this analogy is helpful (Arnal et al. Evol. Appl. 8.6 (2015): 541-544)). The aim of this project is to assess the utility of cancer cells as model systems for understanding the evolutionary ecology of dispersal with the potential for complex epigenetic control, and to use empirical data to generate robust evolutionary models that can be generalised to other organisms. This multidisciplinary project, using data from in vivo and in vitro cell tracking, will involve analysis of large datasets of cell behaviour and lines of descent, and agent-based modelling informed and parameterised by real data. Using video and image analysis, we will quantify variation within populations and correlations between cell relatives, measure population-level responses to environmental change, and examine patterns of motility inheritance. Statistical modelling will help disentangle the influences of ancestry and environment (e.g. cell-maternal effects) on motility. Modelling will involve agent-based simulations and analytical methods to represent the evolution of cell motility under realistic, complex genetic control. Evolutionary processes will be modelled under alternative micro-environments to assess the conditions which drive disparate evolutionary pathways. Insights will be gained into the role of genetic architecture in the evolution of dispersal.

== Multidisciplinary: Disciplines represented: Ecology and evolution; Dispersal ecology; Population and evolutionary genetics; Quantitative genetics; Agent based modelling; Experimental evolution; Biomedical science; Bioimage analysis

== Training: The student will be developing new applications or validation for existing theory/methods; Working with large datasets; Agent based modelling

== Funding notes: Competition funded PhD project. Applicants will have a 2.1 or higher in a relevant undergraduate degree. Relevant post-graduate experience will be considered. NERC-funded studentships are subject to RCUK eligibility requirements, which are outlined under "Student

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UReading FungalPathogenEvolution

The University and Reading, with Imperial College London, UK invites applications for a PhD position in:

Fungal pathogen evolution in a warming world: consequences for human health and biodiversity

Supervisors: Richard Walters and Mike Shaw at the University of Reading, and Matthew Fisher at Imperial College London.

The PhD student will study the thermal adaptation of various important fungal pathogens involved in human and wildlife disease, namely Batrachochytrium dendrobatidis, a global amphibian pathogen causing amphibian chytridiomycosis (Clare et al. 2016), Aspergillus fumigatus, an opportunistic pathogen of plants and animals including humans (Meis et al. 2016) and Fusarium oxysporum, an emerging crop disease. Recent phylogenetic analyses reveals virulence is associated with warmer environments, reinforcing the view that fungal pathogens were the driving evolutionary force behind vertebrate endothermy, homeothermy and (arguably) the extinction of the dinosaurs (Casadevall 2012). The successful applicant will establish the thermal performance of fungal isolates using a novel 'gradient plate' and will explore the evolutionary potential of pathogens under climate change through the development of computer models (e.g. Walters et al. 2012).

The project builds upon evolutionary epidemiology projects currently funded by NERC where several hundred isolates of these pathogens have already been isolated ready for use. Main project aims are to: 1) relate genetic variance in thermal performance e.g. thermal optima and critical maximum temperature, to underlying thermodynamic constraints and the selective environment, 2) validate model predictions by quantifying genetic variance for thermal performance curve biophysical variables using a novel gradient plate approach on a) hundreds of readily available genome-sequenced isolates for B. dendrobatidis, A. fumigatus and F. oxysporum and b) strains subject to laboratory evolution under various thermal regimes, 3) identify genes associated with isolate variation and their possible relationships to biophysical variables and 4) review and adjust the assumptions of the theoretical models given empirical evidence.

The student will develop several skill sets identified as 'most wanted' in the biological and environmental sciences by UK Research Councils, including modelling, data management, numeracy and risk and uncertainty. Specifically, training will be provided in the following areas: 1) mathematical biology and its application to population genomics, enzyme kinetics and epidemiology, 2) computer programming and its application to Individual-Based Modelling, simulations and scenarios and 3) statistically robust experimental design and practice.

We are seeking a strongly motivated person with BSc, and ideally MSc degree, in biology or a related discipline. The applicant should have good English language and presentation skills. We provide training in modelling and quantitative skills but the applicant should highlight evidence of their enthusiasm and aptitude to learn them, such as the type of data analyses undertaken in their previous research projects or their use of R, for example. Previous experience with fungi and experimental design is an advantage.

The position is funded for 3.5 years (competitive funding is obtained through the QMEE CDT). Stipend and conditions are based on NERC PhD studentships. UK residents (3+ years) are entitled to full funding and tuition, EU applicants are entitled to partial funding. Starting date is 1 October 2017.

If you are interested in this position, please send your CV, along with a letter of motivation and the contact details of two references as a single PDF to Richard Walters (r.j.walters@reading.ac.uk). Deadline for applications is 19 January 2017. For questions, please use the same email address as above.

The University of Reading and Imperial College London are strong advocates of equality and diversity in research and teaching and particularly encourage women to apply.

References: Casadevall A (2012) PLoS Pathog. DOI:10.1371/journal.ppat.1002808 Clare F et al. (2016). Phil. Trans. R. Soc. B. DOI: 10.1098/rstb.2015.0454 Meis JF et al. (2016). Phil. Trans. R. Soc. B. DOI: 10.1098/rstb.2015.0460 Walters RJ et al. (2012). Funct. Ecol. DOI: 10.1111/j.1365-2435.2012.02045.x

Weblinks: http://www.imperial.ac.uk/qmee-cdt https://mhasoba.pythonanywhere.com/qmee_cdt/default/view_proposals/view/proposals/36 Richard Walters Ph.D.

Lecturer in Ecology and Evolutionary Biology QMEE CDT Co-Director Reading Ecology Network lead

School of Biological Sciences Harborne Building (Office 8F) University of Reading Whiteknights, Reading, Berkshire RG6 6BX (for Sat. Nat. use RG6 6UR) United Kingdom

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URhodeIsland BiodiversityGenomics

The Lane Lab at the University of Rhode Island is inviting PhD applicants to work on a recently funded NSF GoLife project. The focus of the project is diversity and genomics within the Stramenopiles, Alveolates and Rhizaria - largely microbial eukaryotic taxa that are underrepresented in traditional databases.

The bulk of eukaryotic diversity is microbial and, when compared to plants, animals and fungi, much of this microbial diversity has been undersampled from the standpoint of morphological, phylogenetic and genomic data. This skew in data not only has consequences for our understanding of the biodiversity of eukaryotic life on Earth, but also how we interpret cellular and evolutionary biology in the broadest sense. One of the most diverse major clades of eukaryotes that has recently emerged from phylogenomic analyses united the Stramenopila, Alveolata and Rhizaria into the 'SAR' group.

Initially this clade was controversial because it forced a re-evaluation of the evolution of several characters, most notably the spread of photosynthesis across eukaryotes. However, additional data have robustly supported SAR as an independent clade. Among the diverse lineages within SAR, genomic-scale data are rare and concentrated in only a few areas, Apicomplexa (e.g. malarial parasites), omycetes (e.g.

parasite 'water molds') and diatoms (e.g. ecologically important phytoplankton). Despite their global ecological importance, fewer than 50% of all SAR clades, and only one third of non-photosynthetic SAR clades, are represented by even a single genome in public databases.

This work will add at least 250 novel genomic-scale datasets (transcriptomes, draft genomes, single-cell amplified genomes), focused primarily on capturing diversity within SAR.

Details of the project can be found at http://www.nsf.gov/awardsearch/showAward?AWD_ID=1541510&HistoricalAwardsÃ_olse Interested applicants are encouraged to contact Chris Lane (clane[at]uri.edu) to express interest and for more details.

Information of applying can be found at http://web.uri.edu/graduate-school/apply/ The deadline for full consideration is Jan 15.

Chris Lane Associate Professor Integrated & Evol. Bio. Graduate Director Department of Biological Sciences University of Rhode Island 120 Flagg Road Kingston, RI., 02881 Office: CBLS 277 ph (401) 874-2683 fax (401) 874-2065 http://cels.uri.edu/bio/lanelab/ Chris Lane <clane@uri.edu>

USheffield CompGenomicsStructuralColour

Predicting genomic effects on structural colour Lead supervisor: Dr Nicola Nadeau, Department of Animal and Plant Sciences, University of Sheffield Co-supervisor: Dr Andrew Parnell, Department of Physics and Astronomy, University of Sheffield

Closing date: 6th January

We are looking for a student with advanced numerical skills and an interest in both biology and physics to work on a project predicting genomic effects on structural colour. Structural colours, caused by diffraction or interference of light from nano-scale structures, are some of the brightest and most impressive colours in nature. There has been extensive interest in replicating structural colours, which are produced from simple biological materials that are cheap and non-toxic, and can also have unique properties such as angle dependent colour (iridescence). However, very little is known about how the patterning of such fine structures is controlled in biological systems and the genetic pathways controlling this have yet to be identified in any system. This project would use genomic data from Heliconius butterflies from South America to predict how individual genetic loci control specific aspects of structural variation. The project will involve computational modelling approaches, firstly to predict fine structural characteristics from small angle x-ray scattering data and secondly to predict this morphology from genotype.

The candidate should have a background or training in physics, maths or computer science; or advanced numerical skills from a biology background (e.g. through masters-level training). Some experience or training in data analysis or programming would be ideal. The student should have the enthusiasm to get to grips with concepts from both biology and physics. Interested candidates are encouraged to contact either of the supervisors with informal enquiries.

This project is funded through The Leverhulme Centre for Advanced Biological Modeling (CABM). Studentships are fully funded for 3 years including fees (at UK/EU rate) and a stipend at the standard RCUK rate (currently pounds 14,296, rising slightly each year). These projects are available to UK, EU and overseas applicants, but funding for tuition fees will be provided to successful applicants at the UK/EU rate. This means that students from outside the EU will need another source of funding to cover the difference between UK/EU tuition fees and international fees. To apply go to http://www.sheffield.ac.uk/postgraduate/research/-apply/applying after reading the information contained on that page click the link to the Postgraduate online application form.

Dr Nicola Nadeau Dept. of Animal and Plant Sciences Alfred Denny Building, University of Sheffield Western Bank, Sheffield S10 2TN, UK N.Nadeau@sheffield.ac.uk Tel: +44 (0)114 222 4717 http://nadeau-lab.group.shef.ac.uk/ “n.nadeau@sheffield.ac.uk” <n.nadeau@sheffield.ac.uk>

USheffield GeneticsOfAgeing

The genetics of how environmental fluctuation accelerates the ageing process Supervisors: Dr Mirre Simons (University of Sheffield), Dr Sean Sweeney (University of York) https://acce.shef.ac.uk/the-genetics-of-how-environmental-fluctuation-accelerates-the-ageing-process/ Global warming has changed the average environment experienced by organisms but has also increased environmental variability. Even if organisms are able to adapt to a sudden change in average environmental conditions, rapidly fluctuating ecological conditions are predicted to impose severe constraints on biodiversity. Indeed, we have recently found that fluctuating the diet content of flies (Drosophila melanogaster) can dramatically speed up the ageing process. This novel finding indicates severe physiological costs of fluctuations in the diet and opens up the first possibility to understand these costs in detail. The powerful genetics readily available in flies now allows a rapid and deep insight into these processes with high relevance to understanding how diet impacts on organisms.

You will use a combination of approaches in flies to uncover the physiology responsible for the observed vulnerability to fluctuation in the diet. Through screening a large number of lines for the dietary phenotype, genes regulating this physiology can be implicated using genome-wide association analysis. Such genes can then be manipulated in flies to test whether they are regulating causal physiology. Further experiments can then elucidate the exact physiology responsible. The wealth of different genetic lines of flies available in dedicated stock centres means that many intricate genetic manipulations are only one or a few crosses away.

Recent work on the connection between ageing and diet has suggested that the reward centre in the brain might be key in regulating the valuation of diet and thereby ageing. Such neuronal processes could, therefore, be an important part of how organisms cope with fluctuating environments. You will test the involvement of these brain areas in how flies respond to fluctuations in their diet. With the expertise offered by supervisor Dr Sean Sweeney, you will be able to directly test the connections between neuronal cell biology, accelerated ageing and diet.

We seek a hard-working passionate student with a quantitative mindset and an interest in the biology of ageing. Candidates with a diverse background in life science will be considered. The broad scientific expertise of the supervisors ensures a vibrant environment for the student. We will empower the student to pursue his/her own interests and acquire a wide array of skills. Your research will not only have implications for how we understand a key process in evolution and conservation, but also for biomedical science in which ageing research and in particular the connection to diet is growing in importance.

contact: m.simons@sheffield.ac.uk

“m.simons@sheffield.ac.uk” <m.simons@sheffield.ac.uk>

USouthernCalifornia EvolMitochondriaSexAging

Ph.D. position in Mitochondrial Effects on Sex-Specific Aging

The Edmands Lab at the University of Southern California in Los Angeles (https://dornsife.usc.edu/labs/edmands/) is recruiting a Ph.D. student for research developing the copepod Tigriopus californicus as a new model for the effects of mitochondria and mitonuclear interactions on sex-specific aging. The ideal applicant would have a strong interest in evolutionary genetics and aging, with experience in genomics, transcriptomics and/or bioinformatics.

Prospective students should email Suzanne Edmands (sedmands@usc.edu) to discuss project possibilities. In your email please include brief details about your GPA, GRE, research interests, experience and reasons for pursuing a Ph.D.

Applications should be submitted to the Marine Biology and Biological Oceanography Graduate Program at the University of Southern California (https://dornsife.usc.edu/bisc/meb-admissions/). All Ph.D. students in the program will have five years of support (including tuition remission and student health insurance) through a combination of RAships, TAships and fellowships. To receive full consideration for university fellowships, applications must be submitted by January 15, 2017.

Suzanne Edmands Professor Department of Biological Sciences 3616 Trousdale Parkway, AHF 316 University of Southern California Los Angeles, CA 90089 (213)740-5548 http://dornsife.usc.edu/labs/edmands/ edmandss@gmail.com

UStirling PopStructureAdaptation

Adapt, move or perish? Identifying syndromes of population structure to predict species’ responses to a changing environment

We are seeking a highly motivated individual to carry out PhD research at the University of Stirling that will bridge the research fields of population biology, global change biology and macroecology.

Climate change is already having profound effects on the spatial distribution of many species. To ensure broad coverage, studies often treat species as uniform entities and generate predictions of a species’ overall ability to adapt, move or perish. However, the population is the unit that will respond to a changing climate, therefore making robust predictions on emergent species-level responses should ideally involve consideration of how the populations that make up a species’ range are structured. Population structure has been quantified for individual species, but these data are rarely synthesised across species to identify common syndromes: a main aim of this project.

This is an ambitious PhD project that has the scope to generate novel and significant insights on the role of population structure in determining species’ range dynamics. It will combine generation of a large and unique cross-species dataset of measures of population structure and its potential drivers (from existing literature) with sophisticated modelling techniques to identify syndromes and make predictions on emergent species-level responses. It will suit a quantitatively-minded student with a biological background. For more in-

formation and to apply: https://www.findaphd.com/search/ProjectDetails.aspx?PJID=80692&LID=1455
Lynsey Bunnefeld

Room 4B157, Cottrell Building Biological & Environmental Sciences University of Stirling FK9 4LA, Scotland

01786 467770 lynsey.bunnefeld@stir.ac.uk

lynsey.bunnefeld@stir.ac.uk

USussex FloralEvolution

* PhD position available to study flower evolution during range expansions at the University of Sussex*

Main supervisor: Maria Clara Castellanos (www.sussex.ac.uk/lifesci/plant-evolutionary-ecology-lab); co-supervisor: Dave Goulson (www.sussex.ac.uk/lifesci/goulsonlab)

We are looking for an enthusiastic, independent student interested in plant-animal interactions and plant evolution to explore how new pollinator environments on different continents can generate floral evolutionary innovation. The project will use several plant species that can be studied in their native and new ranges, and combine field and molecular work with greenhouse studies to understand how plants deal with changes in their pollinators. For further details on the project please visit www.sussex.ac.uk/study/phd/fees-and-scholarships/scholarships/view/692 .The student will be part of the vibrant Evolution, Behaviour and Environment subject group within the University of Sussex; our campus is located within a national park, 10 minutes from the seashore city of Brighton.

This 3.5-years fully funded studentship is open to UK and EU citizens. The closing date for applications is 31st January 2017. Applications should be submitted through Sussex University's graduate application system: http://www.sussex.ac.uk/study/phd/apply. Please include a CV, statement of interest and the names and email addresses of two academic referees. The expected starting date is September 1st 2017.

Email me for informal inquires: m.c.castellanos@sussex.ac.uk.

"M.C.Castellanos@sussex.ac.uk"
<M.C.Castellanos@sussex.ac.uk>

UTArlington Evolution

The Department of Biology at the University of Texas at Arlington (http://www.uta.edu/biology/) invites applications for our PhD program beginning in Fall 2017. PhD students are awarded competitive stipends, tuition remission, and health benefits. Research in the department includes a wide range of topics in ecology, evolution, genomics, microbiology, and cell and developmental biology.

For general inquiries about the program, please contact our graduate advisors: Shawn Christensen (shawnc@uta.edu) or Woo-suk Chang (wschang@uta.edu). For more specific questions about research directions, please contact potential advisers directly using the contact information on their webpages (https://www.uta.edu/biology/faculty.php). We will start reviewing applications on December 15th 2016. The on-line application process requires submission of the formal graduate school application, transcripts, GRE scores (general test required), three letters of reference, and, for non- native speakers of English, TOEFL or IELTS scores. Applications can be submitted via the following link: http://www.uta.edu/admissions/graduate/apply/how-to-apply.php . The Department and University have numerous resources including state-of-the-art labs, an Animal Care Facility, a Genomics Core Facility, a Center for Human Genomics, and the newly established Shimadzu Institute for Research Technologies - a major partnership between UT Arlington and Shimadzu Scientific Instruments that offers extensive resources for imaging, proteomics and analytical chemistry. The Department also benefits from access to core UT-system genomics and computational resources at UT Southwestern Medical Center and the Texas Advanced Computing Center (TACC) - one of the leading advanced computing centers in the U.S.

Arlington is a city of approximately 365,000 and is conveniently located in the center of the Dallas-Fort Worth Metroplex. Within a 25-mile radius of the center of Arlington is a workforce of over two million people. The city has 82 public parks, including River Legacy Parks, a 1,300-acre oasis on the Trinity River in the heart of north Arlington. Arlington is the home of the Dallas Cowboys Stadium, the Texas Rangers Ballpark, and Six Flags Over Texas. Cost of living is relatively low for a major metropolitan area. The Dallas-Fort Worth International Airport is the fourth largest airport in the US. More information on the city of Arlington can be found at www.experiencearlington.org . Matthew R. Walsh, Ph.D. Assistant Professor Department of Biology University of Texas at Arlington Arlington TX 76019 Office: 817-272-1546 Lab: 817-272-9079 Email: matthew.walsh@uta.edu

"Walsh, Matthew" <matthew.walsh@uta.edu>

UTubingen FloweringPhenology

The Plant Evolutionary Ecology group (http://www.uni-tuebingen.de/PlantEvoEco) at the University of Tübingen in Germany invites applications for a

** PhD position in Plant Ecology **

The PhD student will combine field surveys with the study of herbarium collections to investigate how land use and climate change affect the flowering phenology of forest understory plants. The project is part of the Biodiversity Exploratories (www.biodiversity-exploratories.de), one of the largest ecology projects in the world, which will allow the student to interact with many other ecological researchers. It will also be in close collaboration with the Ancient Genomics & Evolution group at the MPI for Developmental Biology, who will study genomic changes in the same plants.

The successful applicant will be based in Tübingen. The field work will take place across Germany in the Hainich, Schwäbische Alb and Schorfheide regions. The herbarium work will be in several German herbaria, mainly Tübingen, Stuttgart, Jena and Berlin.

The University of Tübingen is one of the oldest universities in Germany, and Tübingen a beautiful university town with a high quality of life. The Plant Evolutionary Ecology group at the University of Tübingen studies the ecology, evolution and genetics of plants in changing environments.

We are looking for a student with a strong interest in plant ecology and global environmental change. The successful candidate should have a MSc in biology, a good command of English, and a driving licence. Botanical and statistical skills are a plus, but not a must.

The position is funded for 3 years (pending final confirmation by the DFG). Salary is at the scale 13 TV-L (65%). Starting date is 1 March 2017 but can be negotiated.

If you are interested in this position, please send your CV, along with a letter of motivation and the contact details of two references as a single PDF to oliver.bossdorf@uni-tuebingen.de. Deadline for applications is 8 January 2017. For questions, please use the same email address as above.

The University of Tübingen aims at increasing the share of women in research and teaching and particularly encourages women to apply.

– Plant Evolutionary Ecology Institute of Evolution and Ecology University of Tübingen Tübingen - Germany http://www.uni-tuebingen.de/PlantEvoEco "niek.scheepens@biologie.uni-tuebingen.de"

UTubingen PlantPhenotypicPlasticity

The Plant Evolutionary Ecology group (http://www.uni-tuebingen.de/PlantEvoEco) at the University of Tübingen in Germany invites applications for a

** PhD position in Plant Evolutionary Ecology **

The PhD student will study the rapid evolution of grassland plants in response to land use. Specifically, the project will test whether plants evolve greater phenotypic plasticity when environments become more temporally variable in terms of mowing, grazing and fertilization. The successful applicant will collect seeds in three different regions of Germany (Hainich, Schwäbische Alb and Schorfheide), conduct controlled greenhouse experiments in Tübingen to assess plastic responses to experimental treatments, integrate experimental data with land use, vegetation, and molecular data, and analyse and publish results in peer-reviewed scientific journals.

The project is part of the Biodiversity Exploratories (http://www.biodiversity-exploratories.de/), one of the largest ecology projects in the world, which will allow the student to interact with many other ecological researchers. The University of Tübingen is one of the oldest universities in Germany, and Tübingen has a rich student life, a high quality of life and a beautiful old town and surroundings (notably the Swabian Alb). The Plant Evolutionary Ecology group at the University of Tübingen studies the ecology, evolution and genetics of plants in changing environments.

We are seeking a strongly motivated person with MSc degree in biology (or equivalent). The applicant should have good English language and presentation skills. Knowledge of German language is not required, but a driving licence is a must. Previous experience with plant ecological experiments and data analysis (preferably in R) is an advantage.

The position is funded for 3 years (pending final confirmation by the DFG). Salary and conditions are according to a public service position in Germany (TV-L E13; 65%). Starting date is 1 March 2017 but can be negotiated.

If you are interested in this position, please send your CV, along with a letter of motivation and the contact details of two references as a single PDF to niek.scheepens@biologie.uni-tuebingen.de. Deadline for applications is 8 January 2017. For questions, please use the same email address as above.

The University of Tübingen aims at increasing the share of women in research and teaching and particularly encourages women to apply.

– Plant Evolutionary Ecology Institute of Evolution and Ecology University of Tübingen Tübingen - Germany http://www.uni-tuebingen.de/PlantEvoEco "niek.scheepens@biologie.uni-tuebingen.de"

UYork AntHybridisationSpeciation

Hybridisation, speciation and genetic structure in a woodland specialist

Supervisor: Dr Elva Robinson < http://www.york.ac.uk/biology/research/ecology-evolution/elva-robinson/ >

Co-supervisors: Dr Joan Cottrell (Forest Research), Dr Kanchon Dasmahapatra < http://www.york.ac.uk/biology/research/ecology-evolution/kanchon-dasmahapatra/ > , Dr Kevin Watts (Forest Research)

Project description:

Britain's forests offer key habitat for woodland species; however, maintaining biodiversity under the demands of timber production can be challenging. The highly fragmented nature of British woodlands is a further challenge because fragmentation leads to isolation, usually reducing genetic diversity of woodland dwelling species, particularly in species with poor dispersal abilities and exacting habitat requirements such as wood ants (*Formica rufa* group). These species, threatened across Europe, are key components of woodland ecosystems and offer an ideal study system to explore the impact of habitat fragmentation on genetic diversity of a woodland species.

This study will clarify the conservation status of a genetically unusual wood ant population in the North York Moors (NYM) and will use wood ants to study how dispersal and habitat fragmentation influence the formation of hybrids and new species. We will do this by comparing the genetic diversity of the NYM population to samples from across the UK and Eurasia. The data will explain what creates the unusually high diversity in the NYM and allow investigation of how wood ants spread and diversified at the continental scale after the last glacial period.

Research team The collaboration involves the University of York, CASE partner Forest Research, and a project partner (University of Helsinki). The supervisory team provide a range of skills, including genetic techniques, fieldwork skills, landscape analysis, and expertise in forest management and invertebrate ecology/evolution. This combination offers a challenging and well-supported training environment and enables the student to acquire a diverse skill-set with excellent employment prospects.

Applications The results of our research will set the NYM wood ant population in its broader European context which will inform foresters, including Forestry Commission practitioners, and DEFRA policy-makers, in the development of appropriate management strategies for the conservation and promotion of this key woodland species group.

*Funding: *This is a NERC Industrial CASE studentship fully funded for 4 years and covers: (i) a tax-free stipend at the standard Research Council rate (pounds 14,296 for 2016-2017, to be confirmed for 2017-2018), (ii) research costs, and (iii) tuition fees at the UK/EU rate.

Start date: October 2017

The studentship is available to UK and EU students who meet the UK residency requirements.

To discuss your suitability for this project please email: elva.robinson@york.ac.uk <elva.robinson@york.ac.uk>

For more information, see: http://www.york.ac.uk/biology/postgraduate/research/funding/funded-studentships/fullyfundedproject2-robinson/ *CLOSING DATE FOR APPLICATIONS: Sunday 22nd January 2017*

Other related available PhD and MSc projects listed here:

https://pure.york.ac.uk/portal/en/researchers/-elva-joan-hilda-robinson(9c6bafea-ffbb-444c-8d9f-63b9312b9dce).html

– EJH Robinson University of York Elva.Robinson@york.ac.uk Twitter: @Elva_Robinson < http://twitter.com/Elva_Robinson >

Home page < http://www.york.ac.uk/biology/-research/ecology-evolution/elva-robinson/#research > Publications list < http://scholar.google.co.uk/-citations?user=FZZX_koAAAAJ&hl=en > Email disclaimer < http://www.york.ac.uk/docs/disclaimer/-email.htm >

Biology at York holds an Athena Swan Gold Award < http://www.york.ac.uk/biology/about/athena-swan/ >

Elva Robinson <ejhr500@yccsa.org>

UZurich EpigeneticsAdpatation

Joint PhD Position at the Department of Plant and Microbial Biology (IPMB) and the Department of Evolutionary Biology and Environmental Studies (EBES),

University of Zurich

We are looking for a motivated student who is interested in applying molecular approaches to study questions in ecology and evolution. The project will be conducted under the joint supervision of an ecologist and molecular geneticist to investigate the role of epigenetic variation in adaptation (see project description below). Please send your application to Bernhard Schmid <bernhard.schmid@ieu.uzh.ch> and Ueli Grossniklaus <grossnik@botinst.uzh.ch>, including your CV and a short letter of motivation.

Population Epigenomics, Phenotypic Plasticity, and Environmental Adaptation

Bernhard Schmid (EBES), Ueli Grossniklaus (IPMB)

Despite the heritability of epigenetic variation (EV), its ecological and evolutionary significance is largely unknown and being controversially discussed [1-3]. In plants, epigenetic changes can be heritable over generations [e.g. 4,5] and occur more frequently than genetic ones [6,7]. Thus EV may allow rapid responses and has the potential to play a key role in the adaptation to environmental change. However, published results are contradictory, possibly because very small sample numbers were molecularly analyzed and experimental replication is insufficient [discussed in 3,8,9]. Over the last years, we have collected experimental data demonstrating a role for epigenetics in the response to changes in the biotic and abiotic environment using Arabidopsis thaliana as a model. We could demonstrate the selection of new, stable phenotypes in genetically uniform backgrounds in independent, replicated selection experiments, suggesting a role of EV in adaptation [see also 10]. The results, however, depended on the experimental set-up: while we found no evidence for a role in adaptation when starting with seeds from a single individual, stable phenotypes were selected when starting with seeds derived from a population. Although materials and selection scenarios used where highly diverse, this finding indicates that there is standing EV in genetically uniform populations that can be selected upon but that the rate of epigenetic change from generation to generation is too low to generate sufficient variation when starting from an individual. We will test this hypothesis in a highly replicated experiment involving 3 genotypes in 3 environments that should help to settle the controversy on the ecological and evolutionary significance of epigenetic variation.

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[3] Hirsch S, Baumberger R, Grossniklaus U (2012) Epigenetic variation, inheritance, and selection in plant populations. Cold Spring Harb Symp Quant Biol 77:97-104.

[4] Cubas P, Vincent C, Coen E (1999) An epigenetic mutation responsible for natural variation in floral symmetry. Nature 401:157-161.

[5] Manning K, Tor M, Poole M, Hong Y, Thompson AJ, King GJ, Giovannoni JJ, Seymour GB (2006) A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. Nat Genet 38:948-952

[6] Schmitz RJ, Schultz MD, Lewsey MG, O'Malley RC, Urich MA, Libiger O, Schork NJ, Ecker JR (2011) Transgenerational epigenetic instability is a source of novel methylation variants. Science 334:369-373.

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[8] Pecinka A, Rosa M, Schikora A, Berlinger M, Hirt H, Luschnig C, Mittelsten Scheid O (2009) Transgenerational stress memory is not a general response in Arabidopsis. PLoS One 4:e5202.

[9] Pecinka A, Mittelsten Scheid (2012) Stress-induced chromatin changes: a critical view on their heritability. Plant Cell Physiol 53:801-808.

[10] Zuppinger-Dingley D, Schmid B, Petermann JS, Yadav V, de Deyn GB, Flynn D (2014) Selection for niche differentiation in plant communities increases biodiversity effects. Nature 515:108-111.

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Valencia PlantConservation

PhD position_Biotic interactions shaping plant communities Reply-To: Alicia Montesinos <ali.montesinos@gmail.com>

Applications are invited for a PhD position to join the department of Plant Ecology in the Research Center of Desertification (CIDE) in Valencia, Spain

http://www.uv.es/uvweb/desertification-research-centre/en/departments-/plant-ecology-/presentation-1285896767023.html). The successful candidate will work on a project investigating the use of biotic interactions as a tool to improve the success of ecological restauration proposals. The project focuses on the understanding of the environmental filters shaping plant communities in semiarid environments, especially in gypsum soils, and its effects on the phylogenetic diversity and local adaptations of plants in these communities. It will approach how certain biotic interactions such as plant facilitative interactions, plant-mycorrhizal fungi and plant-herbivore interactions can alleviate or promote environmental filters in these stressful environments. This PhD project will contribute to the understanding of biotic and abiotic filters shaping plant communities under stressful conditions in order to design efficient and successful ecological restauration proposals.

The applicant will be encouraged to propose her/his own ideas and research interests within this conceptual framework, and in this sense, the candidate is expected to be highly motivated, and has curiosity and leadership skills in order to propose ideas independently.

The Project will involve fieldwork in gypsum plant communities in south Alicante combined with greenhouse experiments in Moncada (Valencia) (Spain).

Applicants must have a finished her/his degree after the 1st of January of 2013 and have an average grade of academic record above 7.5 (out of 10). Interested applicants can apply via email (ali.montesinos@gmail.com), before the 15th of January of 2017 providing the following information: CV, academic record scores, brief statement of research interests, research experience and motivation, and the email of two researches willing to provide a support letter for the candidate.

Contact information:

Alicia Montesinos Navarro

Email: ali.montesinos@gmail.com Web: https://www.researchgate.net/profile/Alicia_Montesinos-Navarro –

Alicia Montesinos Navarro

Centro de investigacion sobre desertificacion (CIDE-CSIC) Carretera Moncada - Náquera, Km. 4,5 46113 Moncada (Valencia) Spain Tel +34 96 3424126 Fax +34 96 3424160

https://www.researchgate.net/profile/Alicia_Montesinos-Navarro Alicia Montesinos <ali.montesinos@gmail.com>

Vienna PopulationGenetics

Reminder: The 2017 call for PhD students at the Vienna Graduate School of Population Genetics (Twitter @PopGenViennaPhD) is now open:

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:

- Evolution of gene expression

- Understanding thermal adaptation

- The impact of new transposable element insertions on adaptation to a new environment

- *Wolbachia* infection dynamics in evolving *Drosophila* populations

- The adaptive value of diversity produced by recurrent whole genome doubling

- Epigenetic variation in *Arabidopsis*

- Genetic footprints of adaptive introgression

- New methods for modelling and analysis of data from experimental evolution

- Maximum likelihood inference of population genetic parameters using genome-wide data from nearly neutral sites

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics *in a single pdf*) received by *January 08, 2017* will be considered. Two letters of recommendation need to be sent directly by the referees.

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at Julia Hosp <Julia.Hosp@vetmeduni.ac.at>

VirginiaCommonwealthU EvolGenetics

PhD position

The Dyer laboratory (http://dyerlab.bio.vcu.edu) has an opening for a doctoral student in the Integrative Life Sciences Doctoral program (https://goo.gl/qKVrrN) at Virginia Commonwealth University (http://vcu.edu) to work on a landscape epigenetics project.

The successful applicant for this position will be:

- Capable of using R for statistical inferences and spatial analyses, - Able to work successfully in the laboratory creating next-gen libraries, and - Excited about conducting field work in Baja California, Mexico.

To apply, send CV with contact information of at least 3 academic referees to rjdyer@vcu.edu. The application deadline for the VCU ILS PhD program is 10 January 2017.

– Dr. Rodney J. Dyer, Director Center for Environmental Studies Virginia Commonwealth University http://dyerlab.bio.vcu.edu "rjdyer@vcu.edu" <rjdyer@vcu.edu>

VirginiaTech 2 AvianBehaviour

PhD Student, Avian Behavioral Neurobiology, Biological Sciences, Virginia Tech

The Sewall lab in the Department of Biological Sciences at Virginia Tech is recruiting up to 2 PhD students. Research in the lab examines the effects of the ecological and social environment on neural plasticity, communication, and social behavior in songbirds. The successful applicant(s) will conduct field and captive research on songbird communication and cognition, as well as histology, immunohistochemistry, and molecular assays to examine makers of neural plasticity and brain function. Being accepted into the PhD program at Virginia Tech and Dr. Sewall's lab will provide extensive training in animal behavior, neurobiology, and ecology by the PI, lab members, and a group of exceptional researchers in organismal biology, including Drs. Joel McGlothlin, Ignacio Moore, Dana Hawley, and Bill Hopkins. Graduate students at Virginia Tech are provided a stipend and tuition coverage in exchange for service as a teaching or research assistant.

To Apply: Send a cover letter summarizing your prior experience, professional goals, and research interests, as well as a CV and contact information for at least three academic references to Kendra Sewall (ksewall@vt.edu). The application deadline funding through the graduate program is December 31st.

For more information see links below. the Sewall lab: http://vtsewall.weebly.com/index.html Virginia Tech Biological Sciences: http://www.biol.vt.edu/-index.html Kendra Sewall, PhD Assistant Professor Biological Sciences 3024/3026 Derring Hall Virginia Tech 1405 Perry St Mail Code 0406 Blacksburg, VA 24061 540.231.5617 http://vtsewall.weebly.com/ "ksewall@vt.edu" <ksewall@vt.edu>

WashingtonStateU ConservationBiol

PhD positions at Washington State University

The Goldberg Lab at Washington State University, Pullman, is looking for 1-2 new Ph.D. students to start Fall 2017 in the School of the Environment. Our group develops and applies environmental DNA, genomic, and spatial analysis methods to conservation issues throughout western North America and internationally, primarily focusing on amphibians. Applicants should be interested in pursuing quantitative landscape-level questions in a conservation and management context. Students will have the opportunity to work on ongoing projects, develop their own project, or a combination of the two. Projects with anticipated funding include landscape genomics of amphibians, hybridization of endangered amphibians, and eDNA detection of rare aquatic species. Students will be funded on a combination of TA and RAships, depending on project choice and funding availability. TA support is guaranteed for 3 years.

An M.S. degree by Spring 2017 is required. To apply, send a cover letter describing your interests, CV, and contact information for three references as one pdf to caren.goldberg at wsu.edu. An official application must also be submitted to WSU by January 10th, 2017.

Caren Goldberg https://scholar.google.com/-citations?user=XGutsLEAAAAJ&hl=en Caren Goldberg Assistant Professor, Quantitative Spatial Ecology School of the Environment Washington State University (FedEx/UPS) 100 Dairy Rd./404 Heald Hall (USPS only) P.O. Box 642812 Pullman, WA 99164-2812 (509) 335-3673

"Goldberg, Caren" <caren.goldberg@wsu.edu>

WesternWashingtonU GeneExpressionVariation

The Pollard lab at Western Washington University (http://cse.wwu.edu/biology-faculty/pollard) has an opening for a master's graduate student who is interested in the genetic mechanisms of natural variation in gene expression. We use mating pheromone response in budding yeast as a system to study how genetic variation acts at both the transcript and protein levels to modify the dynamics of protein expression.

The ideal candidate will have (1) a strong interest in evolution, genetics, cell biology, and computational biology, (2) experience with basic molecular biology techniques, and (3) the ability to communicate clearly, interact collaboratively, and derive a sense of motivation from within. The lab welcomes qualified applicants with diverse backgrounds.

The Pollard lab is located on the top floor of the WWU Biology building, adjacent to molecular biology and genomics labs and across the sky bridge from biochemistry labs with overlapping interests. We meet weekly to discuss projects and journal articles. Outside of the lab we enjoy going for hikes to collect wild yeasts together.

Western Washington University is a mid-sized public liberal arts university located in Bellingham, WA. Bellingham is a beautiful coastal town in the Northeast corner of Puget Sound, 50 miles south of Vancouver, 30 miles west of Mt. Baker, 90 miles north of Seattle, and 20 miles east of the San Juan Islands.

Interested candidates are strongly encouraged to contact Dr. Pollard by email (dan.pollard (at) wwu.edu) with a description of their interests and carrier goals and a CV including relevant experience, GPA, GRE scores, and the names of 2-3 references.

Official application is due February 1st. Application details: http://www.wwu.edu/gradschool/-how-to-apply.shtml Masters program: http://-catalog.wwu.edu/preview_program.php?catoid=-3D12&poid=3D5419&returnto=2524 Current masters students: https://cse.wwu.edu/biology/graduate-students Pollard lab: https://cse.wwu.edu/biology-faculty/pollard Biology Department: https://cse.wwu.edu/biology Bellingham: http://www.bellingham.org/ "Dan.Pollard@wwu.edu" <Dan.Pollard@wwu.edu>

Jobs

Bayer MicrobialGenomics

GRAD SCHOLAR - MicrobialGenomics/Machine Learning To support R&D projects within Biologics Bayer CropScience (BCS), to drive innovative crop protection and plant health solutions, and to develop and implement b data analysis tools and algorithms. The candidate will work closely with wet lab scientists and computational scientists in West Sacramento, CA and other scientists throughout BCS.

Position: Major Tasks - Proactively identifying and incorporating novel statistical methodologies to link bacterial taxonomy/genomics to function. - Participate in a multi-disciplinary team of scientists who offer comparative genomics, pathway modeling, network analyses, and metagenomics for controlling pests and diseases in plant and promoting plant health using microbes. - Conduct research and collaborate with scientists using machine learning methodologies to examine microbial processes and mechanisms that underlie plant-microbe interactions, produce secondary metabolites, and contribute to primary microbial metabolism. - Help drive the experimental design, analysis, and interpretation of HTS datasets incorporating total community analysis(functional gene analysis, phylogenetic and network analysis), comparative genomics, de novo assembly of targeted specific community,genes and selected microbial genomes. - You will be joining a computational life sciences team which bringstogether expertise in biology, computational science, statistics,bioinformatics and software development. - Be able to communicate effectively through listening, documentation,and presentation, especially using compelling visualization tools to share analysis and interpretation of data. - Provide analysis and feedback about experimental results to supervisors, highlighting important results and defining next step experiments. - Coordinate and cooperate on research activities with peers, supervisors, and subordinates - Communicate effectively by listening, documentation, and presentation.

Position: Skills - PhD in Ecology and Evolution, Microbial Ecology, Microbial Genetics/Physiology/Ecology, Statistics, Applied Statistics, Machine Learning (or nearing substantial completion, provided all Ph.D. requirements are successfully completed within 6 months of employment start date). - M.S. in Ecology and Evolution, Bioinformatics, Microbial Ecology, Statistics, Microbial Genetics/Physiology/Ecology, plus 1+ years of relevant experience. - Proven ability to work within a reproducible framework, handling large data sets efficiently using scripts,databases, and other tools; - Should be highly versed in experimental design methodologies, mixed linear modeling, and machine learning and be able to communicate the output with other scientists around interpretation of these statistical analyses. - Knowledge of R or Python is essential. - Knowledge of other programming languages is a plus (Unix, Perl, C, C++) - Knowledge of microbial physiology an asset.

https://career.bayer.us/job/Graduate-Scholar-Microbial-Genomics--0000182024.html Janette Gardiner <janette.gardiner@bayer.com> Janette Gardiner <janette.gardiner@bayer.com>

CarletonU EvolutionaryHealthSciences

Dear Colleagues,

Please see the job advertisement below for 3 positions at Carleton University in Ottawa, Canada. We welcome applications from scientists using evolutionary and population genetic approaches to address the topics listed, hence we are posting the ad here. The “Big Data” position may be of particular interest to readers of EvolDir.

All the best,

Alex Wong

Assistant Professor Department of Biology Carleton University

Health Sciences - Associate/Full Professors and Department Chair (3 Positions)

Academic unit: Department of Health Sciences, Carleton University

Category of appointment: Preliminary (Tenure-Track)

Rank/Position title: Associate or Full Professor and Chair of the Department (3 Positions)

Start date: July 1, 2017

Closing date for Applications: January 13, 2017

The Department of Health Sciences at Carleton University in Ottawa, Ontario, Canada is inviting applications for three senior Associate or Full Professors, one of whom will be Chair of the Department.

The Department of Health Sciences is an interdisciplinary department in the Faculty of Science at Carleton University, serving as the academic base for 17 full time and cross-appointed faculty members, >200 undergraduate students in the Bachelor of Health Sciences, graduate students, and postdoctoral research fellows associated with our Faculty. Health Sciences is an interdisciplinary department that fosters academic and research collaborations with other departments at Carleton, and with external partners in health-related fields including departments and organisations within the Government of Canada, Government of Ontario, the Institute of Clinical and Evaluative Sciences, and community organisations, hospitals and research institutes in Ottawa, nationally and worldwide.

A distinctive strength of the Department is the interdisciplinary approach to health problems and solutions, and the collaborative nature of our Faculty to address these. The Department is building core strengths in three clusters of excellence: 1) Environment and Global Health, 2) Lifecourse Approach to Health and 3) Big Data. The new Health Sciences Building, slated for opening July 2017, will be the home base for the Department, with state-of-the-art infrastructure for both teaching and research in these health areas and beyond. The Department of Health Sciences and the Faculty of Science have strong commitments to graduate and undergraduate education and research experiences. More information on Carleton’s Department of Health Sciences can be found at: https://carleton.ca/healthsciences/ . We are seeking three senior research faculty, one in each of the three clusters of excellence, and one who will become Departmental Chair. Candidates' research should align with one of these areas: 1) Environment and Global Health: Environmental toxicology/pharmacology, cancer, global health of (re)emerging infectious diseases or climate change. 2) Lifecourse Approach: Biological mechanisms of ageing. A focus on mitochondrial biology, reactive oxygen species and/or metabolism of ageing is ideal. 3) Big Data: Bioinformatics and/or biostatistical approaches to health in one of the clusters of excellence.

Qualifications: Each candidate should have a demonstrated record of success as an independent researcher with an innovative and internationally-recognised research programme, as proven by peer-reviewed publications and funding from CIHR or other nationally and/or internationally-recognised funding agencies (e.g.: NIH, BBSRC, MRC). They should also have demonstrated excellence in teaching, including graduate supervision at the doctoral level, and evidence of administrative and leadership skills. The new Chair will be expected to have exceptional interpersonal skills and serve as a champion of the Department's research and education initiatives, and to develop new academic and research opportunities. Each of the successful candidates must have a PhD and/or MD or equivalent and currently hold the rank of Associate or Full Professor. The position of Departmental Chair will be for a 3-year renewable term.

Application instructions: Interested candidates should submit a CV stating their anticipated Health Sciences research cluster and detailing their experience in this area, a teaching dossier including a statement of which courses offered by the Department they would be interested in teaching, and a statement of administrative experiences and interests. Applicants with interest in the Departmental Chair position should also submit a statement of vision for the Department. Applications, including cover letter, together with the names and contact information of three referees, should be sent as a single PDF to:

Dr. Robert Burk Chair, Department of Health Sciences, Carleton University at: healthsciences@carleton.ca

Please indicate in your application if you are a Canadian citizen or

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CarnegieMuseumNatHist ReaCuratorAmphibiansReptiles

Carnegie Museum of Natural History - William and Ingrid Rea Assistant Curator of Amphibians and Reptiles

Carnegie Museum of Natural History invites applications for the William and Ingrid Rea Assistant Curator of Amphibians and Reptiles. Successful candidates for this endowed position will have research interests involving the systematics, evolutionary biology, ecology, and/or conservation biology of amphibians and reptiles, especially - but not limited to - investigating the consequences of global change on amphibian and reptiles. In addition to developing a strong research program, additional responsibilities will include providing leadership in the care, maintenance and improvement of the collection and participation in the museum's educational programs, exhibitions, and other efforts of public engagement.

Qualifications: Ph.D. in some aspect of amphibian and reptilian biology with a strong background in systematics. The successful candidate will also have a strong record in grants, scientific publications, and science communication. Postdoctoral training is strongly preferred. The appointment is expected to be at the level of Assistant Curator, although exceptional candidates at more senior levels may be considered.

For additional information, please visit: www.carnegiemuseums.org/hr and search "amphibians and reptiles". To apply, a letter of application, CV, contact information for three references, statement of research, and statement of curatorial philosophy (including the curator's role in broader museum efforts) should be emailed to halea@carnegiemnh.org. Review of applications will begin February 1, 2017.

Carnegie Museum of Natural History is one of the four Carnegie Museums of Pittsburgh, with a mission in original scientific research, preservation of collections, and public science education and engagement. The museum has approximately 22 million specimens and artifacts in its collections, including the 9th largest collection of amphibians and reptiles in the US. With access to our 2,200-acre Powdermill Nature Reserve and the museum's placement within blocks of six universities (including two major research institutions: U. of Pittsburgh and Carnegie Mellon U.), there is ample opportunity for collaboration and application of collections-based research to current issues at the intersection of evolution, ecology, conservation biology, and global change.

Carnegie Museums of Pittsburgh is firmly committed to equal employment opportunity for all persons without regard to race, color, religion, creed, national origin, ancestry, sex, gender identity or expression, age, marital status, sexual orientation, citizenship status, veteran status, non job-related disability or genetic information as those terms are defined under applicable law.

"Hale, Alison" <HaleA@CarnegieMnh.Org>

CollegeOfCharleston EvolutionaryMicrobialGenetics

Microbial Genetics

The Department of Biology at the College of Charleston invites applications for a tenure-track position in Microbial Genetics at the Assistant Professor level to begin August 2017. Candidates must have a Ph.D. in Biology or a related field and a strong commitment to teaching and maintaining an active research program involving undergraduates. The area of research is open to any microbial system (eukaryotic, prokaryotic, viral) but we are targeting a microbiologist who asks evolutionary or environmental questions and seek a colleague interested in developing collaborations with existing faculty (http://biology.cofc.edu/about-the-department/-faculty-staff-listing/index.php). Primary teaching responsibilities include undergraduate courses in Genetics, Microbiology, introductory biology and perhaps specialty courses in an area of expertise. The College of Charleston, located in Charleston, SC, is a public liberal arts and sciences institution of 12,000 students, with MS programs in Marine Biology and Environmental Studies, and a commitment to excellence in teaching and research. Information about the department is available at http://biology.cofc.edu/ .Applicants should submit electronic (pdf) copies of their curriculum vitae, statements of teaching and research interests, up to three relevant publications, and a list with names and contact information for three referees, to the following site: http://jobs.cofc.edu/postings/5577 .Questions regarding this position can be directed to Dr. Christine Byrum, search committee chair, at byrumc@cofc.edu. This is a nine-month appointment; salary is competitive and commensurate with experience and qualifications. Review of applications will begin Dec 14, 2016 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>

HowardU VertebrateEvolution

Assistant Professor of Neurobiology (tenure track) *and * *Assistant Professor of Anatomy (tenure track)*

Description

The Department of Biology in the College of Arts and Sciences at Howard University invites applications for two tenure-track positions at the rank of Assistant Professor, one with specialization in neurobiology and the other in comparative vertebrate anatomy. We seek outstanding applicants with a demonstrated track record of excellence in research and teaching.

Qualifications

Successful candidates are expected to develop vigorous, extramurally funded research programs in their areas

of expertise, actively participate in the Department's teaching and curriculum development at the undergraduate and graduate levels, and mentor undergraduate and graduate students.

Candidates must have:

* Earned doctorate in Biology or related field, with a specialization in neurobiology or comparative vertebrate anatomy from an accredited institution,

* Record of scholarship, teaching, and professional service commensurate with the rank of assistant professor,

* Effective communication and organizational skills, and

* Postdoctoral and grant-writing experience preferred.

Application Process

Complete applications consist of a single PDF file containing

1) a cover letter addressing qualifications listed above,

2) a current curriculum vitae,

3) a two-page statement of research accomplishments, interests, and future plans,

4) a two-page statement of teaching experience and philosophy, and

5) the names and contact information for at least three references who will provide letters upon request from the search committee.

Completed applications should be addressed to the Chair of the search committee Dr. Franklin Ampy and emailed to either:

*hubio.neuro@gmail.com <hubio.neuro@gmail.com> *for the* neurobiology position*

hubio.anat@gmail.com <hubio.anat@gmail.com> for the *comparative anatomy position.*

All application materials should be received by February 1, 2017 when screening will begin and continue until the positions are filled.

The starting date for both positions is August 15, 2017.

Additional details and information can be found at http://hubiosearch.wixsite.com/-2017 . "kenneth.hayes@howard.edu" <kenneth.hayes@howard.edu>

IndianaU BioinformaticAnalyst

POSTING: Working as a team member, supports genomics and other 'omics research at Indiana University and for the national audience served by NSF-funded National Center for Genome Analysis Support (NCGAS). Independently consults with biologists and other life science researchers undertaking computational analyses of genomic, transcriptomic, metagenomic, or other 'omics data sets. Initiates installation and configuration of analytical software packages; performs some programming and scripting to develop software; and assists with data management and transformations. Develops research workflows; and directs assistance in executing those analyses and workflows on IU's High Performance Computing systems. Assists with customer requests and work queues, maintains task documentation, and makes programming changes necessary for upgrades, releases and customization.?

REQUIRED: Bachelor's degree in a life science such as biology, microbiology, or biochemistry or in computer science with a specialty in bioinformatics and two years of professional technical experience in analyzing large biological data set.

Combinations of related education and experience may be considered.

Experience with the following: Perl, Python, UNIX shell script, or similar scripting languages; and de novo and reference-based genomics analysis. Experience working withDNA sequence data and analyses for genome assembly, alignment, and annotation; and familiarity with next generation sequencing, Unix/Linux operating systems and one or more programming or scripting languages, and biological data management. An emphasis is put on using existing software (not software development) accepted by the research community. Therefore, broad familiarity with currently available software and ability to match applications to specific research needs, and monitoring of emergent applications.

Excellent interpersonal, written and verbal communication skills including a customer service orientation and ability to interact and communicate effectively with a wide variety of individuals; and willingness and ability to present at the national and international level. Proven ability to work well as part of a team including ability and willingness to work in a collaborative environment where knowledge, code, and effort are shared among colleagues including commitment to sharing knowledge through documentation, communication and collaboration. Demonstrated ability to cooperate and collaborate on projects/operations with other staff while maintaining a positive attitude toward project goals, and take ownership of issues and assigned tasks. Possess a high degree of self-initiative and commitment to expanding skills and expertise through a variety of methods, including self-study, working/mentoring with colleagues, and through internal and external training.

PREFERRED: Experience in/with a DNA sequencing laboratory and familiarity with the current state of the art in 'omics-based life sciences research; experience answering actual biological experimental questions with 'omic sequence sets, with genomic analysis; experience with batch operated clusters or other high performance computing platforms in a university environment.

FOR MORE INFO AND TO APPLY: https://iujobs.peopleadmin.com/postings/30425 Sheri Sanders Bioinformatic Analyst National Center for Genome Analysis and Support (NCGAS)

NCGAS is part of the Research Technologies division of UITS; Research Technologies is a PTI Cyberinfrastructure & Service Center.

"Sanders, Sheri" <ss93@iu.edu>

Liverpool MosquitoBorneDisease

Due to our continuing expansion, we have identified a number of key areas that offer exciting opportunities for impact with tangible potential to shape global health initiatives and deliver health improvement over the next decade. If you have a reputation for excellent research on the biology and/or control of arboviruses and their vectors please get in touch with us. Candidates with research programmes in evolutionary biology, genetics or genomics are strongly encouraged.

The Liverpool School of Tropical Medicine continues to lead in the worldwide fight against infectious diseases working with partners in over 60 countries. Our research reputation has secured funding to lead multiple international consortia and product development partnerships underpinning our translational research focus.

As part of our continuing expansion, we have identified a number of key areas that offer exciting opportunities for impact with tangible potential to shape global health initiatives and deliver health improvement over the next decade. To support this development we wish to strengthen the profile of LSTM in mosquito borne disease through the appointment of a candidate with an established excellent international reputation in this discipline. We are particularly interested in candidates with a reputation for excellent research on the biology and/or control of arboviruses and their vectors.

The post holder will join the Faculty of Biological Sciences which hosts the Departments of Vector Biology and Parasitology and has a vibrant research portfolio with particular research strengths in malaria, filariasis and the Neglected Tropical Diseases. Our activities span the full pipeline from discovery to implementation and we work closely with national and global policy making bodies to maximise research uptake. The faculty has unparalleled facilities for working with vectors and pathogens including category 3 containment facilities, a large suite of controlled insect rearing rooms plus free flight rooms for behavioural studies. Our laboratories are also well equipped with analytical platforms for molecular genetics, proteomics, metabolomics and imaging.

The post is suitable for candidates with an international reputation in mosquito borne diseases and a strong research profile. Candidates will be expected to demonstrate their track record in securing competitive funding and publishing the outputs of their work and have a clearly articulated research vision.

Click here (link is external) < https://livtmli.webitrent.com/livtmli_webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID%3d1175530PZz&WVID=7667700AeE&LANG=USA > to apply http://www.lstmed.ac.uk/senior-lecturer-reader-mosquito-borne-disease Closing Date for completed applications: Thursday 5 January 2017

Martin James Donnelly

Professor of Evolutionary Genetics Department of Vector Biology Malaria Programme Liverpool School of Tropical Medicine & Wellcome Trust Sanger Institute Pembroke Place Hinxton Liverpool Cambridge L3 5QA CB10 1SJ Tel +44(0) 151 705 3296 Fax +44(0) 151 705 3369 Email martin.donnelly@lstmed.ac.uk Web http://donnelly.openwetware.org/Home.html Skype martin-donnelly; Orcid 0000-0001-5218-1497

Martin Donnelly <Martin.Donnelly@lstmed.ac.uk>

Lyon PopulationGenomics

Position: assistant professor, population genomics, Lyon

An assistant professor (maitre de conference) permanent position will be available at LBBE (CNRS/Univ. Lyon 1), a large institute in evolutionary biology/ecology/human health with a special focus on methodological research (https://lbbe.univ-lyon1.fr).

We seek applicants whose research profile is population genomics with a strong methodological emphasis. Applicants should conduct innovative work in population genomics by both developing new methods and applying them to high-throughput data. We are open to all research projects that could fit in the topics of the institute.

Teaching (mainly in French) will be related to biomathematics, bioinformatics and population genetics.

Lyon is one the main (and oldest) French cities, its city center is a world heritage UNESCO site, it is ~2h from the Alps (http://www.lyon-france.com/).

If interested, please contact Dominique Mouchiroud (dominique.mouchiroud@univ-lyon1.fr, +33 4 72 43 26 28).

Gabriel Marais Directeur de Recherches, CNRS

Biométrie et Biologie Evolutive - UMR 5558 Université Claude Bernard - Lyon 1 Bat. Mendel, 16 rue R. Dubois 69622 Villeurbanne cedex, France

Tel: (+33) (0) 4 72 43 29 09 Mob: (+33) (0) 7 82 33 83 51 Fax: (+33) (0) 4 72 43 13 88

Email: Gabriel.Marais@univ-lyon1.fr Web site: http://lbbe.univ-lyon1.fr/-Equipe-Sexe-et-Evolution-.html Gabriel.Marais@univ-lyon1.fr

OregonStateU ResAssist ConservationGenetics

Job: Research Assistant in the Conservation Genetics of Marine and Freshwater Fishes

The O'Malley lab at Oregon State University is looking to hire a highly motivated Research Assistant. The individual will perform research and train students in in the application of both genetic and genomic approaches to address questions related to the ecological and population genetics of marine and freshwater fishes. We are looking for an enthusiastic and responsible individual to join our team. This will be a full time position. Primary responsibilities include: 1) Providing leadership in research, 2) maintaining an efficient laboratory 3) archiving tissue samples and associated phenotypic data 4) training students and visiting scholars in molecular research techniques and 4) serving as the primary liaison to Oregon State University's Center for Genome Research and Biocomputing.

For additional details and how to apply: http://jobs.oregonstate.edu/postings/35284 For questions, please contact Dr. Kathleen O'Malley (Kathleen.omalley@oregonstate.edu)

Kathleen O'Malley, Associate Professor

Oregon State University, Hatfield Marine Science Center

Coastal Oregon Marine Experiment Station

2030 SE Marine Science Drive, Newport, Oregon 97365

ph: (541) 961-3311 fax: (541) 867-0345

http://people.oregonstate.edu/ ~ omalleyk/- "O Malley, Kathleen Gallen" <Kathleen.OMalley@oregonstate.edu>

StCloudStateU Minesota ComputationalMicrobiol

The job title is 'computational microbiologist' and it will be focused on the establishment and evolution of microbial communities within an anaerobic digester.

It is not a tenure-track position, but it will allow for contract extensions if the person chosen will be able to secure more funds beyond the three years of the original project.

The job is currently posted on Nature Jobs.

This is the link:

http://www.nature.com/naturejobs/science/jobs/-600239-biology-computatio nal-microbiologist-fixed-term-non-probationary

Ryan Fink Biology- Computational Microbiologist, Fixed-Term, Non-Probationary : St. Cloud, MN, United States : Naturejobs www.nature.com Biology- Computational Microbiologist, Fixed-Term, Non-Probationary - St. Cloud State University are looking for a Faculty Member - multiple/non-specific in St. Cloud, MN, United States. Salary: unspecified, Hours: Full-time, Type: Temporary

"Fink, Ryan C." <rcfink@stcloudstate.edu>

StockholmU PlantSystematics

Stockholm University seeks to appoint an Associate Professor in Plant Systematics. Closing date: 10 February 2017

The position encompasses research and teaching within the broad subject area of plant systematics, including land plants, algae or fungi.

For a full job description and for how to apply see:

http://www.su.se/english/about/vacancies/vacancies-new-list?rmpage=job&rmjob=2395&rmlang=UK
Contact: Further information about the position can be obtained from the Head of the Department, Professor Ove Eriksson, telephone: +46 8 16 12 04, ove.eriksson@su.se.

For questions regarding the application process, please contact administrator Mikael Stenberg, telephone: +46 8 16 20 86, mikael.stenberg@su.se. (In Swedish: http://www.su.se/om-oss/lediga-anst%C3%A4llningar/lediga-jobb-ny-lista?rmpage=job&rmjob=2393&rmlang=SE)

Aelys Humphreys <aelyshumphreys@gmail.com>

Tanzania 12mnths PrimateProjectManager

The position requires a command of evolutionary theory and behaviour given the scope of our work, but it is a project manager position, so lots else is required as well.

Position Description: The Ugalla Primate Project is seeking a project manager, to be based in a remote field site in western Tanzania for 12 months. Responsibilities include overall Project coordination, management of data collection for multiple ongoing studies (see website) at the research station, finance administration, and schedule organization, among others. The Project coordinator also makes regular trips to the local village/town for supplies and frequently reports to UPP administration concerning ongoing Project developments. Finally, s/he assists especially the logistics of incoming collaborators/students, and often negotiates complex relationships with government institutions and local government officials, e.g. Immigration.

If desired, the successful applicant may also conduct an independent research project of his/her own design, contingent on approval from UPP as well as Tanzanian government research bodies.

Qualifications: A successful candidate should have a bachelor's degree in a related field (evolutionary biology, zoology, biological anthropology), with a strong command of evolutionary theory and behaviour, as well as prior living or work experience in a developing country (preferably in Africa), be extremely fit, able to drive a manual 4x4 vehicle, familiar with Microsoft Excel and Word (GIS a plus), and willing to learn KiSwahili. Additionally, the candidate must be responsible, organized, independent, resourceful, and get along well and easily with others, as the position requires long periods in the forest with a team of Tanzanian field assistants. The landscape is demanding, and so extreme physical fitness is also critical. Previous experience with apes is sought, but not necessary.

Duration: February 2017 - January 2018 (dates flexible).

Compensation: USD300 per month, with in-country & work-related expenses covered by the Project. Candidates must be prepared to pay international travel and government research permits (USD2200) up front. Travel and permit costs are reimbursed upon partial completion of tenure.

Please see ugallaprimateproject.com for more on the UPP.

Interested applicants should create a SINGLE .PDF file that includes a cover letter, updated CV, and the names of two references, emailed to info@ugallaprimateproject.com. We are accepting applications until the position is filled.

"Piel, Alexander" <A.K.Piel@ljmu.ac.uk>

TelAvivU PlantEvolution

The School of Plant Sciences and Food Security at Tel Aviv University is seeking excellent applicants to fill a tenure track position at the levels of Assistant or Associate Professor. Areas of interest include all aspects of plant biology including Plant physiology, Plant ecophysiology, Plant ecology and evolution, Plant development, Crop Sciences, Plant biotechnology, Plant systems biology and other photosynthetic organisms.

Qualifications for the position include PhD in biology or related fields, postdoctoral research experience and publications describing original and outstanding research achievements. The successful appointee is expected to establish an internationally-recognized competitively-funded research program to address contemporary and emerging issues in plant biology. The appointee is expected to develop courses for undergraduate and graduate levels and teach in both Hebrew and English, supervise graduate students and postdoctoral fellows and contribute to the development and operation of the School, Faculty of Life Sciences and University.

Applications will be considered from October 1st (2016) until the position is filled. Recruitment of the successful candidate is expected by October 1st 2017. Applicants should submit the following materials: 1) Curriculum vitae including list of publications 2) Statement of research plans 3) Statement of teaching interests and philosophy 4) Names, addresses, including e-mails, of four professional references.

Materials (combined in one PDF file) should be sent by e-mail to Professor Hillel Fromm, Head, School of Plant Sciences and Food Security, Tel Aviv University (Hillelf@post.tau.ac.il).

Tel Aviv University is an equal opportunity employer. Women and minorities are encouraged to apply.

lilach.hadany@gmail.com

UAmsterdam EvolutionaryBiol

Full professor Population and Evolutionary Biology Faculty of Science - Institute for Biodiversity and Ecosystem Dynamics

Level of education: PhD Salary indication: euro 5,260 to euro 7,659 gross per month Closing date: 11 February 2017 Hours: 38 hours per week Vacancy number: 16-593

The Institute for Biodiversity and Ecosystem Dynamics (IBED) is one of the eight research institutes of the Faculty of Science at the University of Amsterdam. IBED was founded in 2000 by merging research groups with expertise in ecology, physical geography, environmental microbiology and environmental chemistry. The research at IBED aims to unravel how ecosystems function in all their complexity, and how they change due to natural processes and human activities. At its core lies an integrated systems approach to study biodiversity, ecosystems and the environment. IBED adopts this systems approach to ecosystems, addressing abiotic (soil and water quality) and biotic factors (presence, population dynamics and functioning of plants, animals, microbes), and the interplay between these ecosystem components. The IBED vision includes that research encompasses experimental and theoretical approaches at a wide variety of temporal and spatial scales, i.e. from microbes and individual behaviour to patterns and processes occurring at landscape scale. IBED offers advanced and up-to-date research facilities, such as a greenhouse, growth chambers, an electrophysiological lab, a molecular lab, an analytical chemistry lab, a soil erosion lab, a GIS studio, and high-performance computing facilities.

IBED is in search of a new full professor for the department of Population and Evolutionary Biology (PEB).

We are looking for a scientist who has the ambition to lead a diverse research group. Someone who inspires the PEB team, represents the group and increases the international academic visibility of PEB. Someone who has a talent for, and a clear vision on university teaching and research. We welcome a candidate who brings in new approaches, research skills or model systems.

The department of Population and Evolutionary Biology Research of the new department of Population and Evolutionary Biology aims at improved understanding of how interactions between individuals and their biotic and abiotic environment affect population dynamics and evolutionary processes, which ultimately determine speciation and biodiversity patterns. Research is integrative, combining insights from population ecology, community ecology, and evolutionary biology. The Population and Evolutionary Biology department also performs applied research on questions relevant for society.

At present, the department of Population and Evolutionary Biology consists of 10 permanent academic staff members, 10 Postdocs,18 PhD students and 4 technical staff. The department plays an important role in teaching and coordinates a wide range of BSc and MSc courses. The department will comprise the three current chair groups of Population Biology, Evolutionary Biology and Experimental Plant Systematics.

Current research of PEB is organized along 4 lines: - chemical and molecular basis of adaptation and speciation; - adaptive intraspecific variation in exploitation strategies of herbivores and predators; - direct and indirect interactions among plants, predators and prey; - biodiversity and conservation.

Members of the department of Population and Evolutionary Biology collaborate extensively with other research groups within IBED. Within the University of Amsterdam, we work together with colleagues from the Swammerdam Institute for Life Sciences and the Center for Research in Experimental Economics and Political Decision Making. The department of Population and Evolutionary Biology also collaborates with many other national and international institutes and non-academic stakeholders. In particular, we focus on increased collaboration with the related department of Animal Ecology of the Vrije Universiteit Amsterdam. Together, these two groups aim to become a leading center for evolutionary and ecological research.

Job description The new full professor will chair the department of Population and Evolutionary Biology, will develop her/his own research program, and will contribute to the teaching program. The full professor will foster a coherent research profile of the department, will represent the department inside and outside the university, and will mentor and guide the department members in their scientific career development.

Tasks are: - to chair the department of Population and Evolutionary Biology; - to develop and contribute to courses in particular within the BSc and MSc curricula Biology, Psychobiology, Bio-medical Sciences and Future Planet Studies; - to strengthen the existing research lines by bringing in new ideas, skills and innovative research approaches; - to develop her/his own research within the research domain of the

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UBristol 4 EvolutionaryBiol

Three Lecturer/Senior Lecturer Positions, and one Teaching Fellow position available in the School of Biological Sciences, University of Bristol, UK.

We seek at least three new Lecturers and Senior Lecturers across all biological disciplines, but especially in Animal Behaviour and in Behavioural Ecology, with broad-scale approaches using genomics, neuroscience and mathematical modelling, and linking to global environmental challenges.

We are also looking for applications from a broad array of integrative biological disciplines, including metagenomics, epigenetics, phylogenomics, comparative phylogenetics, bio-engineering, and next generation molecular ecology.

We also seek a Teaching Fellow, to provide innovation and guidance in the development of our ambitious undergraduate teaching programmes in Biology and in Zoology. The candidate will have experience in student-focused learning and in introducing innovative approaches to engage large numbers of students in the intellectual and practical challenges of a research-led teaching programme.

The School of Biological Sciences is entering an exciting new phase of development. It moved into the state-of-the-art Life Sciences Building in 2014, which provides extensive laboratory and teaching facilities.

The new building also provides novel opportunities for collaborations with colleagues in other disciplines now located In the new building, particularly Earth Scientists. In 2018, the School will also become a core component of the new Faculty of Life Sciences.

The University of Bristol encourages cross Faculty interactions through various Research Institutes, including the Cabot Institute (http://www.bristol.ac.uk/cabot/), the Elizabeth Blackwell Institute (http://www.bristol.ac.uk/blackwell/) For more details of the jobs and how to apply please see Three PW1 lectureships: http://tinyurl.com/hddjvqg Teaching Fellow (PW3): http://tinyurl.com/zsq2tck See http://www.bristol.ac.uk/biology/ and http://www.bristol.ac.uk/research/ for more details of the School and our research.

The closing date for all applications is 4th January 2017

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>

UCalifornia Davis WildlifeConservation

Job Title: Staff Research Associate II-Wildlife genetics laboratory tech

Dept: VGL

Job Description:

The UC Davis Mammalian Ecology and Conservation Unit is seeking a highly motivated person to fill a position as a molecular genetics laboratory tech (university title: Staff Research Associate II) to assist with research in Ben Sacks's laboratory. Research in the Sacks lab focuses on evolution, ecology, phylogeography, and conservation genetics of wild mammals and other vertebrates. We use both molecular-genetic and field-based approaches in our research. Laboratory facilities include modern and ancient DNA units. Additional details about ongoing projects can be found on the lab website (http://http://www.vgl.ucdavis.edu/cdcg/home.php)

The SRA-II will assist principal investigator, postdoctoral scholars, and graduate students in ongoing research projects by conducting basic molecular genetics lab work and will help recruit, train, and supervise undergraduate interns. Laboratory activities include DNA extractions, PCR, gel electrophoresis, microsatellite genotyping, sequencing, cloning, next generation sequencing library preparation, database entry and management, maintaining laboratory supplies/ equipment, ensuring compliance with laboratory safety regulations, and training students and interns.

Minimum Qualifications: Bachelor's Degree in an appropriate field such as Molecular Biology, Genetics, or Wildlife Biology, along with 1-2 years research experience that included performing DNA extractions and PCR, and routine use of basic computer software. Experience with microsatellite genotyping and/or DNA sequencing is required. Preference will be given to applicants with experience in ecological or evolutionary biology. This position will extend under the SRA-II title for 5 months with possibility to convert to a longer-term position under a different title.

Qualified candidates should submit (via email) a letter of application

describing qualifications for the position and reason for interest,

CV, and contact information for (or letters from) three references who can detail your relevant experience to bnsacks@ucdavis.edu

Annual salary rate: $45,760. Starting Date: When filled. Final Filing Date: December 16, 2016 Interviews may be conducted before the closing date; however, no hiring decision will be made until after that date.

Number of Positions: 1

Ben Sacks

Veterinary Genetics Laboratory

University of California, Davis

One Shields Avenue/Old Davis Rd.

Davis, California 95616-8744 USA

Phone: 530-754-9088 bnsacks@ucdavis.edu

The University of California, Davis is an equal opportunity/affirmative action employer.

"Benjamin N. Sacks" <bnsacks@UCDAVIS.EDU>

UCanterbury NZ Genomics

https://www.seek.co.nz/job/32418493 Applications are invited for the continuing position of Lecturer/Senior Lecturer/Associate Professor in Genomics in the School of Biological Sciences. [Lecturer is equivalent to a (tenured) Assistant Professor in the US system; Senior Lecturer is equivalent to a recently tenured Associate Professor in the US system; Associate Professor is a more senior position equivalent to a Reader in the UK system and a senior Associate Professor in the US system].

We seek an ambitious early-career colleague in the molecular biosciences who will apply modern approaches and augment our existing strengths. The successful applicant will be capable effective research and teaching, and be broadly trained in genomics/bioinformatics with associated laboratory and analytical skills. For the context of their research, they will be motivated to address fundamental questions in at least one of the following subthemes - synthetic/structural biology, cell/molecular biology, genetics, physiology or evolution. It is expected that the successful candidate will establish an externally funded research programme. They will also develop research linkages with research institutes and/or industry groups, and participate in undergraduate and postgraduate supervision and teaching.

Applicants should have a PhD or an appropriate equivalent qualification in biological sciences, an ability and willingness to deliver high quality teaching in molecular and evolutionary biology, and a commitment to do world-class research in an area complementary to current strengths within the School of Biological Sciences.

The successful applicant will demonstrate potential for academic excellence in teaching and research, be able to conduct innovative and effective lectures and laboratory classes from first year through postgraduate level, publish research at a high level as assessed by peer-reviewed publications, and, where appropriate, demonstrate impacts for community stakeholders. We are looking for an adaptable colleague who can work with others to embrace opportunities that contribute to our core mission.

The School of Biological Sciences has a high national and international profile and has an excellent teaching and research infrastructure, including multiple field stations in alpine, lowland and coastal habitats, and new research facilities. We have well-established research programmes from molecular to whole-organism and ecological scales, as exemplified in the Biomolecular Interaction Centre (http://www.bic.canterbury.ac.nz/) and the Centre for Integrative Ecology (http://www.biol.canterbury.ac.nz/-cie/). We have strong linkages with other research institutes. For more information on the School of Biological Sciences see the webpage www.biol.canterbury.ac.nz . The University of Canterbury is committed to promoting a world-class learning environment through research and teaching excellence, and has a vision statement of Tangata Tu, Tangata Ora ('People Prepared to Make a Difference'). You will have the opportunity to work alongside members of a diverse academic community and enrich your own professional and personal development.

Equal opportunity in employment is University policy and the School is strongly committed to equality in the workplace. Applications from all suitably qualified persons are encouraged. The University of Canterbury offers generous leave provisions, including sabbatical and Erskine Fellowship leave. It also has excellent childcare, recreation and staff/graduates club facilities on campus.

For information about the range of benefits in joining UC please visit us online at: http://www.canterbury.ac.nz/-joinus The closing date for this position is: 22 January, 2017.

Interviews for this vacancy are anticipated to take place in March, 2017.

The position will be available from 1 June 2017, although the start date is flexible.

Applications for this position should include a completed University of Canterbury application form, a curriculum vitae, a summary of recent research achievements and a 1-2 page research proposal outlining intended research and research goals. Applicants are also expected to indicate their teaching experience and philosophy and to indicate the ways they could contribute to courses within the School and to curriculum development in the future. They should also indicate the names and contact details of three referees. Applications should be combined into one document and submitted online.

Should you wish to e-mail any additional attachments or have queries in relation to the application process, please forward these to Nikki Gibbs, Recruitment Coordinator, nikki.gibbs@canterbury.ac.nz

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UCollegeLondon HumanGenetics ComputationalBiol

Lecturer/Senior Lecturer (Assistant/Associate Professor) in Human Genetics and Computational Biology (2 posts) University College London Department of Genetics, Evolution and Environment UCL Genetics Institute

The appointment will be full time on UCL Grade 8/9. The salary range will be 42,304 - 49,904 per annum (Grade 8): 54,240 - 58,978 per annum (Grade 9), inclusive of London Allowance.

The UCL Genetics Institute (UGI) is an internationally leading centrefor research and teaching in genetics and genomics. It is part of the Research Department of Genetics, Evolution and Environment (GEE), within the Division of Biosciences. The remit of UGI is to extract biological and medical knowledge from big data in the field of life sciences. https://www.ucl.ac.uk/-biosciences/departments/gee https://www.ucl.ac.uk/-ugi Two lectureships are currently available, one in Human Genetics, and the second in Computational Biology. Appointment to one of these 2 posts may be made at Senior Lecturer (Grade 9) level.

For the post in Human Genetics, the post holder will establish and develop independent and collaborative research programmes with an emphasis on big data. This could be in the areas of chronic or infectious human diseases, human microbiome metagenomics, epigenetics, genetic epidemiology, human population history or other related fields.

For the post in Computational Biology, the post holder will establish and develop independent and collaborative research programmes with an emphasis on big data genomics. This could be in the area of statistical genetics, population genetics, phylogenetics, bioinformatics or systems biology, with some aspects of the research relevant to human health and disease.

The successful candidates will hold a PhD in a relevant subject area and demonstrate an outstanding contribution to the body of knowledge and an international research profile with commensurate, sustained research to the discipline. For appointment at Senior Lecturer level, the successful candidate must demonstrate an international research profile with substantial seminal contributions to knowledge or other outcomes appropriate to the discipline, and evidence of academic leadership and a proven ability to lead, develop and motivate colleagues.

For further details about the vacancy and how to apply online please go to http://www.ucl.ac.uk/hr/jobs/ and search on Reference Number 1616805 (direct link: http://goo.gl/q2gfb4)

Please clearly specify under which specialism you are applying by identifying your application as either 1616805/HG or 1616805/CB.

For informal queries about the posts, please contact Professor Francois Balloux, f.balloux@ucl.ac.uk.

If you have any queries regarding the application process, please contact the Biosciences Staffing Team, biosciences.staffing@ucl.ac.uk.

Closing Date: 31 January 2017. Latest time for the submission of applications: 23:59. Interview Date: TBC.

We particularly welcome female applicants and those from an ethnic minority, as they are under-represented within UCL at this level.

"Pomiankowski, Andrew" <a.pomiankowski@ucl.ac.uk>

UFlorida FacultyResSci ButterflyMothGenomics

The Kawahara Lab at University of Florida is hiring a full-time, fully-benefitted, Assistant Research Scientist faculty.

The primary duty of the researcher will be to help the PI and his team coordinate various projects and analyze data pertaining to research on the evolution and genomics of butterflies and moths. While the position is a faculty position, it is non-tenure track, and the chosen candidate will not be required to meet standard tenure requirements. This is a full-time, permanent position.

Required: 1) A Ph.D. in molecular evolution, systematics, evolution, bioinformatics, genomics, or related field. 2) Familiarity with Next Generation Sequencing, computer programming/scripting in Python, Perl, Java, C++, R or other language. 3) Strong organizational skills and ability to work with colleagues, and help run a lab. Candidates with experience in functional/comparative genomics, genome annotation, and/or phylogenomics will be highly considered. An interest in insect evolution, strong publication record, and some lab management experience is desired.

The research scientist will join the Florida Museum of Natural History (FLMNH), located on the University of Florida campus. The department is one of the largest university museums in the US, and a leading department in the field of biodiversity science research.

Salary: $50,000 USD plus benefits.

The lab's website can be found at: http://www.flmnh.ufl.edu/mcguire/kawahara/ To apply, visit: http://explore.jobs.ufl.edu/cw/en-us/job/500646/assistant-scientist-lepidoptera Application deadline: Jan. 15, 2017 (11:59 pm, US EST time)

Any questions should be addressed to Akito Kawahara at kawahara@flmnh.ufl.edu

– Akito Y. Kawahara Assistant Curator/Assistant Professor Florida Museum of Natural History McGuire Center for Lepidoptera and Biodiversity University of Florida 3215 Hull Road Gainesville, FL 32611 USA 352.273.2018 kawahara@flmnh.ufl.edu

kawahara@flmnh.ufl.edu

UGroningen 10 EvolutionaryBiology

Jobs at Groningen Institute for Evolutionary Life Sciences (GELIFES)

Evolutionary Ecology of Marine Animals 5 in Evolutionary Life Sciences 2 in Evolutionary Medicine Chronobiology Microbial Ecology and Evolution

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Tenure track assistant or associate professor in Evolutionary Ecology of Marine Animals

The Groningen Institute for Evolutionary Life Sciences (GELIFES) was established in 2015 and is the largest institute of the Faculty of Mathematics and Natural Sciences (FMNS) of the University of Groningen.

GELIFES fills a special niche in the life sciences by covering and integrating mechanistic, evolutionary and ecological approaches. GELIFES' main aim is to integrate proximate and ultimate approaches in the Life Sciences. This strategy generates better understanding of fundamental biological processes and contributes to the solution of societal problems. Our research fields include behavioural biology, chronobiology, ecology and conservation biology, evolutionary biology, genetics and genomics, neurobiology, physiology and theoretical biology, using a wide array of research tools from molecular, through the whole organism, to population and community level, under laboratory, semi-natural and field conditions. We study a wide array of species, from microbes, algae, plants and insects to vertebrates such as fish, birds, rodents, marine mammals and humans. Our institute is the driving force of the Adaptive Life Programme, one of four integrative focus research areas of the FMNS.

To further strengthen Adaptive Life, the University of Groningen and FMNS enabled us to hire for 5 new faculty and 25 PhD scholarship positions, as well as to invest in large scale new facilities. This support also facilitated the establishment of the Sustainable Landscape Competence Centre and the Brain and Behavioural Competence Centre, in order to attract external research funds and further organize our outreach.

GELIFES has a vacancy for a tenure track assistant or associate professor in Evolutionary Ecology of Marine Animals

Candidates are expected to set up an independent research line within this field, complementary to ongoing research of the institute. The candidate is expected to have an interest in strengthening the research program and faculty theme called Adaptive Life in which biological adaptation is studied by integrating mechanistic with evolutionary approaches. Candidates are expected to attract funding for new PhD projects and attain a leading international position in the field. They are excellent teachers who can attract students of different disciplines and have an interest in teaching at both the bachelor, master and PhD level.

Research on larger marine animal species that provide opportunities for collaboration not only with ecologists or evolutionary biologists of the institute but also with its behavioural physiologists / neurobiologists is appreciated but not a requirement.

The Netherlands border both the North Sea and the Wadden Sea, the latter being relatively close to the university. Research in the North Sea and Wadden Sea currently provides good funding opportunities and contributes to the regional impact of our university, but researchers working on other ecosystems are also encouraged to apply.

The University of Groningen has adopted an active policy to increase the number of female scientists across all disciplines of the university. Therefore, female candidates are especially encouraged to apply.

For more information on this position, qualifications and conditions of employment, please check the vacancy website: http://www.rug.nl/about-us/work-with-us/job-opportunities/overview. The deadline for application is January 25th 2017.

For more information on GELIFES, its staff and research, please visit: http://www.rug.nl/research/gelifes/ For more information on the Adaptive Life Programme, please visit: http://www.rug.nl/research/fmns/themes/adaptive-life/ —–

The University of Groningen offers 5 Tenure Track Assistant or Associate Professor positions in Evolutionary Life Sciences

The Groningen Institute for Evolutionary Life Sciences (GELIFES) was established in 2015 and is the largest institute of the Faculty of Mathematics and Natural Sciences (FMNS) of the University of Groningen.

GELIFES fills a special niche in the life sciences by covering and integrating mechanistic, evolutionary and ecological approaches. GELIFES' main aim is to integrate proximate and ultimate approaches in the Life Sciences. This strategy generates better understanding of fundamental biological processes and contributes to the solution of societal problems. Our research fields include behavioural biology, chronobiology, ecology and

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UHohenheim CropQuantitativeGenomics

The Faculty of Agricultural Sciences invites applications for the position of a

FULL PROFESSOR (W3) OF QUANTITATIVE GENETICS AND GENOMICS OF CROPS

at the Institute of Plant Breeding, Seed Science and Population Genetics to be filled in the winter semester 2017/2018.

The successful candidate will teach Quantitative Genetics and Genomics of Crops and its application in plant breeding in the study programs Crop Sciences, Environmental Protection and Agricultural Food Production, and Agricultural Sciences in the Tropics and Subtropics both in German and in English.

The successful candidate is expected to conduct innovative research in the investigation and modeling of quantitative genetic variation with a focus on crops. Possible research topics include genotype x environment interactions and yield stability, adaptation to different forms of biotic and abiotic stress, cultivation under low vs. high-input regimes or the quantitative genetics of yield components. Methodological approaches should combine current statistical and quantitative genetics approaches with genome analysis technologies, and/or phenotyping in laboratory experiments or field trials. The successful candidate is expected to cooperate with other groups as well with the interdisciplinary research centers of the University of Hohenheim and to participate in the Regional Research Alliance "Yield stability in dynamic environments", which is a network of plant researchers at the University of Hohenheim, the University of Tübingen and the Max-Planck-Institute of Developmenta l Biology.

The position offers attractive conditions for first-time full professor appointees. Prerequisites for applicants are habilitation or an equivalent research and teaching record that 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.

Application deadline: 12.01.2017

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 as well as education certificates.

Link to the job description and application portal: http://uhoh.de/w3quantgen 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@gmail.com

UKonstanz AquaticGenomics

The Department of Biology of the Faculty of Sciences seeks to fill the W1 - Junior Professorship of Environmental Genomics in Aquatic Systems from October 2017.

Applicants should be internationally recognized in the field of Environmental Genomics in Aquatic Systems. The ideal candidate is supposed to perform research on the response of aquatic communities to environmental change involving the characterization of environmental DNA of eukaryotes in water and sediment samples, and should have excellent bio-informatics skills. The Junior Professor is expected to contribute to the Research Training Group "R3 - Responses to biotic and abiotic changes, Resilience and Reversibility of lake ecosystems". The Junior Professor will be offered to participate in several projects of this RTG and to become a member of the corresponding PhD advisory committees thus receiving immediate support by doctoral researchers. In parallel, we expect the candidate to develop her/his own research ideas in an environment of interdisciplinary research with excellent opportunities of cooperation. Teaching duties include participation in the local BSc and MSc programs of the Department of Biology.

The University of Konstanz encourages disabled persons to apply. They will be given preference if appropriately qualified (contact + 49 (0) 7531 / 88 - 4016 und 88 - 2834).

The University of Konstanz is an equal opportunity employer that tries to increase the number of women in research and teaching.

The University of Konstanz has been certified as a family-friendly institution by the Hertie Foundation and is committed to further the compatibility of work and family life.

The University of Konstanz maintains a "Dual Career Program". Information can be obtained at: http://www.uni-konstanz.de/dcc All application materials (curriculum vitae, publication list, a list of grants and awards, details of teaching experience, as well as statements of current research topics, future research directions and interests) should be sent including reference number 2016/251 as one pdf file and in English to Prof-2016-251@uni-konstanz.de until 8 January 2017. Further information is available on the homepage of the

University (http://www.uni-konstanz.de/stellen) or by contacting Prof. Frank Peeters. (Frank.Peeters@uni-konstanz.de).

Mark van Kleunen <mark.vankleunen@uni-konstanz.de>

ULiverpool 3 EvolBiol

Three positions are available in the Institute of Integrative Biology at University of Liverpool. Two of these are in the area of genomics and would be suitable for candidates in evolutionary, population or statistical genomics.

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. 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 InstituteÂ^{1}s scientists deliver ground-breaking research which spans the complete range of biological scales from genes and genetic regulation through to proteins, post-translational modification and cellular function to whole organisms, populations and ecosystems. The Institute houses state-of-the-art 'omics' facilities and groups working in IIB are applying these technologies to generate large data-sets both within and across these scales and develop new mathematical and computational models to fully exploit these data.

The IIB is now seeking to appoint to three posts within the institute: 1. Head of the Department of Functional and Comparative Genomics (http://www.jobs.ac.uk/job/AVC567/head-of-department-of-functional-and-comp arative-genomics/) 2. Chair/Reader/Senior Lecturer in Genomics/Genome Engineering (http://www.jobs.ac.uk/job/AVO868/chair-reader-senior-lecturer-in-genomics- genome-engineering/) 3. Chair/Reader/Senior Lecturer in metabolomics (due to be posted shortly)

These openings present opportunities to pursue research interest in a very collegial environment that offers research excellence, underpinned by world-leading research infrastructure. We are looking for individuals who demonstrate innovation and leadership, combined with a strong ability to lead on collaborations, both within the IIB and with relevant colleagues elsewhere in the university. Applications should be made online. Informal enquiries can be directed as indicated in the respective job postings.

– Prof Steve Paterson 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/ hwitter: @scottishwormboy

UOklahoma ComputationalMicrobiol

University of Oklahoma's Laboratories for Molecular Anthropology and Microbiome Research (LMAMR.ORG) is seeking an Assistant Research Professor. LMAMR is a NIH and NSF funded leader in anthropologically focused microbiome research. The position requires PhD Degree and five years of experience in bioinformatic and/or computational approaches, with experience working with metagenomic data. Experience with programming and shell scripting languages Perl, Python and/or R is required, with the addition of C or C++ preferred. The Research Professor's primary effort will be working within currently funded projects that study human microbiome variation; there will be opportunities for independently lead research and teaching, if desired.

Start date: Position open until filled, initial application review on January 31st, 2017

Inquiries and applications (CV and three references) directed to Dr. Cecil M. Lewis (cmlewis AT ou.edu) with "Assistant Research Professor | Adjunct Lecturer" in the subject line.

OU is a Carnegie Very High Research institution that comprises three campuses. The University was established in 1890 and enrolls over 30,000 students and more than 2600 full time faculty. It ranks first among all universities in the number of National Merit Scholars enrolled and has developed an award-winning Research Campus, contiguous to the Main Campus, that houses more than a dozen private companies, several Federal agencies, and numerous research programs in a unique synergistic ecosystem. More than a million square feet of new, fully-occupied space now exists on the Research Campus, with the latest additions including a Radar Innovations Laboratory, Life Sciences Complex, and an Innovation Hub that will open in about a year. Norman, with a population of 110,000 has a vibrant arts community with outstanding public schools and a variety of recreational resources. It was ranked #6 among the best places to live by CNN/Money Magazine on America's best small cities.

Located in Norman, Oklahoma, University of Oklahoma's Laboratories for Molecular Anthropology and Microbiome Research (LMAMR.ORG) specializes in anthropological genomics and metagenomics. Current projects include characterizing the ancestral state of the human metagenomics using extraordinary biological samples from traditional indigenous communities, non-human primates, and archaeological "ancient" materials. Our labs are located in the SRTC (http://srtc.ou.edu/index.php), a newer building with several research groups working in environmental genomics (e.g., http://ieg.ou.edu/). Our building also houses part of OSCER, OU's supercomputer (http://www.oscer.ou.edu/). This broad, multidisciplinary research and education consortium is well situated on OU's award winning Research Campus (http://urc.ou.edu/video).

The University of Oklahoma is an Equal Opportunity Employer. Protected veterans and individuals with disabilities are encouraged to apply.

"cmlewis@ou.edu" <cmlewis@ou.edu>

UOregon ResAsst EvolutionHost-Microbe

Research Assistant-Lab Manager http://careers.uoregon.edu/cw/en-us/job/519408/research-assistantlab-manager Department: Institute of Ecology and Evolution Rank: Research Assistant Annual Basis: 12 Month

Review of Applications Begins December 19, 2016; position open until filled

Special Instructions to Applicants Please apply online, providing resume or CV and a brief letter detailing your research background and interest in this position. Please include contact information for three professional references.

Department Summary The Barber lab is recently established at the University of Oregon Institute of Ecology and Evolution.

Current research applies molecular, biochemical, and genetic approaches to study the evolution of host-microbe interactions. Project areas include: - how evolution of host proteins impacts immunity against pathogenic bacteria - how bacteria adapt to survive within animal hosts - mechanisms by which new biochemical functions emerge in microbes and their hosts.

More information is available on our website at evolutionarypath.org.

Position Summary The Research Assistant-Lab Manager position requires an individual who is self-motivated and has excellent organizational skills to oversee daily operations of the lab and participate in new and ongoing research in the lab.

Key Duties include:

- Creation and/or maintenance of lab databases and organizational systems - Conducting research under direction of the laboratory head, including overseeing day-to-day laboratory operations, supervising undergraduate researchers, ordering reagents and supplies, and assisting with graduate students and postdoctoral scholars. - Developing and advancing an independent research project with the laboratory head and collaborating researchers

Minimum Requirements Qualified candidates will have a bachelor's degree in Biology, Chemistry, or a related field from an accredited institution and relevant research and laboratory management experience.

Preferred Qualifications

Master's degree with experience in molecular biology, biochemistry, genetics, genomics, microbiology or cell culture techniques.

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

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

In compliance with federal law, the University of Oregon prepares an annual report on campus security and fire safety programs and services. The Annual Campus Security and Fire Safety Report is available online at http://police.uoregon.edu/annual-report . – INSTITUTE OF ECOLOGY AND EVOLUTION, UNIVERSITY OF OREGON 5289 University of Oregon, Eugene OR 97403-5289 http://IE2.uoregon.edu EO/AA/ADA institution committed to cultural diversity. The University encourages all qualified individuals to apply, and does not discriminate on the basis of any protected status, including veteran and disability status.

“ie2jobs@uoregon.edu” <ie2jobs@uoregon.edu>

USalzburg EvolutionaryBiol

GZ B 00/1-2016

Applications are invited for the position of

Full Professor of “Evolutionary Biology of Animals”

in the Dept. Ecology & Evolution at the Paris-Lodron University Salzburg, Austria. The desired starting date is 01 Oct. 2017.

We seek an innovative scientist with an outstanding track record in research and experience in academic teaching to fill the professorship of “Evolutionary Biology of Animals” at the Dept. Ecology & Evolution (http://www.uni-salzburg.at/ecoevo). The successful candidate must have demonstrated a well-established expertise in evolutionary biology and is expected to combine experimental laboratory and field approaches. The candidate’s research should cover aspects of metazoan evolution with a focus on genotypic and/or phenotypic adaptation of species or species groups (individuals/populations/communities) to long-term or short-term environmental changes. Internationally recognized expertise in research areas such as population genetics/genomics, evolutionary ecology, adaptive trait evolution, speciation, and/or coevolution and the application of state-of-the-art methods (e.g., next generation sequencing, transcriptomics) are expected. The university’s geographic location offers excellent opportunities for researchers particularly interested in alpine environments.

The appointee will be teaching the entire range of animal evolutionary biology and diversity for the university’s Bachelor “Biology” curriculum, the recently implemented Master “Biology/Ecology & Evolution” curriculum, the Teachers’ Education Program, and the Doctoral Studies program, including the university’s newly established Doctorate Schools. Teaching and evaluating students in both German and English will be required.

The new professorship will complement the existing research priorities of the Dept. Ecology & Evolution and further strengthen its scientific profile. Cooperation with researchers from the other biological departments and further related and/or complementary disciplines within the University of Salzburg as well as with local and national non-university research institutions is encouraged. The successful candidate is expected to initiate, acquire and implement novel externally funded national and international research programs, e.g. Austrian Science Fund (FWF), FWF research groups, European or other international joint projects, etc., to establish a research group, to show active participation in the academic self-administration and a willingness and the relevant qualification to take on a leadership position.

Salzburg offers not only an attractive research environment, but also excellent quality of life in a medium-sized city with a rich cultural life, close proximity to mountains and lakes and easy access to the major urban centres of Vienna and Munich.

*Minimum general requirements for the appointment are:

1. A completed PhD compatible with the advertised position; 2. the qualification to teach at the university level (venia docendi or equivalent qualification); 3. excellent scientific abilities; 4. excellent pedagogical and didactical skills; 5. managerial skills necessary to lead an academic organization; 6. evidence of integration within the international research community (e.g. peer review of manuscripts and proposals, international experience and cooperations); 7. proficiency in written and spoken German.

The position is permanent and full time following bylaw UG 2002 and the Employee Act of Austria. The payment will be according to collective agreement for university employees of the group A1, with a minimum salary of euro 4.842,70 before tax (14 annual payments).

The University of Salzburg is committed to increasing the share of women in research and teaching positions and therefore explicitly encourages female candidates to apply. In the event of equal qualifications, preference will be given to women.

Disabled candidates or people with chronic illnesses with the required qualifications are explicitly invited to submit their applications.

Travel and accommodation expenses arising from this application and any potential visit cannot be reimbursed.

Applications, including the standard documents (curriculum vitae, list of publications, teaching record, teaching evaluation, research projects and other relevant activities), as well as a description of the future research and teaching concepts should be addressed to the Rector of the Paris Lodron University of Salzburg, Univ.-Prof. Dr. Heinrich Schmidinger and sent by email to bewerbung@sbg.ac.at. Informal enquiries can be directed to ulrike.berninger@sbg.ac.at.

Applications must be received by 27 Jan. 2017.

Dr. Anja Hörger University of Salzburg Department of Ecology and Evolution Hellbrunnerstr. 34 5020 Salzburg Austria

Email: anja.hoerger@sbg.ac.at Tel: +43 662 8044-5501

Hörger Anja <anja.hoerger@sbg.ac.at>

USouthCarolina EvolutionaryBiology

This is a tenure-track DBER position, open to all areas of biology. One of our search committee members is an evolutionary biologist, and he wanted to make sure this got out to that community. He was worried about getting applicants only from cell/molecular type areas.

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BIOLOGY EDUCATION RESEARCH

UNIVERSITY OF SOUTH CAROLINA

The Department of Biological Sciences in the College of Arts and Sciences invites applications for a tenure-track position at the rank of ASSISTANT PROFESSOR in Biology Discipline-Based Education Research (DBER). Successful candidates will be expected to develop a vibrant, extramurally funded DBER research program in any area of biology education research. We are especially interested in a focus on scholarship of teaching and learning, learner-centered teaching strategies, and evidence-based teaching, learning and assessment practices. This position is part of an anticipated series of new DBER faculty positions in the sciences. Candidates will have a PhD in an appropriate field of biology, research experience in teaching and learning at the university level, and postdoctoral experience is preferred. This person will be responsible for teaching at both undergraduate and graduate levels, in courses appropriate to his/her expertise.

Applications should be emailed in PDF format to, Peggy Breeland, Administrative Coordinator, Biology Education Research Search Committee, Department of Biological Sciences, University of South Carolina, Columbia, SC 29208; (breeland@mailbox.sc.edu). Applications should include a curriculum vitae and a statement (4 page max) describing research accomplishments, future DBER research plans, teaching interests, and teaching philosophy. Applicants should arrange to have at least three letters of reference sent to the committee and provide a list of the names, mail and email addresses, and phone numbers for those referees. Review of applications will begin February 1, 2017, and will continue until the position is filled.

The University of South Carolina's main campus is located in the state capital, close to mountains and coast. The Carnegie Foundation for the Advancement of Teaching has designated the University as one of only 40 public institutions with "very high research activity". The Carnegie Foundation also lists USC as having strong community engagement. The University has over 33,000 students on the main campus, more than 300 degree programs, and a nationally-ranked library system that includes one of the nation's largest public film archives. Columbia, the capital of South Carolina, is the center of an increasingly sophisticated greater metropolitan area with a population of over 800,000.

The Department of Biological Sciences (http://www.biol.sc.edu/) is a multidisciplinary unit of approximately 1,600 Undergraduate Students, 45 Graduate Students, 15 Postdoctoral Associates, and 42 Faculty representing a broad range of research areas, including Molecular and Cellular Biology, Genetics, Biochemistry, Bioinformatics, Cancer Biology, Ecology and Evolution, Plant Sciences and Neuroscience.

The University of South Carolina is an affirmative action, equal opportunity employer. Minorities and women are encouraged to apply. The University of South Carolina does not discriminate in educational or employment opportunities or decisions for qualified persons on the basis of race, color, religion, sex, national origin, age, disability, sexual orientation, or veteran status.

"WHITE, ALAN" <ARWHITE@mailbox.sc.edu>

UVienna PopulationGenomics StatisticalGenetics

The University of Vienna seeks to appoint a faculty member:

Tenure-Track Position (full time) Computational Biology (Statistical Genetics/Population Genomics)

In recent years, Vienna has developed into one of the leading centers in evolutionary biology (www.evolvienna.at, www.popgen-vienna.at). In addition to a stimulating scientific environment, Vienna also offers an extraordinarily high quality of life. Affordable housing, excellent public transport, great restaurants, a range of international schools, two operas, two music centers, many theaters and museums in combination with a pleasant climate make Vienna one of the most attractive cities in Europe.

The position will be allocated to the Centre for Molecular Biology (MFPL - Max F. Perutz Laboratories) of the University of Vienna. MFPL is part of the Vienna Biocenter Campus, a Life Sciences Cluster for world-class research with excellent core facilities (sequencing, bioinformatics, computer cluster). Successful applicants will have access to PhD students and Postdoctoral fellows through highly successful International Programs. The campus hosts an international kindergarten.

Successful candidates should have the following qualifications: - Doctoral degree/PhD and at least two years post-doctoral experience at a university or other research institution - Outstanding achievements and potential in research, excellent publication record, international reputation - Experience in designing and participating in research projects, as well as the willingness and ability to lead research groups - Enthusiasm for excellent teaching, teaching experience at universities or a teaching concept as well as the ability and willingness to teach students in all phases of their studies (bachelor's, master's, or doctoral level), to supervise academic theses and to promoting young academic colleagues

The University of Vienna expects the successful candidate to acquire, within three years, proficiency in German sufficient for teaching in bachelor's programmes and for participation in university committees. In addition, the University of Vienna expects the successful candidate to be prepared to take over responsibility on the organisational level of the Centre and the University, if necessary.

Job description: The announced position is an academic tenure-track position. Within two years' time, the University will offer a qualification agreement if the academic performance suggests that the required high qualification can be reached. With the conclusion of the qualification agreement, the employee will be allocated to the group of "Assistant Professors". If the qualification is achieved according to the agreement, employment, which originally has a six-year duration, will be continued for an indefinite period as an "Associate Professor". Via a further competitive procedure as stipulated in the University's Statutes, associate professors can be directly promoted to full professor. If the qualification goals are not achieved, the employment will end upon expiry of the contract term.

We offer: - the opportunity for a long-time career track, attractive salary - in addition to the statutory social insurance, the University of Vienna offers a pension fund to its employees - a dynamic research location with well-established research funding provisions - attractive working conditions in a city with a high quality of life - a wide range of support services offered by central service institutions - a start-up package to be negotiated

The University of Vienna pursues a non-discriminatory employment policy and values equal opportunities, as well as diversity. The University lays special emphasis on increasing the number of women in senior and in academic positions. Given equal qualifications, preference will be given to female applicants.

Application documents: - Application letter, including a brief description of: - current research interests and research plans for the immediate future - current and planned foci in academic teaching and the supervision of young researchers - Academic curriculum vitae - List of publications, including specification of three key publications - List of talks given, including information about invited lectures at international conferences - Third-party funds list of acquired third-party funded projects, as well as a list of third-party funded projects which the candidate was a member of (subject, duration, origin, volume) - Overview of previous academic teaching and/or teaching concepts as well as supervised theses - Names and contact addresses of three or more referees

Applications must be submitted in English (preferably as a single PDF) to facultyopenings@mfpl.ac.at, c/o Graham Warren. Informal inquiries can be sent to joachim.hermisson@univie.ac.at

The application deadline is 28 February 2017.

– Joachim Hermisson

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

UWashington NoninvasiveGenetics LabManager

Noninvasive Genetics Lab Manager at UW Seattle

The School of Environmental and Forest Sciences at the University of Washington has created a new shared genetics lab directed by Dr. Laura Prugh. We seek an experienced individual to help get the lab up and running, supervise and train lab users, and to carry out noninvasive genotyping projects. Current projects include studies of interactions among a variety of carnivores (wolves, cougars, coyotes, foxes, bobcats, fishers) and ungulates in Alaska and Washington using DNA obtained from scats, puncture wounds, and snow tracks. Other users of the lab may work on varied projects, including those focused on soils, plants, microbes, or other wildlife. We are currently setting up the lab with new equipment, including a droplet digital PCR system that will facilitate cutting edge eDNA work. The lab manager will work independently to arrange equipment, purchase supplies, train and supervise graduate and undergraduate students while in the lab, run genetic analyses, and lead or contribute to publications. The lab manager will be fully integrated into the Prugh lab wildlife ecology research group, with the possibility of assisting with projects outside the lab (e.g., fieldwork). See http://www.prughlab.com/ for more about what we do.

The lab manager will be hired as a full time Research Scientist, at a starting salary of $3600/month with full benefits. Funds are available for at least one year, and the position could be extended pending successful grant proposals. Ideal start date is early January 2017.

Responsibilities and Tasks: - Non-invasive genotyping, extracting and amplifying DNA from hair and fecal samples of wild carnivores - Optimization of PCR protocols - mtDNA and microsatellite analyses for species and individual ID - Use of software such as Genemapper to score alleles - Generation of consensus genotypes from repeated PCR runs - Estimation of genotyping error rates - Purchasing supplies - Training graduate and undergraduate students - Managing use of lab - Assistance with manuscript preparation (with potential for authorship and co-authorship)

Minimum requirements: Bachelor's Degree in an appropriate field of technology or science, plus at least one year of research experience. Proficiency with fecal genotyping and individual identification from microsatellites is required.

Desired qualifications: Master's Degree in an appropriate field of technology or science with at least one year of research experience. Previous supervisory and managerial experience is desirable. Experience with eDNA work would be beneficial.

To apply: Please email a cover letter summarizing your interests and qualifications, your cv, and contact information for 3 references in a single pdf to lprugh@uw.edu. Position is open until filled. To ensure full consideration, submit your materials by Dec 31, 2016.

"lprugh@uw.edu" <lprugh@uw.edu>

UWashington PopGenetics

The Department of Genome Sciences at the University of Washington is continuing a major expansion under its chair, Dr. Robert Waterston. Research in the department encompasses both genetic and genomic analysis of humans and model organisms. The department also has a significant focus in technology development and in computational biology across all levels including sequence, expression, proteomics, single-cell, network, and genetic analysis. The department invites applications for a full-time faculty position at the rank of ASSISTANT PROFESSOR, tenure-track in human genetics, population genetics, computational genomics and/or technology development. The position involves establishing an active research program as well as teaching duties. Applicants must hold an M.D. degree or a Ph.D. in a relevant area. To ensure full consideration complete applications must be received by February 1st, 2017.

Candidates should email their curriculum vitae and statement of research and teaching interests, and arrange to have three signed letters of reference sent to: faculty-search@gs.washington.edu.

For additional information that may be helpful in preparing an application, see the department's web site at http://www.gs.washington.edu . University of Washington is an affirmative action and equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, gender expression, national origin, age, protected veteran or disabled status, or genetic information.

"phg@u.washington.edu" <phg@u.washington.edu>

UWisconsin Milwaukee Dean

The University of Wisconsin-Milwaukee (UWM) invites applications for the position of Dean of the College of Letters & Science. The College of Letters & Science is the largest on campus comprising 45% of ranked faculty at UWM, graduating 27% of all students at UWM annually, and securing 60% of campus research funding. UWM recently received two significant recognitions. The Carnegie Foundation granted the campus the Community Engagement Classification in 2015 for its significant work in Milwaukee and Wisconsin's southeast region. In February 2016, UWM was designated a R-1 Doctoral University - Highest Research Activity, by the Carnegie Classification of Institutions of Higher Education.

As the chief executive and academic officer for the College, the Dean has primary responsibility to plan, develop, and administer all aspects of the College's educational programs, activities, and budget; provide vision in setting priorities and leadership in maintaining academic standards and in strengthening faculty scholarship and research; work with partners across the university; and represent the College within the University, the UW System, the external community and region, with alumni, and with appropriate external agencies and organizations regarding academic programs and standards.

UWM seeks candidates with a strong record of professional accomplishment, commitment to excellence in both research and teaching, and outstanding management and leadership skills to serve as the new Dean. The Dean must be a person with the highest integrity and an educational leader.

Candidates must possess a terminal degree with scholarly qualifications sufficient for appointment as a tenured full professor in a department within the College and have proven leadership and administrative experience. The complete position description is available at: http://www4.uwm.edu/secu/news_events/l-and-s-dean.cfm The Committee will accept applications and nominations until the position is filled. Initial screening of applications will begin in February 2017 and continue until an appointment is made. For best consideration, applications must be received on or before February 12, 2017. Applications received after this date may not be considered.

The Chair of the Search and Screen Committee, Jennifer Doering, welcomes all inquiries and nominations. Nominations should include name, position, e-mail and telephone number of the nominee. Chair Doering may be contacted at doering@uwm.edu or (414) 229-5146.

Applications must include a cover letter, a complete curriculum vitae and contact information for at least five references. These materials must be uploaded through UWM's Applicant Information Management System (AIMS) at: http://jobs.uwm.edu/postings/25764 In accordance with Wisconsin's Open Records Law, requests for confidentiality by nominees and applicants will be honored, if so requested, except that names and titles of the finalists must be disclosed.

UWM is an AA/EOE employer: All applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, or protected veteran status.

Rafael Lucas Rodriguez, PhD Associate Professor Biological Sciences, Lapham Hall University of Wisconsin-Milwaukee 3209 N. Maryland Ave., Milwaukee, WI 53201, USA rafa@uwm.edu www.preferencefunctions.org Rafael L Rodriguez Sevilla <rafa@uwm.edu>

ZFMK Germany HeadOfMolecularLab

Head of Molecular Lab at Zoological Researchmuseum A. Koenig, Germany

The Centre of Molecular Biodiversity Research (https://www.zfmk.de/en/research/research-centers-and-groups/centre-for-molecular-biodiversity-research-zmb) at the Zoological Research Museum Alexander Koenig (ZFMK) seeks creative and highly skilled applicants for a tenure-track position as head of the molecular laboratory. The molecular laboratory is a central facility of the ZFMK and provides service to other scientists at the ZFMK. It is a fully equipped molecular lab, including robot units for high through-put DNA analysis. Two technical assistants are directly associated with the head of the molecular lab.

Required qualifications

It is essential that the applicant has:

* a PhD in Ecology, Evolution or Molecular Biology or a closely related field with strong emphasis on empirical molecular work and computational skills in these subjects; * experience in working with non-model organisms (animals); * experience in molecular genetics, including DNA extractions, PCR, next-generation sequencing, roboting, establishing lab setups; * experience in data management and analysing DNA sequence and genome data (computational skills); * experience in staff management and student supervision; * experience in developing long-term strategies for the lab, meeting the goals of a state of the art central molecular lab service; * motivation to work in a team and take responsibility; * motivation to counsel scientists of the museum in terms of molecular work, strategic development, etc.; * excellent communication skills.

It is desirable that the applicant has/is:

* a good knowledge of the software R for programming, statistical analyses or graphical visualization of data; * experience with soft money acquisition, in particular concerning infrastructure development; * fluent in English; a good understanding of German is advantageous.

Applicants are evaluated based on how well they fulfil the requirements detailed above. Such evidence may include documentation of completed course work, scientific publications, technical and analytical know-how, evidence of organisational skills, and prior experience in lab management. Whenever possible, statements to these effects should be accompanied by objective or independent assessment of the candidate's track record and potential. These may include links to access published or unpublished material or letters of support from supervisors or previous employers. The tenure procedure will evaluate the above listed essential criteria (a high publication output is not mandatory for the getting tenure).

The ZFMK is a Leibniz Institution cooperating with the University of Bonn and funded by the Federal State of NRW and the Federal Government. The Centre of Molecular Biodiversity Research has been established to foster molecular research spanning from genomics and speciation genetic research to developing high-throughput barcoding applications.

We offer a highly motivating environment and flexible working hours. Salary and benefits are according to a public service position in Germany (E13, TVL-13). The ZFMK advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference. The contract will start as soon as possible and will initially be restricted to three years. A tenured position will be subject to personal performance reviewed by a commission. Please send your application by e-mail attachment, including a detailed CV, and names of three referees until January 20th, 2017 to Mrs. Lenz, head of the staff management (e-mail: h.lenz@zfmk.de). In case of questions concerning the position, please contact Prof. Dr. Bernhard Misof, Head of the Centre of Molecular Biodiversity Research (e-mail: b.misof.zfmk@uni-bonn.de).

For more information about the museum see http://-www.zfmk.de Bernhard Misof <bmisof@uni-bonn.de>

Other

AlgaeEvol NormaJLang EarlyCareerFellowships

To anyone using algae as a research subject:

Information on the Norma J. Lang Early Career Fellowships is now available on the Phycological Society of America (PSA) website:

http://www.psaalgae.org/norma-j-lang-fellowships/ Please visit this link to learn more about this award as well as information on the application requirements. The deadline for submission for this award is May 1 each year.

Thank you.

Sincerely, Kirsten

PSA Communications Director

– Kirsten Muller Ph. D. Professor Associate Chair (Graduate Studies) Interim Associate Chair (Undergraduate Studies) Biology, University of Waterloo 200 University Ave. West N2L 3G1 phone: 519-888-4567 ext. 32224 fax: 519-746-0614 kmmuller@uwaterloo.ca http://uwaterloo.ca/biology/-people-profiles/kirsten-m-muller Twitter: @kirstenmmuller

Chris Lane Associate Professor Integrated & Evol. Bio. Graduate Director Department of Biological Sciences University of Rhode Island 120 Flagg Road Kingston, RI., 02881 Office: CBLS 277 ph (401) 874-2683 fax (401) 874-2065 http://cels.uri.edu/bio/lanelab/ Chris Lane <clane@uri.edu>

AmericanGeneticAssoc Awards

The American Genetic Association grants Evolutionary, Ecological, or Conservation Genomics (EECG) Research Awards to graduate and post-doctoral researchers who are at a critical point in their research, where additional funds would allow them to conclude their research project and prepare it for publication.

These awards are open to any graduate student or postdoctoral fellow who is a member of the American Genetic Association at the time of application â€“ visit http://www.theaga.org/ for membership details.

The program is not intended to fund an entire research project, to initiate new research projects, or to provide salary support. Proposals addressing genome-scale questions, or ecological, evolutionary and conservation genetics questions best addressed with genome-scale data, will be given priority for funding. Awards will generally range from $5,000 to $10,000, awarded to the PI or institution (no overhead is provided).

Application deadline is 1 Feb 2017; award outcomes will be announced 15 Apr 2017.

Details and instructions for preparing applications can be found at http://www.theaga.org/ AGAJOH <AGAJOH@oregonstate.edu>

AmericanGeneticAssoc SpecialEventsAwards

SPECIAL EVENTS AWARDS Application Deadline 31 January 2017 Awards announced 31 March 2017 The American Genetic Association grants awards each year for support of special events that advance the mission of AGA, particularly to support students to attend the event.

Eligible events include specialized workshops and short courses in topical areas of organismal genetics and genomics, but any event relevant to AGA's purpose will be considered. Events that could lead to Journal of Heredity articles will receive special consideration. Awards are usually between $5,000-$15,000, with a total of $70,000 available for 2017.

Funding is competitive, and applications must follow the guidelines. Details can be found at http://www.theaga.org/ AGAJOH <AGAJOH@oregonstate.edu>

ArnoldArboretum HarvardU Funding

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.

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/ Faye Rosin <frosin@oeb.harvard.edu>

Drosophilogistis LarrySandlerAwardNominations

LAST CHANCE - Larry Sandler Award Nominations

Only a few days left to nominate your students for the Larry Sandler Award. Thesis advisors can nominate any student completing a PhD in an area of Drosophila research between July 2015 and December 2016. — The winner will present the Larry Sandler Memorial Lecture on the opening night of the 58th Annual Drosophila Research Conference, March 29, 2017, in San Diego. The Award was established in 1988 by colleagues, friends, and students of Dr. Sandler after his untimely death in 1987. The award honors Dr. Sandler for his many contributions to Drosophila genetics and his exceptional dedication to the training of Drosophila biologists. — Nominations should include a curriculum vitae, a thesis abstract of one or two pages, and a letter of nomination from the thesis advisor. The winner receives complimentary airfare, accommodations, and registration for the 58th Annual Drosophila Research Conference as well as lifetime GSA membership. — Nominationmaterials should be sent to Bob Duronio as asingle PDF file no later than December 22, 2016. — Would you still like to submit an abstract for a poster presentation? Late abstracts will be accepted until January 23, 2017 —

— Important Dates

2016 Larry Sandler Award Deadline Dec 22 2017 Late Abstract Deadline Jan 23 Early Registration Deadline Feb 3 Hotel Reservations Deadline Mar 3 —

Genetics Society of America— 9650 Rockville Pike, Bethesda, MD 20814— (301) 634-7300——-—— society@genetics-gsa.org www.genetics-gsa.org —

Drosophila Research Conference <society@genetics-gsa.org>

GenomeSequence DataSchool

If you applied for the Triple A Winter school on how to Assemble, Annotate and Analyse Whole Genome Sequence data you should have received an email detailing the outcome of that application. If you have not received this email please contact me on monteverita@env.ethz.ch

jessica.stapley@env.ethz.ch

Isabelle Olivieri

Isabelle Olivieri has left us on Saturday 10 December at 4 am. She passed away quietly after having fought with an admirable courage against her cancer but also against a paraneoplasic syndrome, which heavily handicapped her for the last years of her life. Isabelle would have passed 60 years in March 2017. She entered the Agronomic College (AgroParisTech) in Paris in 1977, specialized in zoology and then oriented her research towards evolutionary genetics. Her PhD work concerned Mediterranean thistles. These plants were invasive in Australia and one of the goals of the CSIRO where she was based in Montpellier was to find control agents. She will come back to the question of plant-insect interactions later in her life. She did her Post-Doc in Paul Ehrlich's lab in Stanford in 1983 and there, further developed her ideas on the importance of the metapopulation concept for the understanding of the evolution of migration mechanisms. The paper which she will publish on this subject in American Naturalist (after a more than 4 years debate with the editors) will provide her with a congratulation letter from Ernst Mayr (this letter is probably somewhere in her "records", Isabelle has never been very gifted for ordering, her papers as the rest!).

Hired at the INRA (Agronomic Research Institute) in a laboratory near Montpellier on a programme concerning Mediterranean Alfalfa, predominantly annuals, she developed her research on the evolution of genetic systems by studying the evolutionary mechanisms determining the lifespan of organisms according to their ecology. Her DSc thesis will treat of the constitution of an integrative approach of evolution uniting demographic and genetic models on both migration and longevity characters.

Hired as full Professor at Montpellier, she became the first professor in Population Genetics at Montpellier and set up high level courses. She carried on with her quest of evolutionary mechanisms by coming back to thistles and their insects. She studied habitat choice, host specificity, realised a leading study on the Conservation Biology of a local Centaurea, again in relation with the metapopulation concept, and developed experimental evolution studies . The list of questions which she tackled with her team or with diverse collaborators would be too long to be detailed here.

Isabelle also became a recognized actor of international evolutionary biology. John Maynard Smith has once said that she was the fifth column[1] of the French evolutionary biology into the anglo-saxon world. Indeed, she will become president of the European Society of Evolutionary Biology, vice president of the American Society for the Study of Evolution, the Dutch Academy of sciences will attribute her a comfortable grant allowing her to come whenever and wherever she wishes in any University to interact with local scientists, she will belong to the editorial board of numerous journals, the French Society of Ecology will give her its "grand prix" and CNRS its silver medal. Despite all those recognition proofs, Isabelle did not search for honours nor for responsibilities. Actually, she would rather make her best to escape from them. She however used all opportunities to defend her convictions and transmit messages. Invited by the French president to a lunch with other female scientists, she gave an interview to a newspaper criticizing his policy for scientific research. In her national and international activities, Isabelle has established sustainable and fruitful cooperative relationships and tried to gather ideas and people together, bring demography and genetics, ecology and evolution together . It was undoubtedly one of the causes of her charisma, of the fact that a number of us were ready to follow her even on steep paths, just like the Corsican ones she liked so much.

When she passed her DSc, Georges Valdeyron, who had supervised her PhD and who was 45 older than her, stated that the students he was interacting with were a bit like his progeny but that his relation with her was different; actually she had been more like a nursing mother. From that point of view, in a way, we, French evolutionary biologists, are orphans today. The one who dared say things which should not be told, who disputed fiercely, step by step let us admit it, it was sometimes painful any opinion which she did not find rational, the one who oriented the research of a lot of us and who was an example for many, has disappeared. If Isabelle could be severe, brusque sometimes, all of those who have known her have benefited from her exceptional generosity and from her care for collective actions. Her involvement at the collective level has led those who worked with her to establish deep affective relations with her and to build this large family, of which she is the soul, and which will remain united now that she is gone. Her house she shared with her companion was widely open and innumerable

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

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Leipzig CallProposals PostdocsSabbaticalsGroups

sDiv has opened a new call for Working Groups, Postdocs and Sabbaticals.

Deadline: Proposal 15 FEBRUARY 2017 & Deadline for Letter of Intent 18 January 2017

Please for more information: www.idiv.de/sdiv/calls Please spread the word & apply :) Thanks a lot!

With my best regards from sunny Leipzig,

sMarten Winter

Dr. Marten Winter Scientific Coordinator Synthesis Centre sDiv / Wissenschaftlicher Koordinator Synthesezentrum sDiv German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Phone +49(0)341-97-33129 Fax +49(0)341-97-39358 Email marten.winter@idiv.de Homepage https://www.idiv.de/the-centre/employees/details/eshow/winter-marten.html German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig Deutscher Platz 5e 04103 Leipzig Germany

iDiv is a research centre of the DFG - Deutsche Forschungsgemeinschaft

"Winter, Marten" <marten.winter@idiv.de>

MaxPlanckInst Seewiesen Vol SexualSelectionParrots

MaxPlanckInst_Seewiesen. SexualSelectionParrotsVolunteers

Where: Tenerife, Spain When: mid-January until end of August (at least 2 months) What: Volunteer field assistants - Parrot sexual selection

The Department of Behavioural Ecology and Evolutionary Genetics at the Max Planck Institute for Ornithology in Seewiesen, Bayern, Germany (see http://www.orn.mpg.de/2622/Department_Kempenaers), is seeking three volunteers to start working mid-January and until the end of August 2017 (the position requires a minimum of 2 months).

The volunteers will assist in the collection of courtship displays and egg-laying data. This work would be part of a project that aims to understand sexual selection in parrots of the world. The work will be done with captive animals that are held in the facilities of the Loro Parque Fundacion, located in Tenerife, Spain.

Work will include: - recording courtship displays - following up reproduction (sexual displays, mating, and egg laying) - maintenance of electronic equipment - setting up experimental equipment - data collection, entry, and management

Successful candidates should have experience with video-recording equipment. Experience with monitoring animals is desirable. Applicants should also be highly motivated and well organised, with capabilities of working both in a group and independently. Work will be 5-6 days per week.

The working language at the Institute is English, so good knowledge of the language is required. A basic working knowledge of the Spanish language would be advantageous but not mandatory. Eligibility is sadly restricted to UK and EU students. The Max Planck Institute for Ornithology employs a dynamic, dedicated, and international group of researchers who are focused on exploring the fields of evolution, ecology, genetics, and neurobiology.

Benefits will include accommodation and travel-related expenses in Tenerife.

Please apply (including your CV and cover letter) via email to lcarballo@orn.mpg.de

Deadline: 06 January 2017 or until the positions are filled.

Luisana Carballo Department of Behavioural Ecology and Evolutionary Genetics Max-Planck-Institute for Ornithology Eberhard-Gwinner-Straße, House 8 82319 Seewiesen Germany

lcarballo@orn.mpg.de

Phyloseminar XavierDidelot Jan13

Next talk on http://phyloseminar.org/ :

Modelling recombination in prokaryote phylogenomics Xavier Didelot Imperial College London Monday, January 23, 2017, 9:00 AM PST

Recombination happens frequently in most bacterial and archaeal species. Traditional phylogenetic techniques do not account for this, which can greatly limit their usefulness for the analysis of genomic data. The coalescent with gene conversion accurately models the ancestry process of prokaryotes, and this can be used to simulate realistic data, but it is too complex to use in an inferential setting. Approximations have therefore been introduced, which are centred around the concept of the clonal genealogy, that is the phylogeny obtained by following the line of ancestry of the recipient of each recombination event. I will review these mathematical models and ongoing efforts to develop statistical software to perform phylogenomic analysis in recombining prokaryotes.

– Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ ematsen@gmail.com

Seeking GBS facilities

Dear Evoldir members

In our group we seek to use GBS of restriction-enzyme reduced genomes to find SNPs for population genetics of non-model organisms. We are aware of patent problems when using this technique, that's why I would like advice about facilities or companies that are adequately licensed and that offer the service of library preparation (with preliminary enzyme checking and selection) and sequencing. Infos about prices are also welcome

Thanks for your answers, I will prepare a post with them

Regards

Xavier Turon xturon@ceab.csic.es

–

Xavier Turon Dept. of Marine Ecology Center for Advanced Studies of Blanes (CEAB, CSIC) Accés a la Cala S. Francesc 14 17300 Blanes (Girona) Spain

E-mail: xturon@ceab.csic.es Phone: +34 972 336101 Fax: +34 972 337806 http://www.ceab.csic.es/ http://www.ub.edu/beb/english/invertebrates/turon/turon.htm Xavier Turon <xturon@ceab.csic.es>

SummerUndergraduateResearch PlantGenetics

Switchgrass (Panicum virgatum) is emerging as an important biofuel candidate in the United States. Our labs (see list of collaborators below) collectively study the ecology, genetics/genomics, physiology and agronomy/plant breeding of Switchgrass. We are seeking a talented and diverse group of undergraduate students interested in conducting a variety of research in Switchgrass biology across the US.

Program description: This program is an opportunity for undergraduate students to participate in mentored independent research on the biology of Switchgrass. The program is funded through the NSF Research Experience for Undergraduates (REU) program and is associated with our ongoing interdisciplinary work on the ecology, physiology, and genomic responses of switchgrass to future climate change. Summer students will be immersed in research and learn basic and applied biology through active participation in primarily field-based work. Working as part of our research team, they will contribute to group research projects, design short research projects, and present their work in an end-of-summer student symposium.

Each position is supported for 8-10 weeks beginning the first week of June. Students are awarded a $4500 stipend, plus a housing and food allowance, and some funds to help defray the cost of traveling to the designated University.

Who Should Apply: Undergraduates that are not in their senior year (typically 1st to 3rd year students), who are either U.S. citizens or permanent residents studying in the U.S.

Application process: The application deadline is February 19, 2017. Applicants should submit a 1-page cover letter describing any relevant research experience, along with their motivation for joining our research group, and include a copy of their current transcript (unofficial transcript or screenshots are acceptable). Applicants should also ensure that two letters of recommendation are submitted on their behalf. Only applications that are complete will be considered. Applications and requests for further information should be directed to:

Dr. Brandon Campitelli e-mail: brandon.campitelli@utexas.edu Subject: Switchgrass REU 2017

For more information regarding this opportunity, and ongoing research, please visit our website: https://sites.cns.utexas.edu/juenger_lab/summer-research-opportunities – Brandon E Campitelli | PhD Postdoctoral Researcher | Dept. of Integrative Biology | College of Natural Sciences Clinical Assistant Professor | Biology of Biofuels | Freshmen Research Initiative University of Texas at Austin | (512) 471-9920 | Patterson Labs 638

brandon.campitelli@utexas.edu

SystematicsResearchFund

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 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 2017

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 Research Scientist Life Sciences Department The Natural History Museum Cromwell Road London SW7 5BD

Tel: +44 (0) 20 7942 5285

Anne Jungblut <a.jungblut@nhm.ac.uk>

TravelGrants to TexasAMU

The Ecology and Evolutionary Biology Doctoral Program at Texas A&M is pleased to announce the availability of travel grants for prospective PhD students. These travel grants, which will be awarded on a competitive basis, will cover the costs of a domestic flight to and from College Station, hotel accommodations while in College Station, plus a per diem for meals. The aim of the travel grant is to provide prospective PhD students the opportunity to:

- Interview with faculty and meet current graduate students - Tour the department and campus to learn about available resources and facilities - Explore College Station and its surrounding areas

Travel grants will be awarded in January with travel scheduled for February 5-7, 2016. Travel grant awardees will spend time together during their visit, thus gaining immediate insights into their future cohort.

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 fellowships. Texas A&M University is positioned in Blackland Prairie and Post Oak Savannah habitat, which supports great species diversity and a wealth of research opportunities with great year-round climate. 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? To be considered for a travel grant, prospective PhD students first need to contact Jason Martina, the EEB Program Coordinator (email: jpmartina@tamu.edu; phone: 979 845-2114). To receive a travel grant, an official Graduate Application package must be submitted to the EEB Program. For additional information about the EEB Program and the graduate application process please visit: http://eeb.tamu.edu For consideration for merit fellowships, your application needs to be received by January 1, 2017

– Jessica E. Light Associate Professor and Curator of Mammals Department of Wildlife and Fisheries Sciences Biodiversity Research and Teaching Collections Texas A&M University College Station, TX 77843 Phone: 979-458-4357 http://www.jessicalight.org/ Jessica Light <jlight2@tamu.edu>

UBristol FieldInternships EvolFruitflies

Field internship positions available to study the effects of climate change on species interactions in Australian rainforest Drosophila We are looking for two motivated, hardworking volunteers to help conduct fieldwork in northern Queensland, Australia as part of a project examining evolutionary responses to climate change in rainforest Drosophila.

This project is based at the University of Bristol, UK (PI Dr Jon Bridle, postdoc Dr Eleanor O'Brien), and involves collaboration with researchers at the James Cook University in Townsville (Dr Megan Higgie) and the University of Melbourne (Prof Ary Hoffmann), as well as the University of Oxford (Prof Owen Lewis).

For further details of this research, please see our recent (in press in Global Change Biology) http://biorxiv.org/content/early/2016/10/14/068080 These positions represent an excellent opportunity to be involved in exciting research in evolutionary biology, and would suit those seeking direct experience of study or research in this area.

Your role will be to assist with laboratory rearing and field transplant experiments of Drosophila at several locations in the rainforest in northern Queensland. You will also need to help collect specimens, maintain live stocks and perform other duties as required.

Training will be provided in Drosophila identification and maintenance, although previous experience would be an advantage.

Essential requirements: (1) BSc in evolutionary biology, genetics, ecology or a related discipline.

(2) Ability to work carefully and meticulously, paying close attention to detail.

(3) Enthusiasm for biological fieldwork, and the ability to work as part of a team, including in hot, humid conditions.

(5) A full driving licence.

Previous fieldwork experience and 4 wheel-driving experience would also be useful.

Each field intern must be able to spend at least three months in Queensland between March - June 2017, with the possibility of extension beyond this period. Full living expenses (meals and accommodation) will be paid while in the field, and we can contribute 600 GBP (approx.

$US760/ $AU1000) towards the costs of travel to the field site.

Review of applications will begin on the 15th January and will continue until the positions are filled. Applications should include a cover letter and CV, including the names of two referees.

For further information about this position, or to apply, please contact Eleanor O'Brien (e.k.o'brien@bath.ac.uk) or Jon Bridle (jon.bridle@bristol.ac.uk).

– 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>

UTexas ElPase ChihuahuanDesertBiodiversity

REU Opportunity Summer 2017: "Research Experience for Undergraduates in Chihuahuan Desert Biodiversity"

The University of Texas at El Paso (UTEP) Department of Biological Sciences invites applicants for the NSF sponsored Research Experience for Undergraduates (REU) in Chihuahuan Desert Biodiversity. This is a 10 week summer program. The goal of this program is to provide undergraduate students with experience in hypothesis-driven collaborative research utilizing field based and/or laboratory methods and fully engage students in projects associated with the ecology and evolution influencing Chihuahuan Desert biodiversity.

The program provides:

* High quality research experience in ecology and evolutionary biology in the field and/or lab * Research opportunities at the Indio Mountains Research Station (IMRS), a 40,000 acre facility controlled by UTEP * One-on-one and group mentoring from active research faculty in multidisciplinary fields * Training in bioethics and other relevant professional skills

The program includes

* $5250 stipend for 10 weeks

* Housing in shared apartments and field station * Travel reimbursement of up to $600

For more information on the program, research projects or to apply please visit: http://science.utep.edu/cdb-reu/ Enquiries: CDB-REU@utep.edu

"mlmoody@utep.edu" <mlmoody@utep.edu>

WillametteU VolField YuccaCoevolution

The Smith lab at Willamette University is soliciting applications for volunteers to participate in field research studying the pollination biology and coevolution of Joshua trees (*Yucca brevifolia*) and yucca moths (genus *Tegeticula*) from mid March to mid April of 2017. Volunteers will assist in the completion of pollination experiments in a plant hybrid zone located in central Nevada, which will involve collecting flower and leaf tissue samples, installing pollinator exclusion cages over Joshua tree flowers, collecting moths, and sorting insects to species. All travel, food, and accommodation costs will be covered by the project.

Participation will require living at a remote field camp continuously for approximately four weeks. Meals are communal, prepared in a small RV kitchen, and evenings are typically spent around the camp fire. Many past participants have returned for additional years, and many have used the experience gained on this project to secure other positions in agency, private conservation organizations, and graduate programs in ecology, evolution, and entomology.

However, prospective participants should be aware that conditions in the field are challenging. The field site has no running water. Apart from personal tents and walks in the desert there is little opportunity for personal space and time, and there are no cell phone/internet services at the field site. (Wifi and cell service are available in the nearest town, a 30-minute drive away). Daily temperatures may drop below freezing or exceed 90 F. Wind and sandstorms are very common. So, it is important that prospective volunteers be enthusiastic about living and working closely with others in challenging conditions. Volunteers should also be capable of hiking up to 6 miles per day while carrying heavy and awkward loads, and able to climb a 6' ladder.

Prospective volunteers should submit a CV or resume, the name and contact information for one or more professional references, and a letter describing their interest in the project by email to csmith@willamette.edu . There is no degree requirement, but a familiarity with and an interest in ecology and natural history are necessary.

Please include the words 'Volunteer Field Assistant' in the subject line of your message.

Screening of applicants will begin on January 15th, 2017, and continue until all positions are filled.

More information about our research can be found here:

http://www.nsf.gov/discoveries/disc_summ.jsp?cntn_id=115956&org=NSF http://www.reviewjournal.com/news/water-environment/joshua-tree-yucca-moth-co-evolution-fascinates-researchers https://knpr.org/knpr/2013-01/joshua-tree-researcher-searching-citizen-scientists Christopher Smith <csmith@willamette.edu>

Wolbachia-infected Ephestia kuehniella

Dear all,

I'm trying to get hold of some (live) Ephestia kuehniella (Mediterranean Flour moths) that are infected with Wolbachia. If anyone is able to send me some, that would be most appreciated. My email address is Z.Lewis@liverpool.ac.uk.

Thanks in advance, and best wishes,

Zen

Dr Zenobia Lewis

Senior Lecturer, Director of Studies, Biological Sciences

@Zen_of_Science

Room G53, Ground Floor, Biosciences Building

School of Life Sciences

University of Liverpool

Liverpool

L69 7ZB

UK

+44(0) 151 795 4384

logos

"Lewis, Zenobia" <Z.Lewis@liverpool.ac.uk>

PostDocs

AMNH NewYork MetabolicNetworkAnalysis

A postdoctoral scholar position is immediately available in the Sackler Institute of Comparative Genomics at the American Museum of Natural History in New York City. The research will involve computational reconstruction of metabolic pathways of ancient organisms using a combination of network analysis and phylogenetics and will involve the development of new computational resources along those lines. The successful candidate will have extensive computational background in network and graph based analysis and in scripting and programming languages (e.g. python, perl, R, C/C++) to complement the team with expertise in biology, genomics, and phylogentics. Additional experience in the development and application of theoretical models to biological problems (e.g. machine learning methods) would also be of interest.

The Sackler Institute of Comparative Genomics is a preeminent center for research, collections, and training in the field of non-human comparative genomics and in the pursuit of seminal research in the study of gene variation, which informs our understanding of the human genome, the evolution and history of life, and the conservation of Earth's biodiversity.

The American Museum of Natural History is a leading research institution with world-class facilities and researchers. It is home to more than 200 scientists who work across the broad disciplines of anthropology, astrophysics, biology, Earth and planetary sciences, and paleontology, as well as to one of the world's most extraordinary collections of specimens and artifacts. Through the Richard Gilder Graduate School, it is the only U.S. museum to award the Ph.D. degree.

Qualifications: PhD in Biology, Bioinformatics, Computational Biology, Computer Science, Physics, or a related degree.

The position is funded for 2 years with a starting salary of $56,000.

Please send a C.V. with a list of recent or relevent publications, a cover letter, and a list of references to jburns@amnh.org and anarechania@amnh.org.

John A. Burns Postdoctoral Fellow Kim Lab American Museum of Natural History Sackler Institute for Comparative Genomics 212.769.5838 jburns@amnh.org

John A Burns <jburns@amnh.org>

ArnoldArboretum 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/ Faye Rosin <frosin@oeb.harvard.edu>

Berlin Fellowship

Fellowships College for Life Sciences - GAIN TIME TO THINK

Wissenschaftskollegzu Berlin - Institute for Advanced Study, Berlin, Germany

Deadline: January 8, 2017

The College for Life Sciences, a junior program of the Wissenschaftskolleg zu Berlin (Institute for Advanced Study), announces the availability of a small number of short-term fellowships for early-career postdoctoral life scientists to live and work in a unique, interdisciplinary environment on the Wissenschaftskolleg's campus. The fellowship enables you to step back from your demanding lab work and teaching duties and provides time to work on your research questions, to develop your career goals, to establish crucial collaborations, and to broadenyour horizon. You will work among leading scientists of all academic disciplines as well as outstanding intellectuals who are Fellows of the Wissenschaftskolleg.

The fellowships are intended for residencies of 3-6 months during the academic year 2017-18. There are no restrictions regarding life science discipline, nationality, or age.Applications from scientists working at institutions in Berlin cannot be taken into consideration.

We offer a stipend covering your prior salary, studio accommodation on the campus of the Wissenschaftskolleg in Berlin, and access to its library and IT services, daily meetings and lively discussions with all Fellows, weekly colloquia, annually changing focus groups on contemporary scientific questions, scientific exchange with the research community of Berlin, Germany and beyond, the possibility to invite your ;scientists of interest to the Wissenschaftskolleg and to organize workshops on scientific topics you are interested in and to invite related scientists.

We do not offer any lab space. We invite applications from post-doctoral researchers andjunior principal investigators (lecturers, junior/assistant professors) from all life science disciplines. If you have been a principal investigator for longer thanfive years, though, you are advised to apply for a regular Fellowship. Application includes a project proposal, a letter of motivation, your CV and publication list.

Please apply here: https://www.wiko-berlin.de/-institution/college-for-life-sciences/ Thank you for posting..

Sincerely

Ulrike Pannasch

Dr. Ulrike Pannasch Wissenschaftliche Koordinatorin/Scientific Coordinator College for Life Sciences Wissenschaftskolleg zu Berlin / Institute for Advanced Study Wallotstr. 19, 14193 Berlin Tel. +49 - 30 - 89 001 - 255 http://www.wiko-berlin.de/institution/college-for-life-sciences/ Ulrike Pannasch <paul@wiko-berlin.de>

Bordeaux France PopulationGenomics

Post doc position in Population Genomics Bordeaux, France

Job description: A two years post doc position is available at UMR BIOGECO. Starting date as soon as possible or as agreed upon.

The general goal of the research will be to conduct genome wide exploration of evolutionary changes that occurred in recent times in European white oaks. Investigations will be conducted on whole genome resequencing data of extant populations sampled along geographic gradients or known historical trajectories. The aim will be to disentangle changes associated to demographic events, admixture with other related species, and natural selection. Special emphasis will be given to the detection of evolutionary changes over short time scales (last 3-4 centuries). This research is part of a larger ERC project investigating rates of genomic and phenotypic changes based on allochronic and synchronic approaches (http://www.treepeace.fr/).

Scientific environment: The working location will be at the BIOGECO research unit (20 km southwest of Bordeaux, France (https://www4.bordeaux-aquitaine.inra.fr/biogeco_eng/). BIOGECO is a joint research unit between INRA and the University of Bordeaux and has long standing experience in studying evolution and genetic variation of forest trees. The research group is multidisciplinary with competences in population and quantitative genetics, ecology, evolution, genomics and ancient DNA. The research environment is international and offers opportunities for interactions with other postdocs and researchers working on similar projects. Pool-seq data, access to the annotated oak genome sequence and access to supercomputation facilities are available to carry out the work.

Required Qualifications: The ideal candidate will have a strong expertise in population genomics and genetics, as well as strong programming, bioinformatics and statistical skills. Previous experience working with genome wide data or whole genome resequencing data is a requirement. Candidates should be fluent in English.

Application: Application with CV, a brief statement of research interests, contact information for two professional references and publication list should be submitted in an electronic form to Dr. Antoine Kremer (antoine.kremer@inra.fr). Review of applications will begin on January 1st. Applications can be accepted until the position is filled. Do not hesitate to contact us for further details or questions. Salary will be determined according to the pay system of INRA, considering qualification and experience.

Examples of recent publications:

Plomion C, Aury JM, Amselem J, Alaeitabar T, Barbe V, Belser C, Berges H, Bodénès C, Boudet N, Boury C, Canaguier A, Couloux A, Da Silva C, Duplessis S, Ehrenmann F, Estrada-Mairey B, Fouteau S, Francillonne N, Gaspin C, Guichard C, Klopp C, Labadie K, Lalanne C, Le Clainche I, Leplé JC, Le Provost G, Leroy T, Lesur I, Martin F, Mercier J, Michotey C, Murat F, Salin F, Steinbach D, Faivre-Rampant P, Wincker P, Salse J, Quesneville H, Kremer A. 2016. Decoding the oak genome: public release of sequence data, assembly, annotation and publication strategies. Molecular Ecology Resources 16: 254-265

Leroy T, Roux C, Villate L, Bodénès C, Romiguier J, Paiva JAP, Dossat C, Aury JM, Plomion C, Kremer A. 2016. Extensive recent secondary contacts between four European white oak species. New Phytologist (In press)

Rellstab C, Zoller S, Walthert L, Lesur I, Bodénès C, Pluess AR, Sperisen C, Kremer A, Gugerli F. 2016. Signatures of local adaptation in candidate genes of oaks (Quercus spp.) in respect to present and future climatic conditions. Molecular Ecology (doi: 10.1111/mec.13889)

See also: http://www.oakgenome.fr/?page_id“ cfirmat <cyril.firmat@inra.fr>

CarnegieMuseumNatHist CuratorAnthropocene

Carnegie Museum of Natural History - Post-Doctoral Fellow and Interim Curator for the Anthropocene

Carnegie Museum of Natural History invites applications for a Post-Doctoral Fellow and Interim Curator for the Anthropocene. The primary responsibility for this position will be to work with the Director, museum senior leadership and science staff, as well as Carnegie Museums of Pittsburgh central staff to develop an intellectual and infrastructural framework for the new Center for Anthropocene Studies. The Center is intended to be interdisciplinary in its foci across art and the humanities with science at its core. The successful candidate will demonstrate a plan for developing a research program that results in publications of high quality and visibility. The position has a limited term of two years, although there is the possibility of extension if the fellow/curator is successful and further funding is developed.

Qualifications: Ph.D. in an area embedded in or cognate to Anthropocene science, while demonstrating a broad awareness of cultural, historical and artistic themes associated with advanced considerations of Anthropocene themes. Prior postdoctoral training or equivalent professional experience is desirable.

For additional information, please visit: www.carnegiemuseums.org/hr and search “anthropocene”. To apply, a letter of application, CV, contact information for three references, statement of research, and statement of curatorial philosophy (including the curator’s role in broader museum efforts) should be emailed to halea@carnegiemnh.org. Review of applications will begin February 1, 2017.

Carnegie Museum of Natural History is one of the four Carnegie Museums of Pittsburgh, with a mission in original scientific research, preservation of collections, and public science education and engagement. The museum has approximately 22 million specimens and artifacts in its collections, making it the 5th largest natural history collection in the US. With access to our 2,200-acre Powdermill Nature Reserve and through collaborations with museum staff, adjacent universities, and museums throughout the world, there is an exceptional opportunity to develop the Carnegie Museum of Natural History as a vibrant hub in a knowledge and inquiry network engaged in understanding human existence, responsibility, and capability at the dawn of the age of the human.

Carnegie Museums of Pittsburgh is firmly committed to equal employment opportunity for all persons without regard to race, color, religion, creed, national origin, ancestry, sex, gender identity or expression, age, marital status, sexual orientation, citizenship status, veteran status, non job-related disability or genetic information as those terms are defined under applicable law.

"Hale, Alison" <HaleA@CarnegieMnh.Org>

CharlesU Prague SexChromosomeEvolution

CharlesU_Prague.Postdoc.SexChromosomeEvolution

Postdoc position in Evolution of sex chromosomes in squamate reptiles

One postdoc position is currently open in the research team of Dr. Lukas Kratochvil, Department of Ecology, Charles University, Czech Republic. The successful candidate will join our current projects on the study of the evolution of sex chromosomes in squamate reptiles with molecular and cytogenetic methods.

Project description: The aim of the project is to examine the evolution of sex chromosomes and their homology based on gene content in selected lineages of squamate reptiles (eg. lizards and snakes). Squamate reptiles possess lineages with either XX/XY, ZZ/ZW or temperature-dependent sex determination. Despite the recent advances in the field, our knowledge about their sex determination systems and sex chromosome homology is limited only to few groups of reptiles (eg. iguanas, advanced snakes), while the majority of reptilian lineages remain unstudied. The successful candidate will collaborate with the other team members and will study the evolution of sex chromosomes in a multidirectional approach, involving cytogenetics (eg. FISH, chromosome painting), molecular genetics (eg. qPCR) and bioinformatics (eg. transcriptomics). More information about our current research activity can be found in the following publications:

https://www.ncbi.nlm.nih.gov/pubmed/27037610
http://www.ncbi.nlm.nih.gov/pubmed/26702042
http://www.ncbi.nlm.nih.gov/pubmed/24433436
Qualifications: The ideal candidate would have a Ph.D. diploma and proven expertise in a related field of biology: evolutionary biology, cytogenetics, phylogenetics, genomics and/or bioinformatics. Previous experience in herpetology is not necessary. The applicant should be scientifically motivated, have good communication skills and demonstrate publication record in reputable journals. High standard of spoken and written English is required.

Application: The applicant should send a short letter explaining his/her background and motivation, full CV and contact information for two references to both Dr. Michail Rovatsos (michail.rovatsos@natur.cuni.cz) and Dr. Lukas Kratochvil (lukas.kratochvil@natur.cuni.cz).

The successful candidate will be financially supported, with a salary sufficient for a comfortable living in Prague, Czech Republic, relevant to qualifications, which will be further increased based on performance.

Prague is often included in the top lists for best cities, considering safety, culture, popular travel destinations and quality of living. Some useful links:

Charles University website: http://www.cuni.cz/UKEN-1.html Faculty of Science, Charles University: www.natur.cuni.cz/en Student life in Prague: http://studyinprague.cz/about-prague/student-life-in-prague/ Cost of living: http://www.studyin.cz/living-costs/ Tourism guide: http://www.myczechrepublic.com/prague/ The position is valid until a suitable candidate is selected and the starting date is flexible, with closest date 1/1/2017. Suitable candidates will be interviewed until January 31th 2017. For any additional information, do not hesitate to write an email (michail.rovatsos@natur.cuni.cz).

Michail Rovatsos

Researcher Department of Ecology Faculty of Science Charles University Vinicna 7, 128 43 Praha 2 Czech Republic

Michail Rovatsos

Researcher Department of Ecology Faculty of Science Charles University Vinicna 7, 128 43 Praha 2 Czech Republic

"Michail Rovatsos, Ph.D." <michail.rovatsos@natur.cuni.cz>

ColoradoStateU PlantGeneticsEvolution

The Sloan Lab at Colorado State University has funding to support a postdoctoral researcher or masters-level research associate in plant molecular genetics and evolution. Specific project goals are flexible and may be tailored to the skills and interests of the researcher. The overarching theme in our lab is the evolution of mitonuclear and plastid-nuclear interactions. We are interested in someone to build off of ongoing and planned experiments that are investigating these interactions through genetic manipulations in both model and non-model plant systems. More information about our lab is available here:

https://sites.google.com/site/danielbsloan/home

We are particularly interested in researchers with experience in genetic transformation and crossing techniques in plant model systems. Interests and experience in computational biology, including genomics, molecular evolution, and population genetics are also desirable. Above all, we are seeking researchers who are enthusiastic about answering biological and evolutionary questions and who will contribute to a positive and collaborative research environment.

Start date is flexible but preferably by July 1, 2017.

For more information or to discuss opportunities, please e-mail Dan Sloan (dbsloan@rams.colostate.edu) and include a CV, a very brief statement of research/career goals, and contact information for at least two references. Inquiries will be evaluated on a rolling basis until a candidate is identified.

Dan Sloan Assistant Professor Department of Biology Colorado State University Fort Collins, CO 80523 USA

dbsloan@rams.colostate.edu

CzechRepublic RepeatomeBioinformatics

In the project "Repeatome dynamics in the earliest evolutionary stages of apomictic plants" funded by the Czech Science Foundation, a

Postdoc Position in Bioinformatics

is available at the Institute of Botany (www.ibot.cas.cz/-en/) of the Czech Academy of Sciences. Project begin is January 2017; the position is for 3 years and shall be filled as quickly as possible, with an option to be prolonged after the end of the project.

The project is aimed at a better understanding of mechanisms underlying the transition from sexual to apomictic reproduction. It brings together an interdisciplinary and international team of researchers who will tackle a complex biological question from various angles (cytogenetics, genomics, embryology, reproductive biology).

Tasks involve the de novo identification and quantification of genomic repeats from high-throughput sequencing data in the non-model hawkweed genus Hieracium in order to investigate genome repatterning following hybridization. The successful applicant will be involved in experimental design and statistical analysis, collaborate with wet-bench biologists and help to integrate the results into the bigger picture.

Prerequisites are a PhD in Biology, Genomics, Bioinformatics or a related field with at least two years of experience in Bioinformatics (preferably with a background in eukaryote genomes), a profound interest in the topic, the capacity to work independently as well as to contribute creatively to a team, and the proven ability to publish in renowned IF journals.

We offer an excellent infrastructure and a friendly working atmosphere in a marvellous environment (Pruhonice Park, UNESCO World Heritage Site, http://-www.pruhonickypark.cz/en/the-pruhonice-park/) in the close vicinity of Prague and an option to become engaged in the future establishment of a central Bioinformatics unit at the Institute of Botany.

For more information, please contact Dr. Judith Fehrer (fehrer@ibot.cas.cz). Applications containing a motivation letter, a short CV, a full publication list and two references should be sent until 15. January to fehrer@ibot.cas.cz.

Dr. Judith Fehrer Institute of Botany Czech Academy of Sciences Zámek 1 25243 Pruhonice near Prague Czech Republic

phone +420 271015415 fax +420 267750031 fehrer@ibot.cas.cz

Fehrer Judith <Judith.Fehrer@ibot.cas.cz>

DalhousieU MicrobialGeneTransfer

11 December 2016

Dear colleagues,

The Archibald Lab is hiring a postdoc to work on experimental and computational aspects of gene transfer in microbial eukaryotes. If you know of anyone please feel free to forward this message.

The lab is located in the Department of Biochemistry & Molecular Biology at Dalhousie University in Halifax, Nova Scotia, Canada. The successful applicant will join an internationally recognized research team embedded within Dalhousie's collaborative and vibrant Centre for Genomics & Evolutionary Bioinformatics (www.cgeb.dal.ca). Expertise in comparative genomics and/or molecular biology is essential.

Interested persons can contact John Archibald for more information (john.archibald[at]dal.ca) or directly submit (i) a complete CV and (ii) the names and contact information of three academic references.

best wishes,

john

John M. Archibald, Ph.D. Distinguished University Research Professor Senior Fellow, Canadian Institute for Advanced Research, Program in Integrated Microbial Biodiversity Department of Biochemistry & Molecular Biology, Dalhousie University Sir Charles Tupper Medical Building 5850 College Street PO BOX 15000 Halifax, Nova Scotia, B3H 4R2, Canada Phone: (902) 494-2536 Fax: (902) 494-1355 Webpage: http://myweb.dal.ca/-jmarchib/ One Plus One Equals One: Symbiosis and the Evolution of Complex Life Oxford University Press, Paperback September 2016

John Archibald <John.Archibald@Dal.Ca>

ETHZurich EvolutionaryMicrobiology

ThePathogen Ecology group at ETH ZuÌrich are looking for a highly motivated postdoctoral researcher to work on a project funded by the Swiss National Science Foundation.

Theproject combines (i) experimental evolution of bacteria exposed to viruses and/or antibiotics, (ii) quantitative analysis of natural and clinical isolates and (iii) development of an experimental system for culturing, manipulating and analyzing enteric bacteria ('model gut'). The postdoc will focus on the 'model gut' subproject. Therefore advanced knowledge of evolutionary microbiology, bacteria-virus interactions and/or gastrointestinal microbiology will be advantageous. Development of this subproject will be done in collaboration with the group of Angus Buckling (University of Exeter, UK). The postdoc will also interact with group members working on other subprojects and have the opportunity to develop new research projects.

Ourgroup is part of the Institute of Integrative Biology (IBZ) in the Department of Environmental Systems Science at ETH ZuÌrich. The institute has three main research themes: ecology, evolution and infectious diseases.

Applicationdeadline: open until filled. Startingdate: as soon as possible. Employmentterm: full time for twoyears. Salary:fixed rate for ETH postdocs (86,300 chf p.a. in the first year).

Toapply send alex.hall@env.ethz.ch a single PDF file with a one-page summary of your research interests and motivation, a CV and publications list plus contact details of three referees.

www.pe.ethz . alex.hall@env.ethz.ch

FloridaStateU EvolutionBehaviorMosquitofish

Postdoctoral Position, Indirect genetic effects in mosquitofish Hughes and Travis Labs Florida State University

We are seeking a full-time postdoctoral scholar to investigate indirect genetic effects and the maintenance of genetic polymorphism in natural mosquitofish populations. We currently have NSF funds to support a postdoctoral research scholar for 2 years, with possibility for extension beyond that. In addition to the funded work, there will be opportunities to develop related empirical or theoretical projects.

The selected postdoc will work at the main FSU campus in Tallahassee, FL, USA, and in nearby field sites. The region is a hotspot for biodiversity and offers ready access to diverse habitats including terrestrial, freshwater, and marine ecosystems, many of which are relatively undisturbed. The postdoc will work closely with both PIs on the project (Joe Travis and Kim Hughes) and with the other members of our labs. There will also be opportunities to interact and collaborate with other members of the Ecology and Evolution group at FSU. This group includes 24 research-active faculty, and has particular strengths in research at the interface of ecology and evolutionary biology.

Requirements: Ph.D. in a relevant field, demonstrated expertise in techniques such as DNA extraction, PCR, and sequence or fragment-length based genotyping, excellent command of spoken and written English, and experience in statistical analysis of complex phenotypic or genetic data.

Additional valuable skills and experiences include: experience with paternity assignment, experience working with live vertebrates in lab or field settings, familiarity with quantitative-genetic methods, expertise in constructing high-throughput sequencing libraries, experience collecting and analyzing behavioral data, and experience mentoring undergraduate research students.

Florida State University, the Department of Biological Science and the Hughes and Travis labs are interested in candidates who are committed to the highest standards of scholarship and professional activities, and to the development of a climate that supports equality and diversity. Florida State University is an affirmative action/equal opportunity employer.

Salary: $47,658-$49,000 USD plus benefits

Start date: Position available Feb 1, 2017 or until filled. Evaluations of applications will begin Jan. 12, 2017

Duration: The appointment can be up to 2 years, but will be made on a yearly basis given satisfactory progress.

To ensure full consideration please email the following to Kim Hughes (kahughes@bio.fsu.edu) or to Joe Travis (travis@bio.fsu.edu) by Jan 12, 2016: (1) a cover letter, (2) an up-to-date CV, and (3) names of 3 mentors/colleagues from whom you can request letters of support. The cover letter should describe your previous research and training and your qualifications for the position as described in this advertisement. The letter should also explain how this postdoctoral position will further your long-term research/career aspirations. The email subject line should read: “Postdoc_GambusiaProject”.

Kimberly A. Hughes Professor and President, Society for the Study of Evolution Department of Biological Science Florida State University 319 Stadium Drive Tallahassee, Florida 32306-4295

Ph: 850-645-8553 FAX: 850-645-8447 Office: 4062 King Life Sciences Building http://www.bio.fsu.edu/faculty-hughes.php “Please note: Florida has very broad public records laws. Most written communications to or from state/university employees and students are public records and available to the public and media upon request. Your e-mail communications may therefore be subject to public disclosure.”

Kimberly Hughes <kahughes@bio.fsu.edu>

Geneva EvolutionaryEcologyParasites

Subject area

Evolutionary and ecological processes driving parasite speciation

Description of the project:

This is a project on how species radiations affect interspecific interactions, such as host- parasite associations. Analogous to how a diverse habitat can support a diverse community of free-living species and lead to species radiations, a species-rich or genetically divergent pool of hosts may provide variable but resource-rich habitats that may promote diverse parasite communities and in some instances, parasite species radiations.

The aims of this project are: 1. to test general ecology theory regarding whether parasite diversity follows the habitat heterogeneity hypothesis 2. to develop general theory for the interplay of ecological and evolutionary processes promoting parasite diversification in an inter-species interaction context

The model system used to address the theoretical framework above will be whitefishes and their parasite communities in Swiss and Scandinavian lakes.

A major part of the research will involve fieldwork in Norwegian and Swiss lakes, parasitological examination of fish and morphological characterisation of parasites. This will be followed by community ecology analyses, extensive population genomic [single- nucleotide polymorphisms (SNPs)] of parasites and phylogeography analyses.

The position involves working closely with field assistants and students at different institutions.

Skills desired and experience

The candidate will hold a PhD in biological science and possess the following skills and experience (E=essential, DÃsirable):

-

Fieldwork, preferably in freshwater environments (E) -

Knowledge of parasitology and parasitological dissections (E) -

Library preparation for RAD-seq or other next generation technologies (E) -

SNP analyses, bioinformatics, data management and building workflows (D) -

Experience with population genetics and phylogenetics analyses (E) -

Experience in using R for statistical analyses (D) -

Experience using cloud computing (D) -

Good interpersonal skills (E) -

Able to deal effectively with international and national collaborations (E) -

Demonstrated experience in management (D)

Job position

Postdoctoral researcher based at the Natural History Museum of Geneva, in close collaboration with the UNIGE and EAWAG. Duration: Up to 2 years (1 year, renewable once); salary 80K CHF/year. Open to CH and EU citizens.

Starting date 1 July, 2017

How to apply

Please send a motivation letter together with your full CV and the name and contact details of two preferred referees to Isabel.Blasco-Costa[at]ville-ge[dot]ch by January 20, 2017

isa.blasco.costa@gmail.com

Glasgow Evodevo Epigenetics

We seek a theory-driven postdoc to join us to focus on questions related to evolutionary developmental biology and genomics including the genetic and epigenetic basis of phenotypic change. We offer a highly interdisciplinary group and generous funding support from a recently awarded NERC Highlight topics grant to Dr Kevin J. Parsons (PI), Prof. Neil B. Metcalfe, Dr Shaun S. Killen and Dr Jan Lindstrom.

The project provides an opportunity to take evo-devo and genomics in a new direction by investigating the impact that long-term increases in temperature can have on evolution. The postdoc will be in charge of leading and applying large-scale population genomic and QTL mapping approaches to sticklebacks that have evolved within geothermally-heated and ambient temperature locations in Iceland. A substantial portion of this research will also involve the use of genomics to understand patterns of methylation in response to temperature in both wild and lab-reared populations. While these genomic approaches will be used, the lab is phenotype-first orientated and works at the intersections of ecology, evolution, physiology, and development. The postdoc will therefore also have the opportunity to take part in the design of experiments used to assess developmental changes in a range of phenotypes.

You will have previous postdoc experience or be near to completing a relevant PhD and be experienced with genomics, developmental genetics, and/or epigenetics. Interest and experience with questions surrounding parallel evolution and phenotypic plasticity would be an asset. As part of a team funded by this NERC grant, you will work closely with another postdoctoral scientist who will focus on running lab experiments and behavioural assays, and a full-time technician who will aid in the running of a breeding programme and lab work.

Passion for research, team spirit and enthusiasm are essential. Our team is multidisciplinary with additional major projects funded by the European Research Council (ERC) and NERC. Additional PhD student projects in the lab of the PI involve collaborations with engineers, statisticians, and physicists demonstrating the highly active and collaborative research environment in the University of Glasgow. Further information on the post can be obtained from Dr. Kevin Parsons (kevin.parsons@glasgow.ac.uk). Formal applications are due by January 8th, 2017, and can be made at:

reference # 015558 http://www.gla.ac.uk/about/jobs/vacancies/ Dr. Kevin Parsons Lecturer, Institute of Biodiversity, Animal Health, and Comparative Medicine University of Glasgow https://sites.google.com/site/kevinparsonslab/home http://www.gla.ac.uk/researchinstitutes/bahcm/staff/kevinparsons/ Dr. Kevin Parsons Lecturer, Institute of Biodiversity, Animal Health, and Comparative Medicine University of Glasgow https://sites.google.com/site/kevinparsonslab/home/people http://www.gla.ac.uk/researchinstitutes/bahcm/staff/kevinparsons/ Kevin Parsons <Kevin.Parsons@glasgow.ac.uk>

GreifswaldU EvolutionaryBiomathematics

Dear Evoldir members,

I currently invite applications for a postdoc position in my working group, starting asap, but the starting date is negotiable.

It is a 100% position (paid according to German TVL 13) with 4 hours per week teaching obligation. If the candidate prefers a part-time position with reduced teaching load, this would also be possible. Teaching may include lectures if the candidate wants to gain experience, but will mainly consist of tutorials (4 hours per week amount to two tutorials per week during the semester; no teaching is done during the long summer break from mid-July to mid-October and from the end of January to early April).

Research in my group is focussed on biomathematics with a special interest in mathematical phylogenetics and population genetics, i.e. evolutionary research from a mathematical perspective. The ideal candidate has a strong background in mathematics and / or theoretical computer science, preferably with some biological pre-knowledge (and, if not, at least a strong interest in biology in general and evolution in particular). Mathematical areas needed for our research include, but are not limited to, graph theory, probability theory, combinatorics and complexity theory. Programming skills in at least one mathematical programming language (such as Mathematica, Maxima, Matlab, Maple or R) are required; additional programming skills are also desirable.

Knowledge of the German language is desirable, but is not a must at first (teaching at the Master's level can be done in English). Greifswald university offers affordable German language courses for researchers. However, the candidate must be proficient in both written and spoken English.

The offer: - PostDoc position for 2 years with a possible extension if funding permits.

- No pre-set fixed project, i.e. the work focus is negotiable and will be chosen to match the candidate's interests and ideas. - 4 hours teaching duties per week. - The application deadline is January 31st 2017 (starting date flexible, but as soon as possible), but the offer will be kept open until a suitable candidate is found.

- A small but highly specialized maths institute with a renowned research focus on biomathematics, located in Greifswald in North-Eastern Germany, directly at the Baltic Sea with lots of nearby beaches and generally good living quality.

For more information, do not hesitate to contact me: mareike.fischer@uni-greifswald.de or to read the official job offer online (in German): https://www.uni-greifswald.de/universitaet/information/stellen ausschreibungen/oeffentliche-stellenausschreibungen/wissenschaftliches-personal/institut-fuer-mathematik-und-informatik-16sa34/

Please send your applications electronically to mareike.fischer@uni-greifswald.de IN A SINGLE PDF FILE and refer to job number 16/SA34.

Best wishes,

Mareike Fischer

Prof. Dr. Mareike Fischer Biomathematics and Stochastics Institute for Mathematics & Computer Science Ernst-Moritz-Arndt University Walther-Rathenau-Str. 47 Office 3.15 17487 Greifswald GERMANY +49 (0) 3834 86 46 43 mareike.fischer@uni-greifswald.de

Mareike Fischer <email@mareikefischer.de>

IndianaU BehavioralPlasticityEvolution

Postdoc: IndianaU.BehavioralPlasticityEvolution

A postdoctoral position is available in the laboratory of Kimberly Rosvall, Department of Biology, Indiana University, Bloomington. Our lab investigates the genomic and physiological bases of behavioral plasticity, and how these mechanisms change over evolutionary time. We approach these questions by combining conceptual and analytical tools from animal behavior, neuroendocrinology, evolutionary ecology, physiology, and genomics, almost entirely by studying free-living songbirds. We are especially interested in hormonal and genomic mechanisms of social competition and aggression, how they differ between males and females, and how they are shaped by experience. We are seeking a candidate to develop an original research project within these areas of research.

For the position, we seek a collegial and intellectually driven individual with a recent Ph.D. in animal behavior, behavioral genomics, behavioral endocrinology, or a related field. A strong background in animal behavior is essential. Experience with RNA/DNA extraction, qPCR, avian neuroanatomy, EIA, avian field ecology, and/or genomic/informatic skills is strongly desired, but relevant training will be provided as necessary. The position will be renewed annually for two years, assuming sufficient progress, with the potential to extend for a third year. Salary will be commensurate with experience, and full benefits are included.

To apply, please submit (i) a letter of application, (ii) a full CV, (iii) a statement of research interests, and (iv) contact information for three references electronically to http://indiana.peopleadmin.com/postings/3259 or send cover letter, C.V., statement of research interests & contact info for 3 references to Kimberly Rosvall, 1001 E. 3rd St., Bloomington, IN 47405 (email preferred: krosvall@indiana.edu).

Review of applications will start January 22, 2017 and will continue until the position is filled. The exact start date is flexible, but could begin as early as March 2017 or as late as Fall 2017. Inquiries about the position can be directed to Kimberly Rosvall (krosvall@indiana.edu). Additional information about research in the Rosvall lab can be found at http://www.indiana.edu/˜krosvlab/ . Bloomington is a vibrant college town located in scenic southern Indiana, close to several natural parks and wilderness areas, and it enjoys a local culture exceptionally rich in music, art, and theater. 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.

– Kimberly Rosvall, Ph.D. Assistant Professor Indiana University Jordan Hall A318A, 812-856-2375 http://www.indiana.edu/˜krosvlab/ Kimberly Rosvall <krosvall@indiana.edu>

LeedsU PlantFungiSymbiosis

Leeds University - Plant-fungal physiology

Fixed Term for 3 years, latest start date 16 January 2017 Project Title: Shifting symbiotic scenarios at the dawn of land plant- fungus associations

We are looking for a highly motivated and enthusiastic postdoctoral researcher for this exciting NERC-funded post as part of a multidisciplinary team of scientists from the University of Leeds, Kew Royal Botanic Gardens, the Natural History Museum in London, University of Sheffield and the Sainsbury Laboratory in Cambridge.

Working as a key member of the research team, you will be based in the laboratory of Dr Katie Field (School of Biology) and undertake cutting-edge research to uncover the functioning of symbiotic fungal associations in early diverging clades of land plants. You will be responsible for growing and maintaining plants in controlled environment growth chambers and in axenic/monoxenic cultures, managing experiments using isotope tracers and analysing large biological datasets. You will be highly motivated and be able to manage multiple tasks, with a strong ability to assimilate and evaluate the relevant literature and write high quality, scientific papers.

You will have a PhD (or be close to completion) in plant science or plant/mycorrhizal physiology or a related discipline. You should have strong analytical and experimental skills and have experience in plant biology and physiology and/or biochemistry. You must have the ability to work well independently and as part of team, together with excellent time management, laboratory and communication skills.

Informal enquiries may be made to Dr Katie Field, tel +44 (0)113 343 2849, email K.Field@leeds.ac.uk

Interviews to held on the 5 or 6 January 2017

https://jobs.leeds.ac.uk/vacancy.aspx?ref=FBSBY1058 "m.bidartondo@imperial.ac.uk" <m.bidartondo@imperial.ac.uk>

LundU EvolutionaryBiology

Dear all,

A 12 month position as a research in Evolutionary Ecology is open at Lund University. Topic: Evolution in variable environments, Phenology in interactive communities

Please find more details here: https://lu.mynetworkglobal.com/en/what:job/jobID:124855/ Best, Jörgen Ripa

Jörgen Ripa Theoretical Population Ecology and Evolution Group Dept. of Biology, Lund University, Sweden Sölvegatan 37, SE-223 62 Lund, Sweden phone: +46-46-222 3770, +46-70-999 3570 email: jorgen.ripa@biol.lu.se<mailto:jorgen.ripa@biol.lu.se> www: http://www.biology.lu.se/jorgen-ripa Jörgen Ripa <jorgen.ripa@biol.lu.se>

MonashU MitochondrialGenomics

Postdoctoral position in evolutionary genomics / evolutionary ecology the role of the mitochondrial DNA in evolutionary adaptation.

Monash University Melbourne Australia

The Opportunity

Research in Damian Dowling's laboratory is focused on the role the mitochondrial genome plays in evolutionary adaptation and in the evolution of sex differences. Maternal inheritance of the mitochondrial genome renders the mitochondrial DNA vulnerable to the accumulation of mutations that are harmful to males, but neutral or beneficial to females.

We seek a talented and highly-motivated postdoctoral researcher to join our laboratory group, to study the contribution that mitochondrial genetic variation makes to mediating sex-specific trajectories of life-history evolution. The project will integrate experimental techniques in evolutionary ecology, genomics and evolutionary physiology.

As the successful candidate, you will have a PhD degree, a record of publication in international journals, and strong quantitative or bioinformatic skills. You will have opportunities to develop and pursue your own research interests within the bounds of the advertised project, and to co-supervise undergraduate and Master's level research projects within the Dowling group.

The position is a full-time, fixed-term appointment available for 24 months. Flexible working arrangements may be negotiated.

The job description, complete with the position description, and instructions on how to apply, can be found at:

http://careersmanager.pageuppeople.com/513/cw/en/job/555895/research-fellow-mitochondrial-genetic-variation Please direct enquiries to Dr Damian Dowling

damian.dowling@monash.edu

The closing date for applications is Wednesday 18th January 2017, 11:55 pm AEDT.

Information about Damian Dowling's lab is available at:

http://www.damiandowlinglab.com/index.html Five publications from our lab that are relevant to this position:

1. Innocenti P, Morrow EH, Dowling DK (2011) Experimental support for a sex-specific selective sieve in mitochondrial genome evolution. Science 332, 845-848.

2. Reinhardt K, Dowling DK, Morrow EH (2013) Mitochondrial replacement, evolution, and the clinic. Science 341, 1345-1346.

3. Camus MF, Wolf, JBW, Morrow EH, Dowling DK (2015) Single nucleotides in the mtDNA sequence modify mitochondrial molecular function and are associated with sex-specific effects on fertility and aging. Current Biology 25, 2717-2722.

4. Camus MF, Clancy DJ, Dowling DK (2012) Mitochondria, maternal inheritance and male aging. Current Biology 22, 1717-1721.

5. Yee WKW, Sutton KL, Dowling DK (2013) In vivo male fertility is affected by naturally occurring mitochondrial haplotypes. Current Biology 23, R55-R56.

Information about Monash University

Currently ranked 74th in the Times Higher Education World University Rankings, Monash University is a member of Australia's "Group of Eight" a coalition of research-intensive universities, and is internationally recognized for excellence in research and teaching. The School of Biological Sciences (http://monash.edu/science/about/schools/biological-sciences/) is home to a collegial and world class research environment, with key strengths in evolutionary ecology and genomics.

Melbourne

Monash is located in Melbourne, a vibrant cultural and recreational centre, and is consistently rated one of the world's most liveable cities (http://en.wikipedia.org/wiki/World's_most_livable_cities)

"damian.dowling@monash.edu"
<damian.dowling@monash.edu>

OIST Japan InsectEvolutionAndGenomics

The Okinawa Institute of Science and Technology Graduate University (OIST) is a model for change in education and research with the best international graduate students, working side by side with world-class faculty in modern well-equipped laboratories. Beautifully situated on the island of Okinawa, OIST relies on a cross-disciplinary approach, with an emphasis on creativity and exchange, to offer unique, individualized graduate training. OIST is a university with no departments, eliminating artificial barriers between people working in different fields, but many nationalities, with students and faculty being attracted from all over the world. Concentrating initially on Neuroscience, Molecular Sciences, Mathematical Sciences, Environmental and Ecological Sciences and Physical Sciences, OIST is bringing some of the best brains in the world to Okinawa to transform the way science and education is done in the global academic world.

Position summary:

The Evolutionary Genomics Unit is seeking for a postdoctoral researcher with skills in insect ecology and evolution, and with ability to analyze high throughput sequencing data. The researcher will work around on one or more of these promising topics: molecular evolution of the symbiosis between insects and microorganisms, molecular phylogenetic of insects, historical biogeography of termites, and molecular mechanisms of insect defense.

Position:

The Evolutionary Genomics Unit is a research group recently established at OIST with interests in evolution of insects in general. Our main research topics include molecular evolution of the symbiosis between insects and microorganisms, molecular phylogenetic of insects, historical biogeography of termites, and molecular mechanisms of insect defense. We address all these themes using high throughput sequencing. We are looking for a postdoctoral candidate with extensive experience in high throughput sequencing and who is keen to work on one of our insect models: cockroaches or termites. The candidate is expected to work in collaboration with members of the Evolutionary Genomics Unit, and she/he will be given relative independence to develop her/his own research within the frame of the Unit's research agenda.

Some possible research topics include, but are not restricted to:

- Studying the role of termite gut microorganisms in soil-feeding termites using metagenomic analyses. Many species of termites feed on soil but they are not studied as intensively as wood-feeding termites. Metagenomics can help us understanding the function of these microorganisms.

- Studying the evolution of genome reduction in the cockroach endosymbiont Blattabacterium. Most cockroaches are associated with Blattabacterium, a bacterium that recycles nitrogen wastes and provides amino acid to their host. The number of genes varies between strains of Blattabacterium, and one question is therefore what are the factors responsible of gene erosion in some strains?

- Studying the historical biogeography of termites using molecular phylogenies. Termites are distributed worldwide and often make up a large part of animal biomass in the tropics. We are studying the origin of their distribution using mitochondrial genome phylogenies, to determine the timing and direction of their spread across the globe.

Working Location:

Onna-son, Okinawa, Japan

Responsibilities:

1. Carrying out lab experiments
2. Data analysis
3. Writing papers
4. And possibly carrying out fieldwork

Qualifications:

(Required)

1. Ph.D. in Biological Science, with relevant research experience

2. Proficiency in written and spoken English

3. Good track record of publications

4. Ability to analyze high throughput sequencing data

5. Highly motivated and with strong social skills

(Preferred)

1. Previous fieldwork experience, especially of insect sampling

2. Experience with insect breeding

Term:

Full-time, fixed term appointment for 2 years. Contract initially with 3 month probationary period (inclusive). This contract may be renewed.

Working hours:

9:00-17:30 (Discretionary)

Compensation:

In accordance with the OIST Employee Compensation Regulations

Benefits:

- Relocation, housing and commuting allowances

- Annual paid leave and summer holidays

- Health insurance (Private School Mutual Aid http://www.shigakukyosai.jp/), welfare pension insurance (kousei- nenkin), worker's accident compensation insurance (roudousha-saigai-hoshou- hoken)

Submission Documents:

- Cover letter in English

- Curriculum vitae in English, including a list of publications

- Names and contact information of 3~5 referees, one of which should be a previous employer

* Please be sure to indicate where you first saw the job advertisement.

Starting Date:

May-June, 2017

Application Due Date:

Applications are due by January 10, 2017

Application Address:

Please submit all required application materials by email to:

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

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PasteurInst BacterialEvolutionaryGenomics

POSTDOCTORAL POSITIONS IN MICROBIAL EVOLUTIONARY GENOMICS

Two postdoc positions for highly motivated and talented young researchers are available in the Microbial Evolutionary Genomics unit (head: Eduardo Rocha) of the Pasteur Institute, Paris, France. Our lab has been at the forefront of the study of mobile genetic elements (MGE) using comparative genomics and is part of the C3BI ambitious program to create an interdisciplinary center focusing on quantitative biology in the Institute.

Topic. The exact projects for these two postdoc positions are adaptable to the candidate's interests, but should use comparative genomics, population genetics, metagenomics, and/or phylogenomics to tackle: - What do MGE bring to bacterial genomes in the short and in the long term? - How to identify the mechanisms of mobility and stabilization of MGE? - What is the interplay between MGE and bacteria in microbiomes?

Representative publications: Nogueira, Curr Biol, 09; Guglielmini, PLoS Genet, 11; Treangen, PLoS Genet, 11; Bobay, PNAS, 14; Remigi, PLoS Biol, 14; Oliveira, PNAS, 16; Touchon, ISMEj, 16.

Profiles. We invite young researchers with PhDs in domains relating to bacterial evolution and genomics with some computational or quantitative background, including programming skills (shell, R, and/or Python), and experience in large-scale sequence analysis. A taste for collaborations and the ability to discuss with a variety of researchers are strictly necessary.

Conditions. The positions are funded by ANR and ERC projects. The salary corresponds to the standard in France (2100€to 2600€after tax, depending on the experience), including extended health coverage. The contracts will be for 18 months minimum, renewable when successful. The candidates must have passed their PhD less than 5 years ago. The position is available immediately but the starting dates are negotiable up to September the 1st of 2017.

Application: Send a single pdf document with a detailed CV (2-3 pages, with lists of publications, presentations, and computational skills), a cover letter explaining your research interests, projects, and motivations to join us (1-2 pages), and three references who we'll contact to obtain advices on your application. Deadline: January 10th, 2017.

Contact: For information on how to contact us and to know more of our work check the lab web-site: https://research.pasteur.fr/en/team/-microbial-evolutionary-genomics/ Eduardo Rocha <erocha@pasteur.fr>

Rockville Maryland PhylotasticProject

post-doc position with Phylotastic project (Rockville, MD)

Applications are invited for a Postdoctoral Associate position with the Stoltzfus group at the University of Maryland Institute for Bioscience and Biotechnology Research (IBBR) in Rockville, MD.

While experts continue improving the Tree of Life, the focus of the Phylotastic project (www.phylotastic.org) is on getting this knowledge into the hands of scientists, educators, and the general public, so that they can get online species trees as easily as they get online driving directions. Based on a design initially prototyped at a NESCent hackathon, NSF has funded this project to develop an open, distributed system of web services to provide convenient, computable access to ToL knowledge. The successful applicant will join a distributed virtual team with key personnel from IBBR, NMSU, UTK, OpenTree and GlobalNames. Responsibilities will include software design, development, and evaluation, with opportunities for research on topics such as the quality and coverage of available phylogenetic and taxonomic resources.

For the job requirements and application instructions, please see https://ejobs.umd.edu/postings/48392 . The position is available now: applications will be considered immediately, until a suitable candidate if found. If the aforementioned web site is still available, the position is still open. Pre-submission inquiries to arlin@umd.edu are encouraged.

Please feel free to redirect this message to anyone who might be interested. Thanks,

Arlin Stoltzfus

Arlin Stoltzfus (arlin@umd.edu) Research Biologist, NIST; Fellow, IBBR; Adj. Assoc. Prof., UMCP IBBR, 9600 Gudelsky Drive, Rockville, MD, 20850 tel: 240 314 6208; web: www.molevol.org Arlin Stoltzfus <arlin@ibbr.umd.edu>

Rockville MD MutationInformaticsEvol

The Stoltzfus group at IBBR is looking for a post-doc interested in computational work in a relevant area of molecular evolution, evolutionary genetics, or informatics. This position is available through a competitive fellowship offered by the US National Research Council (http://sites.nationalacademies.org/pga/rap/). Awardees must hold U.S. citizenship, and have held the Ph.D. < 5 years at time of application. The award is very generous ($67K plus $3K travel allowance), the location is Rockville (MD), and the time-period is 2 years.

The application requires a brief research proposal that reflects a plan of your own, or a plan that we develop together. Especially welcome are proposals that relate to mutation-biased evolution, following previous work [1-3], or anything that leverages a valuable unpublished resource (some of it used in [2]) consisting of carefully vetted data on fitness effects of mutations from high-throughput mutation-scanning studies (over 100K mutations), classic DFE studies, and evolution experiments. I welcome anything that supplements the Phylotastic project [10] (http://www.phylotastic.org), particularly a system to access fossil data and use them in calibrations via methods such as [5]. I welcome proposals for other computer-based work in molecular evolution or evolutionary genetics [1-8].

The upcoming deadline for proposals is February 1, 2017 (there is another deadline August 1). If you are interested, contact me with a brief introduction, and we'll go from there.

Arlin Stoltzfus (arlin.stoltzfus@nist.gov)

Research Biologist, NIST (Genome-scale Measurements; Office of Data & Informatics)

Fellow, IBBR; Adj. Assoc. Prof., UMCP; IBBR, 9600 Gudelsky Drive, Rockville, MD, 20850 tel: 240 314 6208; web: www.molevol.org 1. Stoltzfus A, McCandlish DM. (in progress) Mutation-biased adaptation in natural cases of parallel evolution.

2. Stoltzfus A, Norris RW. 2016. On the Causes of Evolutionary Transition:Transversion Bias. Mol Biol Evol 33:595-602.http://mbe.oxfordjournals.org/content/33/3/595.abstract 3. Stoltzfus A, Yampolsky LY: Climbing mount probable: mutation as a cause of nonrandomness in evolution. The Journal of heredity 2009, 100(5):637-647. http://jhered.oxfordjournals.org/content/100/5/637.full.pdf 4. Stoltzfus A: Constructive neutral evolution: exploring evolutionary theory's curious disconnect. Biology direct 2012, 7(1):35. http://www.biologydirect.com/content/7/1/35 5. Norris, R., C.L. Strope, D.L. McCandlish, and A. Stoltzfus. Bayesian priors for tree calibration: Evaluating two new approaches based on fossil intervals. http://biorxiv.org/content/early/2015/01/24/014340 6. Stoltzfus A, Yampolsky LY: Amino Acid Exchangeability and the Adaptive Code Hypothesis. J Mol Evol 2007, 65(4):456-462.

7. Yu G, Stoltzfus A: Population diversity of ORFan genes in E. coli. Genome Biology and Evolution 2012.

8. McCandlish, D. M., and A. Stoltzfus. 2014. Modeling Evolution using the Probability of Fixation: History and Implications. Q Rev Biol. 89(3):225-52. http://www.ncbi.nlm.nih.gov/pubmed/25195318 9. Vos RA, et al: NeXML: Rich, Extensible, and Verifiable Representation of Comparative Data and Metadata. Systematic Biology 2012, 61(4):675-689.

10. Stoltzfus, A., H. Lapp, N. Matasci, et al. 2013. Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. BMC Bioinformatics 14:158. http://www.biomedcentral.com/1471-2105/14/158 Arlin Stoltzfus <arlin@ibbr.umd.edu>

Southampton UK 2 ModellingEvodevo

Postdoctoral Research Fellows in Modelling Evolutionary Processes (eco-evo-devo) (2 posts)

Dept Computer Science/Institute for Life Sciences University of Southampton, UK

We welcome applications for two postdoctoral researchers in the area of 'evolutionary systems biology' at the lab of Richard Watson at the University of Southampton. Two positions are available, each for a duration of two years, starting June 1st 2017.

The positions are part of a (7.7M) umbrella project which aims to put to the test the predictions of the extended evolutionary synthesis (Laland et al. 2015, PRSB, 282:1813). The two positions available at Southampton will build on recent developments unifying evolutionary theory with learning theory (Watson & Szathmary, 2016, TREE, 31(2), 147-157). This work converts theoretical tools of learning systems, already well-developed in computer science, to deepen and expand our understanding of natural evolution. Both positions will use computational and/or mathematical modelling to explore the adaptive capabilities of different functional processes and different assumptions about the processes of and feedbacks within natural selection: the selective conditions in which it takes place, the variation on which it can act, and the heritability of that variation. We focus on modelling how these components of the Darwinian Machine (i.e. selection, variation and inheritance) change over time as a function of past evolution. Themes addressed within these projects include:

* The evolution of developmental organisations, plasticity, and evolvability (evo-devo). * The evolution of ecological organisations, collective function and niche construction in ecosystems (evo-eco). * The evolution of reproductive organisations and transitions in individuality (evo-ego).

Co-investigators include John Odling-Smee (Oxford), Michael Wade (Indiana), Andrew Gardner (St Andrews), Charlie Cornwallis (Lund), Kevin Laland (St Andrews), Gunter Wagner (Yale) and Tobias Uller (Lund). As a part of this team, the candidates will also work closely with several PhDs dedicated to this project and on related projects.

The successful candidates will build mathematical/simulation models to develop our understanding of how ecological, developmental and reproductive feedbacks alter evolutionary dynamics and test the utility of learning theory to characterise them. Appropriate skill sets include gene-expression dynamics/gene-regulation network modelling, ecological dynamics/community network modelling, theoretical population genetics, mathematical modelling of biological evolution, social evolution theory, comparative phylogenetics, theoretical quantitative genetics, adaptive dynamics, evolutionary game theory, computational individual-based modelling, complex adaptive systems, algorithmic/functional modelling of evolutionary adaptation.

Applicants must have a PhD in a relevant subject and be capable of building bridges that link between evolutionary biology and computer science. For example, i) A PhD in theoretical evolutionary biology (e.g. evolutionary systems biology, theoretical population genetics, mathematical biology, social evolution theory), with strong mathematical skills and experience in simulation modelling/programming, or ii) A PhD in computer science/maths/physics (e.g. complex systems/dynamical systems modelling, machine learning, optimisation) with strong knowledge/experience of working on applications in theoretical evolutionary biology.

Applications must include a CV, publications list, the names of three referees and a covering letter explaining your current interests and relevant background.

Salary range 29,301 to 36,001 per annum, depending on experience. Full Time Fixed Term 2 years Closing Date: Sunday 29 January 2017 Reference: 811616FP

Further information: - http://users.ecs.soton.ac.uk/-raw/PostDocAdvertWatsonEES.htm - https://-jobs.soton.ac.uk/Vacancy.aspx?ref=3D811616FP Dr. Richard A. Watson Associate Professor Institute for Life Sciences/Electronics and Computer Science, University of Southampton http://www.ecs.soton.ac.uk/people/-raw R.A.Watson@soton.ac.uk

R.A.Watson@soton.ac.uk

TexasTechU PlantFungalInteractions

A Postdoctoral Research Associate positon is available in the Sharma Lab at Texas Tech University in Lubbock, Texas, U.S.A. We seek a highly motivated individual with a Ph.D. to participate in an NSF funded project (http://www.nsf.gov/awardsearch/-showAward?AWD_ID=1355155) that is exploring the role of plant-fungal interactions in explaining plant species distributions in a tropical rainforest in Costa Rica. The research team includes scientists from the University of New Mexico, the University of Hawaii, and the University of Costa Rica. This position is based in Lubbock, TX, but intense field work will be required during the rainy season in Costa Rica (typically 3-4 weeks per year).

Competitive candidates will possess the following attributes: 1. A record of achievement in fungal molecular ecology, orchid mycorrhizal ecology, metagenomics, community ecology, evolutionary ecology, and / or ecological phylogenetics.

2. Extensive laboratory molecular ecology experience and strong quantitative analytical skills (bioinformatics and multivariate statistical analyses).

3. Demonstrated proficiency in communicating research results (i.e., peer reviewed publications and scientific presentations).

4. Strong time management and organizational skills, with an ability to manage a number of competing priorities.

5. Enthusiasm for intense work schedules in the laboratory and in challenging field conditions. Strong capacity to undertake lab work independently and also interact productively with project PIs and personnel.

6. Leadership and initiative in developing creative and relevant research proposals and projects.

Salary: Competitive and commensurate with experience

Duration: Two+ years, but contingent upon satisfactory research performance.

Application: Please submit the following in a single PDF file to jyotsna.sharma@ttu.edu. Subject line of the e-mail and the PDF file name should read - 'Applicant last name_postdoc' 1. Cover letter 2. A brief description of past research accomplishments and future research goals (under two pages) 3. Curriculum Vitae along with reprints of no more than four most relevant publications 4. Names and contact information for three academic references, including the Ph.D. advisor.

Timeline: Review of applications will begin on 20 January 2017 and will continue until the position is filled. The targeted start date is 15 March 2017, but is somewhat flexible. Strong applicants will be contacted to schedule an informal Skype interview.

"Sharma, Jyotsna" <jyotsna.sharma@ttu.edu>

UAngers France RosaBioinformatics

Call for applications for a 17 months Postdoctoral Fellowship on "Evolution of genomes in the genus /Rosa/" at the Research Institute in Horticulture and Seeds (Angers, France)

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A 17-months postdoctoral researcher position is available at the University of Angers (France). The project is a collaboration between the "Research Institute of Horticulture and Seeds" in Angers, astride two teams "Genetics and Diversity of Ornamentals" (GDO, http://www6.angers-nantes.inra.fr/irhs_eng/-Research/GDO) and "Bioinformatics" (BioInfo, http://www6.angers-nantes.inra.fr/irhs_eng/Research/-BioInfo), and the group of Pr Thomas Debener from the "Institute for Plant Genetics" at the Leibniz University of Hannover (Germany; http://www.genetik.uni-hannover.de/index.html?&L=3D1). The project will be a bio-informatic analysis of the evolution of genomes in the genus /Rosa/, at two levels: (/i/) the research of structural variants (SVs), and (/ii/) the study of the evolution of resistance gene families (see details below). Applications are open for candidates who did not have spent more than 12 months in France within the last 3 years immediately prior to the expected date of recruitment. The net salary (after taxes) is 2409.58 /month. The opportunity to apply for AgreenSkills programmes (https://www.agreenskills.eu/) may allow to increase this salary. The beginning of the contract is expected for February or March 2017. The postdoctoral researcher will be based in Angers, regularly cited as the most pleasant city to live in France, and at proximity to the Loire Valley. Travels are planned between Angers and Hanover.

*_Summary of the project: _*The rose bush is the most economically important ornamental plant and the model plant for many studies about ornamental traits (flowering, fragrance, disease resistance). The rose bush, constituting the genus /Rosa/, has a complex evolutionary history with interspecific hybridization events and polyploidizations. Little information about these events is presently available, mainly hypotheses drawn from sparse molecular markers. Recently, as part of an international consortium, co-coordinated by the GDO team, the first version of the genome sequence of a variety of rose (/Rosa chinensis/ cv. 'Old Blush') has been obtained. In this genomic context, we propose to study the evolutionary history of the genus /Rosa/ by resequencing different species of the genus /Rosa/. *The objective is to understand the evolution of genomes in the genus /Rosa/*, and especially to focus on the processes that led to the creation of wild species, including polyploid ones, which are at the base of cultivated modern roses. From short reads (paired-end) obtained from different representative /Rosa/ species involved in cultivated rose breeding, (/i/) _the research of structural variants (SVs as insertions, deletions, duplications, inversion, translocations)_, and (/ii/) _the study of the evolution of resistance gene families_ will be conducted.

//

*_Mission of the postdoctoral fellow_*://The//production of raw reads will be done before the postdoc arrival. The hired postdoc with a strong background in bioinformatics or genome analysis will make a survey of the best methods to analyze structural variations in rose genomes. He/she//will then be in charge of the computer bio-analyses to research the structural variants and to study gene family evolution.

*_Expected skills:_*The desired applicant is expected to be a bioinformatician or a bioanalyst with an expertise in genome assembly and genetics. Expertise in the detection of genomic rearrangements, identification of homologous relations within gene family and/or gene family evolution study would be appreciated. Programming skills for one or several languages are needed. Social skills are also important for the success of interactions.

Applications should be sent by email to jeremy.clotault@univ-angers.fr, fabrice.foucher@inra.fr, debener@genetik.uni-hannover.de and include a letter of motivation, a CV, and names and contact information of three referees. *The dead line for application is January 3^rd , 2017.***

"jeremy.clotault@univ-angers.fr" <jeremy.clotault@univ-angers.fr>

UBristol EvolutioaryRescue

A 3-year NERC-funded postdoctoral position in plant ecological genetics and evolutionary rescue available at the University of Bristol, UK We are looking for an enthusiastic postdoctoral researcher for a NERC project on "evolutionary rescue and the limits of phenotypic plasticity", beginning in April 2017. This project will transplant ecologically divergent but closely related Senecio ragwort species on the slopes of Mount Etna, Sicily.

This project is a new collaboration between the Universities of Bristol, Oxford, Napoli (Italy), Catania (Sicily) and CNRS Montpellier.

It will combine extensive field transplant experiments with ecological and demographic analysis, quantitative genetics, and transcriptomics, in order to develop and test theory for the role of phenotypic plasticity in helping or hindering evolutionary responses at ecological margins.

The successful candidate will be based in Sicily for the first 15 months of the project, and then at the University of Bristol. A major part of the research will involve the extensive propagation and transplant of large numbers of Senecio seedlings along an elevational gradient, monitoring their fitness, and quantifying variation in their traits and phenotypes. This will be followed by extensive ecological and quantitative genetic analysis, and transcriptomic analysis of the genomic basis of adaptive and non-adaptive plastic responses.

The post will involve working closely with a field assistant based in Sicily, as well as a postdoctoral bioinformatician based at Oxford, and a Bristol-based technician to assist with morphometric and molecular analysis. Experience in extensive field experiments (particularly in plants), plant propagation and quantitative genetics would be highly desirable. A passion for evolutionary biology and the interaction between population genetics and genomics with population ecology is essential. Demonstrated experience in management, and proficiency in Italian would also be a big advantage.

Applications are invited from applicants regardless of their citizenship or country of origin.

http://www.bristol.ac.uk/jobs/find/-details.html?nPostingID5337&nPostingTargetID 019&option(&sortSC&respnr=1& ID=Q50FK026203F3VBQBV7V77V83&JobNum102335& Resultsperpage&lg=UK&mask=uobext The closing date for applications is 4th January, 2017 Please direct informal enquiries to Dr Jon Bridle (jon.bridle@bristol.ac.uk), Prof Simon Hiscock (simon.hiscock@obg.ac.uk), or Prof Dmitry Filatov (dmitry.filatov@plants.ox.ac.uk) in the first instance.

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>

UBritishColumbia TroutGenomics

Landscape Genomics Postdoc at UBC

A research team at the University of British Columbia's Department of Zoology and Biodiversity Research Centre is seeking a postdoctoral researcher in landscape genetics of native rainbow trout (Oncorhynchus mykiss). This project is part of a larger Genome Canada project on genetics and physiology of adaptation to climate change in rainbow trout, and the population genomics component is in the labs of Eric Taylor and Michael Whitlock. The landscape genomics component primarily involves whole genome sequencing approaches to understanding the genomic basis of adaptation to features of habitat, but also to provide insights into phylogeography and the influence of watershed structure on population subdivision in rainbow trout. A PhD in a related field with expertise in basic theory and bioinformatic analysis of population genomics data is required. The position is available for one year with renewal for up to three additional years. Salary is $55,000 per year plus benefits. To apply, please send a brief cover letter summarizing your qualifications for the position, a CV, and the names, addresses, phone numbers and emails of three references. Review of applications will begin January 16, 2017. Address application materials to etaylor@zoology.ubc.ca to whom any questions can also be addressed.

etaylor@zoology.ubc.ca

UCalifornia LosAngeles CapuchinMonkeyEvol

Call for Postdoctoral Fellow Applications!

ISG Capuchin Genomics Post Doc Fellowship, 2017-2018

Application deadline is February 15, 2017

The UCLA Institute for Society and Genetics (ISG) is recruiting a post-doctoral scholar with a proposed start date of July 1, 2017, to help lead research on a capuchin monkey comparative and population genomics study funded in part by a FAPESP grant on "Phenotypic plasticity in robust capuchin monkeys (Sapajus): effects of distinct ontogenetic trajectories and context-dependent activation." This one-year position (renewable for one additional year pending positive review) is for a researcher who can (1) engage in genomic and bioinformatics analyses of capuchin genomes to understand evolutionary changes and functional differences across ten species and in comparisonto other Neotropical primates and more broadly; and (2) use recently available techniques to design and implement a genome-wide sampling approach for neutral and coding markers, to beused for non-invasive genomic sampling for wild capuchin monkey populations, in collaboration with Brazilian colleagues who will collect samples and perform sample preparation and sequencing in Sao Paulo, Brazil. The postdoc will lead population genomics analyses to test hypotheses about phenotypic plasticity versus genetic variation in individually identified wild capuchins, in conjunction with an extensive behavioral dataset on these populations.

We encourage applicants from fields in genetics, biomathematics, biological sciences and biological anthropology. The most competitive candidates will have a strong background in population or evolutionary genetics and expertise acquired from working with NextGen sequencing platforms (e.g. Illumina) for sequence analysis in a Unix environment. Background in computer sciences, mathematics and/or bioinformatics is aplus, due to the use of perl or python scripts and downstream analyses using R. Brazilian Portuguese language skills preferred but not required. This position is primarily based at UCLA in Los Angeles, but a short field research component in Brazil would be a possibility for this position.

Candidates are expected to collaborate with Jessica Lynch Alfaroand Patrícia Izar on the FAPESP-funded project, producing publications and public presentations related to capuchin functional and population genomics, development, biology and behavior. Candidates will be expected to actively participate in ISG activities, which will include teaching or co-teaching one quarter-length class (10 weeks) per year in the Human Biology and Society undergraduate major (B.A. and B.S., course can be cross-listed with another major; seminar format with 15-20 students).

The salary is competitive and includes health insurance, plus a $1500 stipend for conference fees, travel, research equipment/supplies, and other approvedresearch-related expenses. Salary will be determined based on experience and percent time of the position. Eligibility: Applicants who received the Ph.D. degree after September 2008, or who will complete all Ph.D. requirements by June 30, 2017, are eligible to apply. Certification of completion of Ph.D. degree requirements must be in hand at the time of the appointment start.

Applicants are requested to submit a letter of application, curriculum vitae, research statement, writing sample, and the names and addresses of three references. Please submit all applications and application materials online via UCLA's Academic Recruit Online at the following URL: https://recruit.apo.ucla.edu/apply/-JPF02742. Any questions about the position or the application process may be addressed to Jessica Lynch Alfaro (jlynchalfaro@g.ucla.edu[DEL:). The research statement should include an explanation of the candidate's research experience and interest in the topic, as well as methodological orientation and skills. The cover letter should include a description of a course the candidate would be interested to teach in the Institute. :DEL] The deadline for applying is February 15, 2017.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy, see: UC Nondiscrimination & Affirmative Action Policy (http://policy.ucop.edu/doc/4000376/-NondiscrimAffirmAct).

Application deadline is February 15, 2017

3D"ISGLogoAmisha" Administrative Assistant UCLA Institute for Society and Genetics 621 Charles E. Young Dr. South, 3360B LSB Los Angeles, CA 90095-7221 MC: 722105

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UCalifornia SanFrancisco ComputationalBiology

Postdoctoral Fellow - Computational Biology / Bioinformatics / Viral Population Genetics : San Francisco, CA, United States

Postdoctoral Fellow - Computational Biology / Bioinformatics / Viral Population Genetics

The Pillai Lab at Blood Systems Research Institute (BSRI), (www.bsrisf.org), an affiliate of the University of California San Francisco (UCSF), is looking for a highly motivated Postdoctoral Fellow with expertise in computational biology, with special emphasis on phylogenetics, viral population genetics, transcriptomics, and analysis of next generation sequence data. The fellowship is focused on HIV cure research, and involves extensive training within the UCSF Center for AIDS Research (CFAR) and collaboration with the recently-founded amfAR Institute for HIV Cure Research.

The ideal candidate will be interested in using a systems biology approach to investigate the effects of host gene expression patterns and viral genetic variation on HIV pathogenesis and persistence in vivo.

RESPONSIBILITIES - Phylogenetic analysis of ultra-deep HIV sequence data generated from clinical samples - Analysis of RNA-sequencing data to characterize host and viral gene expression patterns - Compilation and curation of next-generation sequence data - Computational modeling of virus-host interactions

REQUIRED QUALIFICATIONS - Ph.D. degree in bioinformatics, biostatistics, biology, computer science, or related fields - Minimum two-year experience in coding (python and R preferred) and expertise in Unix/Linux environments. - Knowledge of applied statistics - Minimum one year of basic biology knowledge. - Highly motivated, quick learner.

PREFERRED QUALIFICATIONS - Specific expertise in deep sequencing genomics and genetic analysis - Background in computational virology - Familiarity with web programming, Amazon cloud computing, SAS, SQL plus - Expertise in data management and "Big Data" analytical approaches

EEO/Minorities/Females/Disabled/Veterans

Our organization is an equal employment/affirmative action employer. If you need accommodation for any part of the employment process because of a medical condition or disability, please send an e-mail to accommodation@bloodsystems.org or call 1-844-220-2612 to let us know the nature of your request. A representative will respond to accommodation requests within two business days. Please note that this email/phone number is for medical/disability accommodations only and any other inquiries will not receive a response.

To express your interest please submit your CV by January 27, 2016 using the following link:

https://bloodsystems.taleo.net/careersection/-bsi/jobsearch.ftl?lang=en&radiusType=-M&searchExpanded=true&organization=5620010 0500&radius=1

Enter Job Number 16001425 into the search field.

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C. Brandon Ogbunu The Broad Institute of M.I.T. and Harvard Department of Organismic and Evolutionary Biology, Harvard University ogbunugafor@oeb.harvard.edu

"C. Brandon Ogbunu" <ogbunugafor@oeb.harvard.edu>

UCDavis FishDiversification

Postdoctoral Position in Fish Diversification Wainwright Lab University of California, Davis

A position is open in my lab group for a postdoctoral researcher interested in the diversification of fishes. Areas of expertise that are of particular interest include knowledge of the diversity of fishes and their biology, phylogenetic reconstruction, divergence time estimation, comparative analysis of discrete and continuous characters, fish morphology, and functional morphology. I am especially interested in extending knowledge about how functional morphology and innovations impact the evolutionary dynamics of fishes. The position is annually renewable for at least two years. Start date for the position is negotiable but is anticipated to be summer or fall of 2017. Salary will be based on experience level and will follow the University of California, Davis postdoctoral scholar salary scale. The position will come with full benefits (including health, dental and vision insurance).

If you are interested in this position, please send me an email with a summary of your interests and background, and include a copy of your cv.

The University of California, Davis, the Department of Evolution & Ecology, and the Wainwright lab are interested in candidates who are committed to the highest standards of scholarship and professional activities, and to the development of a climate that supports equality and diversity. The University of California is an affirmative action/equal opportunity employer.

Peter Wainwright Department of Evolution and Ecology University of California, Davis Davis, CA 95616 Email: pcwainwright@ucdavis.edu Website: http://-fishlab.ucdavis.edu pcwainwright@UCDAVIS.EDU

UChicago ComplexDiseaseModels

Our lab at the University of Chicago has an immediate opening for an NIH-funded postdoc to contribute to a study of complex disease models of misfolded stress response and of diabetes in the fly. This work is a continuing collaboration between Martin Kreitman (Department of Ecology & Evolution), Graeme Bell (Department of Medicine) and Matthew Stephens (Human Genetics/Statistics). We are now at the stage of research where we are collecting large amounts of NGS data (DNA and RNA-Seq) from synthetic cage populations for a variety of traits. We are looking for someone with background and experience analyzing large complex datasets to identify genetic modifiers of disease.

Contact martinkreitman@gmail.com if interested.

Project Summary: Drosophila, can be genetically manipulated to recapitulate human diseases. We have constructed a complex disease model of misfolded proteins by expressing a mutant diabetes-causing human proinsulin protein (INSC96Y) in the Drosophila eye and other tissues. The severity of proteostatic disease phenotypes in this model varies when the mutant transgene is placed in different wild-derived genetic backgrounds and this genetic variation can be mapped with high resolution by genome-wide association studies (GWAS), bulk segregant analysis of extreme phenotypes, and gene expression studies. Here we propose innovative experimental approaches to enhance the value of Drosophila as a model for investigating naturally occurring genetic variation influencing the severity of proteostatic disease or other complex traits. The research has four specific aims: (1) Map genetic variation and expression QTL's that modify cellular response to proteostatic challenge in two developing tissues, the eye and notum. We have developed a novel application of bulk segregant analysis of extreme phenotypes in an array of 16 synthetic fly populations to enhance the signals from both common SNPs and rare variants with effect sizes not detectable by conventional GWAS; (2) Screen the synthetic populations to identify alleles that are suppressed by the inhibition of apoptosis. The approach is a novel population genomic analog of a classical genetic suppressor screen; and (3) Investigate the interaction between environmental and genetic inputs to the breakdown of proteostasis; (4) Explore genetic modifiers of diabetes-like symptoms in the fly induced by a high sugar diet.

Martin Kreitman <martinkreitman@gmail.com>

UConnecticut SymbiontPhylogenomicsEvolution

Postdoc positions in molecular phylogenomics, host-symbiont diversification in the Simon Lab (See also our PhD student advertisement).

The Simon lab at the University of Connecticut seeks creative and motivated Postdoctoral candidates interested in phylogenetics, molecular phylogenomics, bioinformatics, and/or symbiont-host interactions (endosymbionts and/or microbiomes) to begin in the summer or fall of 2017. Experience in the preceding subjects preferred but not required.

Applicants will participate in an NSF sponsored project entitled: Exploring Symbiont Biodiversity and Complexity in the Family Cicadidae. The major goal of this proposal is to study the co-diversification 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? Similarly, we ask whether the changes in the gut microbiota affect primary endosymbionts (keeping in mind that gut microbiota are known to synthesize essential amino acids for some hosts). Other hypotheses concern changes in symbiont consortium membership related to changes in the biotic or abiotic external environment coincident with the invasion of new biogeographic areas characterized by different climates and host plants. Broader impacts will involve teaching collaborations with team members in the US, Brazil, China, India, NZ, and Fiji. Field trips to Brazil, Chile, Argentina, Fiji, and India are planned.

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), and Peter Lockhart (NZ, FJ), and numerous cicada researchers around the world.

Interested, qualified Postdoctoral candidates should send an email describing their motivation, skills, and research experience/interests along with a CV, and copies of relevant publications. Applicants should also arrange to have letters sent by three referees who are familiar with the candidates work (including the PhD advisor). Postdoctoral support is available through our NSF award but applications to outside funding sources are also strongly encouraged. Send all material to chris.simon@uconn.edu. Strong applicants will be contacted to schedule an informal Skype interview.

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 75 North Eagleville Road, University of Connecticut Storrs, CT 06269-3043

chris.simon@uconn.edu

Office (860) 486-4640; Lab (860) 486-3947; Fax (860) 486-6364, Office: Biopharm 305D, Lab: Biopharm 323,325

C. Simon Home page: http://hydrodictyon.eeb.uconn.edu/projects/cicada/simon_lab/member_pages/c_simon.php Simon Lab Home: http://hydrodictyon.eeb.uconn.edu/projects/cicada/simon_lab/lab_pages/current.php Reprints: http://hydrodictyon.eeb.uconn.edu/projects/cicada/resources/reprints.html

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UFlorida 3 LifeHistoryTiming

Postdoc: 3 postdoc positions in diversification, host-parasite interactions, and rapid evolution of seasonal phenology

Animals and plants must synchronize their life-history timing to exploit good times and avoid bad times of the year. Synchronization among interacting species makes seasonal responses a critical organizational component of ecological communities. Adaptation in seasonal timing can create and maintain biodiversity. Reproduction is often seasonal. Therefore, shifts in seasonal timing can disrupt reproductive timing among populations, catalyzing speciation. Moreover, formation of new taxa creates opportunities for other, interacting organisms to diversify in kind. Shifts in seasonal timing can have reverberating effects generating new biodiversity "sequentially" through ecosystems. Contemporary climate change is driving changes in seasonality. The capacity of ecological communities to evolve in concert with changing conditions will impact whether interactions among community members will be maintained or disrupted under new climatic regimes.

Our research team, including Jeff Feder at Notre Dame, Greg Ragland at University of Colorado-Denver, Tom Powell at Binghamton University New York, and Dan Hahn at University of Florida will investigate the role of seasonal adaptation in the origin and maintenance of insect biodiversity. Rhagoletis pomonella, the apple maggot fly, is a fruit-feeding agricultural pest that has recently evolved (since the mid 1880's). Seasonality drives diversification; apple flies evolved an earlier life cycle than their hawthorn-feeing ancestors to feed on earlier ripening apple fruits. Superimposed on seasonal partitioning of plant-feeding flies are additional "sequential" radiations involving parasitic wasps. Three wasps have similarly diverged in life cycle timing to match the seasonal shift of their R. pomonella hosts to earlier fruiting apples.

This multidisciplinary project will test whether the same physiological, molecular, and genomic mechanisms underlying the shift in life history timing allowing Rhagoletis to attack apples are also involved in sequential shifts and seasonal adaptation of the parasitic wasps attacking apple flies. This project will also manipulate environmental conditions to assess the potential for climate change to disrupt the fly and wasp community or if sufficient genetic diversity exists in populations of these insects for them to rapidly respond and co-evolve.

One postdoc each will join:

Greg Ragland's lab at University of Colorado-Denver (GREGORY.RAGLAND@ucdenver.edu - https://seasonaladaptation.org)

Tom Powell's lab at Binghamton University, New York (powellt@binghamton.edu - http://www.powellevolab.com)

Dan Hahn's lab at University of Florida. (dahahn@ufl.edu - http://entnemdept.ifas.ufl.edu/people-directory/daniel-hahn/)

This group of laboratories has a strong history of inter-institution collaboration and communication so while postdocs will have a single home lab, they will interact frequently with other members of the larger team. We are especially interested in folks with experience and passion for population genetics, genomics, multi-trophic ecology, climate change, physiological ecology or evolutionary developmental biology.

For more information or to apply to the Hahn or Ragland labs, please contact each PI directly at the e-mail addresses above. Applications to the Powell lab should be directed through the open position posting of the SUNY Research Foundation's employment website. Please note that access to this position in that application system will become available shortly. For applications to any of the labs, please provide a single PDF document including your CV, a brief statement of previous research, and contact information for three references to each PI you may be interested in working with by January 30th. Review of applications will begin February 1st and continue until the position is filled.

Please note that both Greg Ragland and Dan Hahn will be at the SICB meetings in New Orleans if you wish to talk in person, you can also see related work in the symposium "Evolutionary Impacts of Seasonality" (http://www.sicb.org/meetings/2017/symposia/seasonal.php).

Some publications related to the project include:

Meyers, P., T.H.Q. Powell, K. Walden, A. Shieferecke, J.L. Feder, D.A. Hahn, S.H. Robertson, S.H. Berlocher, and G.J. Ragland. 2016. Evolutionary divergence of the diapause transcriptome in apple maggot flies: winter chilling and post-winter transcriptional repression. Journal of Experimental Biology 219: 2613-1622.

Hood, G.R., A.A. Forbes, T.H.Q. Powell, S.P. Egan, G. Hamerlinck, J.J. Smith, and J.L. Feder. 2015. Sequential divergence and the

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UFlorida ButterflyMothGenomicsEvol

Full-timePostdoc, Kawahara Lab:

TheKawahara Lab at the University of Florida, Gainesville, FL, is hiring a full-time postdoc.

Thepostdoc will help various projects pertaining to research on the evolution of butterflies and phylogenomics/comparative genomics of sensory system evolution in bombycoid moths, as part of two, recently-funded National Science Foundation projects (NSF DEBNERC and NSF GoLife).

Theselected postdoc will work at the Florida Museum of Natural History's McGuire Center in Gainesville, FL, USA. The selected candidate will need to be able to communicate well in verbal and written English and have the ability to train students and analyze genomic libraries for NGS, including insect transcriptomes and target capture approaches. The selected candidate will join a team of 4 postdocs, 9 graduate students, multiple undergraduates, and staff in the Kawahara Lab. The postdoc will also work closely with local and international collaborators.

Required:A Ph.D. in molecular evolution, systematics, evolution, bioinformatics, genomics, or related field. Familiarity with Next Generation Sequencing, computer programming/scripting in Python, Perl, Java, C++, R or other language. Candidates with background experience in functional/comparative genomics, genome annotation, and/or phylogenomics will be highly considered. An interest in insect evolution and strong publication record is desired.

Salary:$47,500-$50,000 USD plus benefits. Startdate: Position available Feb 1, 2017 or until the position is filled. Evaluations of applications will begin Dec. 20, 2016. Duration:The appointment can be up to 2 years, but will be made on a yearly basis given satisfactory progress.

Toensure full consideration please email the following to Akito Kawahara at kawahara@flmnh.ufl.edu by December 20, 2016: (1) a cover letter, (2) your updated CV, and (3) letters of support from 3 mentors/colleagues.

The cover letter should describe your previous research and training, your qualifications for the position as detailed in this advertisement, and should explain how this postdoctoral position will further your long-term research/career aspirations. Specify in the email subject line: "Postdoc_KawaharaLab"

Aboutthe University of Florida TheUniversity of Florida (UF) is one of the nation's leading research institutions with 35,000 undergraduates, 15,000 graduate students, and over 4,500 faculty and academic staff. UF offers all resources of a top research university to study evolution, genomics, and systematics. The Florida Museum of Natural History (FLMNH) serves as the iDigBio HUB, and is now one of the primary centers for research in evolutionary biology.

TheFLMNH is also closely tied to the UF High-Performance Computing Center (HPC) and HiPerGator2 (https://www.rc.ufl.edu/) allowing for the chosen postdoc to utilize this rich computational resource. UF also has a state-of-the-art next-generation genome sequencing facility at the Interdisciplinary Center for Biotechnology Research (ICBR), the Florida State Collection of Arthropods (FSCA), and collections of the McGuire Center for Lepidoptera and Biodiversity. The Kawahara Lab also has strong ties to UF's the Department of Biology, Department of Entomology and Nematology, School of Natural Resources and Environment, Department of Wildlife Ecology and Conservation, School of Forest Resources and Conservation, and Department of Microbiology and Cell Science. Further information on the Kawahara Lab can be found at: http://www.flmnh.ufl.edu/mcguire/kawahara/ Recent-publications from the lab include:

- Barber, J., Leavell, B.C., Keener, A.L., Breinholt, J.W., Chadwell, B.A., McClure, C.J.W., Hill, G.M., Kawahara, A.Y. 2015. Moth tails divert bat attack: Evolution of acoustic deflection. PNAS 112(9): 2812-2816 - Kawahara, A.Y., Barber, J.R. 2015. Tempo and mode of anti-bat ultrasound and jamming in the diverse hawkmoth radiation. PNAS 112(20): 6407-6412. - Kawahara, A.Y., Breinholt, J.W. 2014. Phylogenomics provides strong evidence for relationships of butterflies and moths. Proceedings R. Soc B 281: 20140970

kawahara@flmnh.ufl.edu

UFZ Halle ButterflyBiodiversity

The Department of Community Ecology at the Helmholtz Centre for Environmental Research - UFZ and the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig offer the following position under the supervision of Prof Dr Josef Settele:

Postdoctoral researcher (f/m) in the field of community ecology of butterflies

Global change restructures species assemblages with severe consequences for biodiversity and ecosystem functioning. The basic processes underlying this include environmental filtering, niche partitioning and a number of spatial and stochastic processes. The key question of the project will be to understand the relative importance of these underlying mechanisms. Using European butterflies as a model system, we will integrate multiple data sets on species distribution and abundance with high temporal and spatial resolution and extent across Europe . In combination with comprehensive information on species traits and phylogenetic relationships we will (1) analyse butterfly trait and niche evolution, (2) identify the impact of global change drivers on spatial and temporal patterns of species richness, functional and phylogenetic diversity and their mismatches, and (3) analyse scale - dependencies of taxonomic, functional and phylogenetic diversity.

planned starting date: 1 April 2017 full-time employment two-year contract job location: UFZ Halle (Saale), Germany salary: Pay grade (Entgeltgruppe) 13 TV-L (100%) position number: 34600515#10

Applications are accepted until 1 January 2017.

The recruitment symposium will take place in Leipzig on 27-28 February 2017.

more information (PDF): https://www.idiv.de/-fileadmin/content/Files_Flexpool/pdfs/-PD_34600515_10_Settele.pdf – Dr. Martin Wiemers Department of Community Ecology Helmholtz Centre for Environmental Research - UFZ Theodor-Lieser-Str. 4 06120 Halle Germany Tel. +49 345 558-5322 e-mail: martin.wiemers@ufz.de http://-www.ufz.de/index.php?en=31235 Martin Wiemers <martin.wiemers@ufz.de>

UGhent EvolutionAnimalColouration

Post-doc on animal coloration/sensory ecology and evolution.

DEADLINE DEC. 20, 2016

Supervisor: Dr. Matthew D. Shawkey

Evolution and Optics of Nanostructures (EON) Group, Department of Biology

University of Ghent, Belgium

http://users.ugent.be/~mshawkey Deadline: December 20, 2016

A 3-year post-doc position on animal coloration/sensory ecology is available in the Evolution and Optics of Nanostructures (EON) group at the University of Ghent, Belgium. Research projects should be within this broad theme, but will be collaboratively designed by the post-doc and I. Anyone with an interest in multidisciplinary research is encouraged to apply, including those trained in fields outside biology. The post-doc will also have the opportunity to do some teaching on an ad hoc basis, but this will be limited to <30% of their time.

Funding: Competitive salary is offered for three years. Research and travel funds will be available in varying degrees depending on the project.

Eligibility: Open to all nationalities. A PhD in any field of science (preferably Biology, Physics or Materials Science) is required by the time of admission. Proficiency with the English language (both written and spoken) is required, and basic skills in Dutch (or a willingness to learn) are advantageous.

Location: The University of Ghent is a large research-oriented university that is consistently ranked within the top 100 Universities worldwide. The Department of Biology has broad research expertise with an active community of faculty, post-docs and students. Ghent is a beautiful small city in the heart of Europe that combines medieval architecture with a thriving arts and food scene.

How to apply: You can formally apply at https:/-/career012.successfactors.eu/career?career%5fns=-job%5flisting &co mpanyÃ€000956575P
&navBarLevel=JOB%5fSEARCH
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You are encouraged to first contact Dr. Matthew Shawkey (matthew.shawkey@ugent.be) to discuss your application, but this is not required.

Matthew Shawkey <Matthew.Shawkey@UGent.be>

UHawaii BactroceraFruitFlies

Postdoctoral research position to study population genetics/diagnosis of fruit flies

The University of Hawaii in cooperation with the USDA Mission Laboratory in Texas is in search of a Junior Researcher (Postdoc) to work on the population genetics and identification of exotic pest fruit flies as part of a project to understand invasion pathways. The project will develop and examine new resources for molecular identification of fruit fly species and populations in the genus Bactrocera. The junior researcher will examine fruit flies using principles of population genetics and systematics. These data will be evaluated for trends in species composition and movement pathways through comparison to offshore and domestic fly collections. There is an opportunity to contribute to analysis of Next Generation Sequence data in support of the goal to distinguish populations.

The research will be performed at the USDA Mission laboratory in southern Texas. The laboratory has the molecular biology instrumentation and fruit fly collections needed to complete the study. The candidate will conduct molecular experiments to generate data, perform statistical analysis of data sets, organize samples and records, and develop publications and presentations. The successful applicant will be expected to work independently as well as part of a team. This includes working with colleagues at the Mission Laboratory and collaborating with scientists at the University of Hawaii Insect Biodiversity and Systematic Lab.

Requirements: Minimum of a PhD in biological sciences. Prior experience generating and analyzing molecular data sets, as demonstrated through publications. Knowledge of both molecular phylogenetic and population genetic methods are highly desired.

The position is for one year, with the possibility of continuation based on productivity. If interested please submit a CV and contact information for at least 3 references to co-PI Dr. Norman Barr (Norman.B.Barr@aphis.usda.gov). Review of applicants will begin immediately. For full consideration submit CV and references by January 15, 2017.

"Barr, Norman B - APHIS" <Norman.B.Barr@aphis.usda.gov>

UHelsinki HostPathogenCoevolution

POST DOC position in HOST-PATHOGEN COEVOLUTION

Applications are invited for a three year post doc in the research group of Professor Anna-Liisa Laine. The successful applicant will join the Centre of Excellence in Metapopulation Research at the University of Helsinki.

The project is centered on the interaction between host plant Plantago lanceolata and its fungal pathogen Podosphaera plantaginis in the Ãland Islands. With 16 years of epidemiological data complemented with intensive disease sampling since year 2010, molecular resources and solid experimental protocols, this system offers unique opportunities for testing classic hypotheses regarding host-pathogen coevolution with direct links to epidemiological dynamics. One of the key aims of the project is to link molecular variation to phenotype data and population dynamic data of both host and pathogen. Depending on the background and interests of the candidate, the focus of the research can be more molecular or ecological.

Recent relevant publications include:

Jousimo, J, Tack, AJM, Ovaskainen, O., Mononen, T., Susi, H., Tollenaere, C. & Laine, A.-L. 2014. Ecological and evolutionary effects of fragmentation on infectious disease dynamics. Science, 344: 1289-1293.

Susi, H., Barres, B., Vale, P. & Laine, A.-L. 2015. Coinfection alters population dynamics of infectious disease. Nature Communications, 6: 5975.

The successful candidate should have PhD / post doctoral experience with host-parasite interactions, evolutionary genetics, bioinformatics, plant pathology, evolutionary biology or similar, and a strong interest in studying disease in natural populations. Excellent written and verbal communication skills, and the ability to think independently and creatively are required. You must demonstrate the ability to work as part of a team, and participate in supervision of more junior group members.

More information: http://allaine.it.helsinki.fi/ Starting date: Winter/Spring 2017

Application deadline: 15 January 2017

Mail your application (CV with publications included, contact details of two references, and a letter (MAX 1 page) with a description of your research interests and why you would be a suitable candidate for the project) as a single pdf file to biotiede-mrg@helsinki.fi, with title POST DOC COEVOLUTION.

Informal inquires to anna-liisa.laine@helsinki.fi

For information on the University of Helsinki, please visit: http://www.helsinki.fi/university/index.html
Professor Anna-Liisa Laine

Center-of-Excellence in Metapopulation Biology

Department of Biosciences

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allaine.it.helsinki.fi

helsinki.fi/science/metapop/

twitter: @annaliisalaine

Anna-Liisa Laine <allaine@mappi.helsinki.fi>

UIceland Transcriptomics

Postdoc at the Institute of Life and Environmental Sciences, University of Iceland

A full postdoctoral research position is available at the Institute of Life and Environmental Sciences, University of Iceland. The research field is transcriptomics of non-model organisms, whelks and groundwater amphipods. The position is supported for two years by the Icelandic Research Council with a possibility of extension. The goal is firstly to unravel the causes behind the high colour variation in Common whelk Buccinum undatum in Icelandic waters by analysing existing unassembled transcriptome data, and secondly to analyse assembled transcriptome of Crangonyx islandicus, an endemic groundwater amphipod in Iceland, in comparison with the transcriptome of the surface living amphipod Crangonyx pseudogracilis.

Qualifications: PhD degree in biology or related fields. Research experience in the field of bioinformatics, genetics and evolutionary theory. Good communication and collaboration skills. English speaking/writing skills.

Application deadline is December 19th 2016, please apply here: http://english.hi.is/vacancies_list Interested applicants need to send the following with their application: I. Written application (max one page), listing the applicant's interest in the project and how they envision they can contribute to the project II. CV III. Certificates of education IV. Two reference letters and information how to reach the referees

The work will be supervised by Zophonias O. Jónsson zjons@hi.is (http://starfsfolk.hi.is/en/simaskra/1476) SnÃbjörn Pálsson snaebj@hi.is (www.hi.is/˜snaebj), who can provide further information about the position.

Appointments to positions at the University of Iceland are made in consideration of the Equal Rights Policy of the University of Iceland. The salary for the position will be in accordance with the grant and salary agreement between the Union of University Teachers and the Minister of Finance.

At the School of Engineering and Natural Sciences 380 people are employed in research and teaching. The School offers an international environment, with the number of international employees and students increasing each year. Currently 25% of all employees and postgraduate students are international. There are around 2200 students at the School, divided into six faculties, thereof are 350 graduate students and 150 doctoral students. Research institutes at the school are the Science Institute that divides into the Institute of Earth Sciences and Institute of Physical Sciences, Institute of Life and Environmental Sciences, Engineering Research Institute and the Institute for Sustainability Studies which is an interdisciplinary institute and belongs to the five schools of the University of Iceland.

The University of Iceland is the largest teaching, research and science institute in Iceland and is ranked among the top 250 universities in the world by Times Higher Education.

Information on the University of Iceland can be found here and more information can be found at the International office and Relocation Service

snaebj@hi.is

UKansas BiodiversityInstitute

TheUniversity of Kansas' Biodiversity Institute is excited to announce a postdoctoral position for a Genomics Specialist who will conduct collaborative research and oversee the Biodiversity Institute's shared-use molecular genetics laboratory (https://biodiversity.ku.edu/-research/molecular-genetics-lab). The Biodiversity Insitute's molecular laboratory is a recently renovated facility with ample bench space and state of the art equipment that is located in the KU Natural History Museum. This laboratory is used by a diverse and highly interactive group of approximately 25 scientists who are addressing a range of research questions in systematics and population genetics using organisms from across the tree of life (e.g., insects, spiders, plants, fish, birds, reptiles, amphibians, mammals, invertebrates [incl. parasites], and viruses).

Becausethis position is supported by the Biodiversity Institute rather than an individual PI, it offers considerable intellectual freedom. Our goal is to hire someone who is interested in developing collaborative projects with one or more members of our group. Collectively, we have numerous ongoing projects involving acquisition and analysis of genomic sequence data underway, and are looking to to add some outside talent capable of taking this work in new directions. Our ideal candidate will be someone with prior genomics and bioinformatics experience who also has strong organismal interests and would enjoy working in one of the world's finest natural history museums.

Theposition will be for a two year term (with possible renewal for a third year) and offers a competitive salary ($47-48K, depending on prior experience). We will start reviewing applications on January 12th, 2017. More information about the molecular genetics group, including a list of molecular laboratory users and projects, can be found at our website: https://biodiversity.ku.edu/-research/molecular-genetics-lab. The official job posting and application site can be found a KU's employment pages https://employment.ku.edu/staff/7361BR. Please feel free to contact us if you have any questions.

GenomicsSpecialist Search Committee RichGlor, chair of search committee (glor@ku.edu) KirsenJensen (jensen@ku.edu) RobMoyle (moyle@ku.edu) LenaHileman (lhileman@ku.edu) AlanaAlexander (alana.alexander@ku.edu) glor@ku.edu

ULaval FishPopulationGenomics

The Bernatchez's Lab at Univerity Laval (Québec City, Canada) is currently searching for a postdoctorate researcher to be involved in our ongoing research program pertaining to the comparative and population genomics of fishes. This research program is very well supported from multiple funding agencies (Natural Sciences and Engineering Research Council of Canada, Canadian Research Chair Program, Genome Canada, Genome Québec, Fonds nature et Technologie Québec) and involves numerous collaborators, both national and international from over 20 countries. Our research program aims to enhance fundamental knowledge pertaining to the evolutionary processes responsible for generating and maintaining genetic diversity within populations of aquatic animals, with relevance for management and conservation.

Depending on his/her specific expertise and qualifications, the selected candidate can be involved in one or several of the specific projects currently conducted including either marine (Halibut, Capelin), anadromous/catadomous (Salmon,Eel) or freshwater (Trout, Whitefish), among others. Details of specific ongoing projects can be found on our website (see below).

Required Qualifications: We are primarily searching for a prospective candidate with strong and demonstrated bioinformatics skills in whole genome assembly who is also familiar with scripting and programming. The ideal candidate should also be familiar with population genomics analyses of data sets derived from whole genome resequencing, high density SNP chips, RADseq/GBS genotyping, as well as epigenome (methylation) data sets. Candidates must be fluent in English, both written and spoken.

The position is available now and for 2 years, likely renewable for a third year, and to be filled as soon as possible. Salary is established according to local University standards.

To apply, please send a cover letter describing your research interests and qualifications, a complete CV and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca

Do not hesitate to contact me directly for any further details or questions.

To learn more about.

Our lab, research program, publications, people: The Canadian Research in Genomics and Conservation of Aquatic Resources https://www.bio.ulaval.ca/-louisbernatchez/research_programs.htm Laval University : https://www.ulaval.ca/en/research.html Québec City : http://www.quebecregion.com/en/ Louis Bernatchez, Canadian Research in Genomics and Conservation of Aquatic Resources Institut de Biologie Intégrative et des Systemes, Pavillon Charles-Eugene Marchand, Universite Laval, Québec, QC G1V 0A6 Canada

Tel: 1 418 656-3402 Fax: 1 418 656-2043 Couriel: Louis.Bernatchez@bio.ulaval.ca

Louis Bernatchez <Louis.Bernatchez@bio.ulaval.ca>

ULiverpool PopulationGenetics

Popgen and bioinformatics postdoc in Liverpool

We are seeking an individual with expertise in computational population genetics, statistics and informatics to join a multi-institution research network that is using several species of British Lepidoptera, with contrasting demographic histories, to study the rate of evolutionary responses to ecological change. You will be working with the Liverpool team, led by Ilik Saccheri, with responsibility for analysing whole genome scan data from contemporary and museum samples to identify genomic regions, and functional candidates within them, showing evidence of recent selection. You should have a PhD degree in population/evolutionary biology, bioinformatics or statistics, and experience of genomic analysis. The post is available for 2 years from the time of appointment (ideally around April/May).

Informal enquiries to saccheri@liv.ac.uk are welcome.

For further details and how to apply go to https://recruit.liverpool.ac.uk and search for Job Reference 004064. Closing date 12 January 2017.

DR ILIK J. SACCHERI Institute of Integrative Biology University of Liverpool The Biosciences Building Crown Street Liverpool L69 7ZB UK Tel. 44 (0)151 795 4522 email saccheri@liv.ac.uk

"Saccheri, Ilik" <I.J.Saccheri@liverpool.ac.uk>

UMichigan AvianEvolutionSpeciation

The Winger lab in the Department of Ecology and Evolutionary Biology and the Museum of Zoology at the University of Michigan is accepting applications for a postdoctoral scientist position in avian evolutionary genomics and speciation. We conduct research on diverse topics related to avian evolution and evolutionary ecology, including speciation, the evolution of geographic range, the assembly of regional biotas, and avian movement ecology (seasonal migration and dispersal). We are particularly interested in topics that bridge one or more of these themes. The primary focus of this postdoctoral position is to test the historical and ecological factors that regulate speciation in Neotropical montane birds. Specifically, the project seeks to develop a comparative genomic framework to test how ecological and social selection pressures interact with population history to influence trajectories of speciation in the Andes. Duties may involve development of genomic libraries and sample preparation in a molecular lab, assembly and analysis of genomic data, project organization, training of graduate and undergraduate students, and collaborative grant and manuscript writing. "Wet lab" molecular work will take place in a highly collaborative, multi-PI, biodiversity-focused genomic laboratory in the Department of Ecology and Evolutionary Biology. Depending on expertise, the postdoc may also contribute to other research endeavors in the Winger lab that involve genomic, phylogenetic, distributional or morphological (specimen-based) datasets.

A successful applicant would have a PhD in evolutionary biology, evolutionary or ecological genomics, population genetics, phylogenetics or biodiversity informatics by summer, 2017; demonstrated success in publication and grant writing of original research; a passion for biodiversity and natural history of birds or other taxa; and a track record of and interest in mentorship of undergraduate students. Ideally, a successful applicant would also have expertise in at least one of the following areas: genomic and bioinformatic methods such as whole genome sequencing and assembly, sequence capture and/or short-read sequencing and assembly; population genetic and/or phylogenetic analytical methods, particularly as pertains to genomic data; and/or fluency in scripting languages such as Python or R. This Postdoctoral Fellowship is intended to be a two-year position, pending a successful performance review after the first year. Desired start date is September 1, 2017, but may be negotiable. Applicants should send a letter of interest, CV, and list of three references to Dr. Ben Winger (wingerb@umich.edu) by December 9th, 2016.

Ben Winger, PhD Assistant Professor & Curator of Birds, Dept. of Ecology & Evolutionary Biology and Museum of Zoology University of Michigan Ann Arbor, MI 48109 USA www.benwingerbiology.com
"wingerb@umich.edu" <wingerb@umich.edu>

UMunich PlantGenomics

Postdoc position in evolutionary botany at the Ludwig-Maximilians University in Munich to work on floral sex determination

Our lab is seeking to recruit a scientist at the postdoctoral level ('Wissenschaftlicher Mitarbeiter' position) to work on sex determination in the economically important Cucurbitaceae family, specifically on the assembly of a PacBio-sequenced genome of a species in the Cucumis/Citrullus clade. The project involves collaboration between the labs of Abdel Bendahmane (Head of Translational Research Group, Institute of Plant Sciences Paris-Saclay) and Susanne Renner. Paired-end Illumina Nextera sequenced male and female total genomes are already in hand. Much higher coverage will be achieved now, and the assembly will focus on three gene families known to be involved in floral sex determination, with the specific goal of inferring chromosomal location and re-arrangements in a group of related species. The functional characterization of X- and Y-linked sex genes will be carried out in the Bendahmane lab.

The position is for initially two years, starting on 1 April 2017, with the possibility of an extension. Candidates must have a doctoral degree in the areas of plant biology or genomics and experience in bioinformatics, for example, with the Python language. Knowledge of spoken German is required because the position involves assistance in basic botany courses, some of which are obligatory for future biology teachers.

Candidates should submit their CV, including a list of publications and a statement of research interests, along with the contact information of two referees to Professor Susanne Renner (renner@lmu.de). Deadline: 30 January 2017.

What we do: https://scholar.google.de/citations?user=-uzOGmTgAAAAJ&hl=en Susanne Renner <renner@lrz.uni-muenchen.de>

UOtago PopGenTheory

Postdoctoral Fellow in Evolutionary Biology-1602140

Applications are invited for this full-time, fixed-term position of Postdoctoral Fellow in Evolutionary Biology 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 and is available for three years.

The project is 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 researchers 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.

You will have a strong interest in applying quantitative methods in biology. In addition, you will demonstrate a good record of publication in peer-reviewed journals, together with high quality oral and written communication skills. Previous experience in modelling population-genetic theory is desirable but not essential.

Our research group and the wider Department includes world-class research staff, facilities and strong international collaborations, offering you excellent opportunities to gain a variety of highly pertinent research and technical skills.

For details about living in Dunedin, in the South Island of New Zealand, 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 personal statement of suitability and the names and contact details of two referees via the University of Otago's website (https://otago.taleo.net/careersection/-2/jobdetail.ftl?lang=3Den&job=3D1602 140).

Applicants must have been awarded the degree of Doctor of Philosophy before taking up this position.

Specific enquiries may be directed to Professor Hamish Spencer (hamish.spencer@otago.ac.nz).

Applications must be filed via the University of Otago's website (https://otago.taleo.net/careersection/-2/jobdetail.ftl?lang=3Den&job=3D1602 140) quoting reference number 1602140 and will close on Wednesday, 18 January 2017.

Hamish Spencer <hamish.spencer@otago.ac.nz>

UPennsylvania EvolutionaryGameTheory

Post-doctoralpositions in Evolutionary Theory and Social Norms at Penn

JoshuaPlotkin's laboratory in Evolutionary Theory at the University of Pennsylvania seeks one or two postdoctoral researchers to begin as soon as possible (summer or fall 2017 at the latest). Post-docs will join a vibrant research group of scientists with diverse backgrounds who share common interests in evolutionary theory and population biology.

Weseek and value individuals who have strong intellectual motivations of their own. But we are especially interested in scientists who want to use mathematical models to study how social norms might arise, be maintained, or be disrupted in populations. Familiarity with some body of mathematical modeling (population biology, game theory, and/or evolutionary theory) is required, and computational skills (Monte Carlo simulations, scientific computation) are a plus. Strong communication and writing skills are also highly valued. In addition to the development of formal theory, there are opportunities for funded collaborations with behavioral experimentalists using economic games for empirical study of social norms.

Fundsfor conference travel and visits with collaborators will be available to the fellow, as well as the many opportunities for collaboration in by the Penn community. Post-docs will also have the opportunity to help mentor undergraduate and graduate students in the lab. Individuals with a Ph.D., or those expecting to complete their Ph.D. in Spring 2017, are encouraged to apply.

Applicationswill be reviewed on a rolling basis. Please send CV, statement of interest (two pages max), two papers (published or pre-prints), and arrange for at least two reference letters to be sent to: jplotkin (at) sas (dot) upenn (dot) edu. Also visit http://-mathbio.sas.upenn.edu Universityof Pennsylvania is an EOE/Affirmative Action Employer. Female, underrepresented minority and LGBT candidates are particularly encouraged to apply.

jplotkin@sas.upenn.edu

UPennsylvania SocialEvolutionTheory

Postdoctoralfellowships in social evolution theory at Penn

Multiplefunded postdoctoral fellowships are available in the research group of Erol Akcay at the University of Pennsylvania to work on the theory of animal and human social behavior and social structure. We are seeking enthusiastic and talented individuals to conduct original research on topics related to the lab's interests. Specific potential topics include: dynamics of social networks, evolution of social preferences and social norms, and collective behavior. There will also be opportunity and encouragement to develop own research questions within these broad areas.

Theideal candidate will have a strong background in mathematical or computational theory in ecology, evolution, and/or social science (and a Ph.D. in a related field), and will have demonstrated ability to conduct original research. The fellow will join a vibrant research group working on diverse questions in social evolutionary theory. Start date is flexible, from as soon as possible to the Fall of 2017 at the latest. Funding is available for multiple years, contingent on satisfactory progress.

Moreabout the lab: The Akcay lab (http://-erolakcay.wordpress.com/) is based in the Department of Biology at the University of Pennsylvania in Philadelphia, PA. We study social evolution, broadly conceived, across the tree of life. Work in the group addresses a range of questions at the interface of ecology, evolution, and social dynamics, including: the evolution of social behaviors and social systems of animals and humans, evolutionary ecology of species interactions such as mutualisms, the interplay between physiology and social behavior, dynamics of coupled natural and human systems, and others. More information about the lab's research and links to recent publications can be found at: http://erolakcay.wordpress.com/research and http://erolakcay.wordpress.com/publications. The Biology Department and the University of Pennsylvania provide a vibrant intellectual environment for research in theoretical biology and social evolution, and ample opportunity for cross-disciplinary collaborations. The University of Pennsylvania is in an urban campus in the heart of Philadelphia, one of the most livable big cities in the US.

Toapply: send a CV, statement of research interests (2 pages max), two representative papers (published or preprints), and contact information for 3 references to Erol Akcay at eakcay@sas.upenn.edu. Applications will be considered on a rolling basis; informal inquiries are welcome.

TheUniversity of Pennsylvania is an EOE/Affirmative Action Employer. Female, underrepresented minority, and LGBT candidates are especially encouraged to apply.

– ErolAkcay AssistantProfessor Departmentof Biology Universityof Pennsylvania PhiladelphiaPA 204E Lynch Labs http://erolakcay.wordpress.com eakcay@sas.upenn.edu

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USussex EvolutionaryGenetics

Postdoctoral position in evolutionary genetics/genomics of sexual antagonism

University of Sussex School of Life Sciences

Full time, Fixed term for 1 year Salary range: starting at 32,004 and rising to 38,183 per annum Closing date for applications: 12 January 2017

Description

The Morrow lab wishes to appoint a postdoctoral researcher as part of project investigating the genetics of sexual antagonism in the fruit-fly Drosophila melanogaster. The position will be focussed on analysing molecular data from an experiment into the reproductive success of flies with known genotypes in a mass-action experiment that has already been carried out. The aim being to determine reproductive success of the different haplotypes and infer selection at individual genetic loci. The main duties will involve designing the genotyping strategy (using microsatellites and/or SNP markers), pre-processing genotyping data, statistical modelling and contributing to writing-up the experiment. The post-holder is expected to work closely with the PI and other members of the group. There may be an opportunity to extend the position based on the availability of other funding.

The position would be ideal for a highly motivated individual with an interest in sexual antagonism or more generally in evolutionary biology and/or genetics/genomics. The candidate should be familiar with principles of molecular biology and have training or experience with bioinformatics or advanced statistical analysis. Direct experience of working with data generated from molecular markers (microsatellites or SNPs) would be a distinct advantage. Knowledge of or experience with genomic or genetic data from Drosophila is not necessary but may be advantageous. A proven record of publishing peer-reviewed articles as a main author is essential. The candidate should have excellent organizational and communication skills and work conscientiously. The post-holder must have a PhD in a biological or related subject.

Further information on the research of the Morrow lab can be found at: http://www.sussex.ac.uk/lifesci/morrowlab/index A recent paper on the large genomic dataset that is available has just been peer-reviewed at F1000 Research: https://f1000research.com/articles/5-2644/v1 Candidates are welcome to make informal enquiries to the PI via email: ted.morrow@sussex.ac.uk

An overview of research within the Evolution, Behaviour and Environment theme can be found at http://www.sussex.ac.uk/lifesci/ebe/ The School of Life Sciences is at the forefront of research in the biological sciences in the UK, coming in the top 10 in the REF 2014. The School is committed to equality and valuing diversity, and currently holds an Athena SWAN Silver Award. Applications are particularly welcomed from women and black and minority ethnic candidates, who are under-represented in academic posts in science and engineering at Sussex. The School of Life Sciences welcomes applications to academic posts from candidates who wish to work part-time or as job-sharers.

The University offers various schemes to provide real benefits to parents, these can be found at http://www.sussex.ac.uk/humanresources/personnel/familyfriendlypolicies Brighton is a lively multicultural city on the south coast of England, 20 minutes from Gatwick International Airport and around 1 hour from the centre of London (by train). Apart from the famous sea front and piers of Brighton and Hove, and the stunning white chalk cliffs along the south coast, the University of Sussex campus at Falmer is nestled in the beautiful South Downs National Park - next door to Stanmer country park and from the picturesque village of Lewes.

Ted Morrow <Ted.Morrow@sussex.ac.uk>

UtahStateU Macroevolution

Hello everyone,

I'm looking for a post-doc to join my lab at Utah State University. The position would suit anyone with a good background in macro-evolutionary models and/or community ecology, and would be desk-based. I've copy-pasted the details at the bottom of this email; if you're interested, please email me (will.pearse@usu.edu) to ask for more details.

Thanks,

Will Pearse

Website with details and application instructions: http://usu.hiretouch.com/job-details?jobid=1983 We are seeking a post-doctoral researcher to participate in a project linking the macro-evolution of species' traits with their present-day ecological distributions. The project is aimed at understanding how ecological assembly processes affect the evolution of species' traits and speciation/extinction rates. The post-doctoral researcher will be expected to develop new methods to address questions at the interfaces of community ecology, biogeography, and evolutionary biology. The position is for one year with the likelihood of extension up to 2 years total.

Responsibilities: The successful candidate will be responsible for a number of duties and be expected to:

* Work well in a collaborative, inter-disciplinary environment. * Develop novel analytical approaches. * Maintain a solid publication record. * Analyze data and prepare material for publication and presentation both in written and oral formats. * Take an active role in the lab. This includes working with and mentoring (where appropriate) lab members, and giving feedback on manuscripts and grant proposals.

Minimum Qualifications:

* Ph.D. in biology or a closely related discipline * Good understanding of literature in at least one of the fields of macro-evolution, community ecology, and biogeography * Expertise in statistical analysis in an open source environment (e.g., R) * Strong oral and written communication and interpersonal skills * Experience mentoring undergraduate students

Preferred Qualifications:

* Experience working with large datasets * Comfortable working across fields * Good understanding of literature in several of the fields of trait evolution, community ecology, and biogeography * History of previous research funding success

Will <will.pearse@gmail.com>

UTurku HumanLifeHistory

Post-doctoral research position in human evolutionary ecology

Overview: Our multidisciplinary research team is looking for a post-doctoral researcher for a three-year project investigating life history, social integration and the influence of kin in forced migrants in a 20th century Finnish population. The project is an exciting opportunity to investigate the consequences of forced migration of over 400000 people during World War II from an evolutionary ecology and sociology viewpoint. These migrants encountered much the same traumas and faced similar prejudices and resentment that current migrants face today, making the study of this population particularly appropriate to gain insight into the present and future of current migrants.

The project, headed by Dr. John Loehr, is funded by Kone Foundation for the period 2017-2020. http://www.koneensaatio.fi/en/hanke/learning-from-our-past/ Job description: We are looking for an enthusiastic and motivated new member to our team who will develop new research questions along with contributions and guidance from other team members, independently manage and statistically analyse large and complex datasets, and write scientific publications from the results.

Start date for the position is February 1, 2017 or as agreed. The position is funded for 3 years, and an initial contract of 1 year will be offered with a 3 month trial period. Payment is in the form of a grant (2700euro/month, largely tax free income). The work location is flexible and can be done at The University of Turku, Lammi Biological Station (University of Helsinki), Family Federation of Finland (Helsinki) or University of Jyväskylä or a combination of these places. The successful candidate will join the Human Life History Group headed by Finnish Academy Professor Virpi Lummaa; a group internationally renowned for its innovative and cutting edge research on human life history (http://human-life-history.science/).

Ideal candidate descriptors:

- PhD degree in evolutionary ecology, sociology or related field
- Strong statistics background, preferably with experience in Bayesian analysis
- Background in population level analyses of large data sets
- Good publication track record
- Self-motivated and enthusiastic with good teamwork and communication skills
- Ability to lead and supervise research assistants
- A keen interest in human evolutionary ecology

How to apply: Application deadline: 30 December 2016 at 24:00. Submit an e-mail to John Loehr (john.loehr@helsinki.fi) with the subject heading 'POST-DOC APPLICATION', with the following documents combined into ONE pdf file:

- A cover letter describing your research interests and suitable for the job - A detailed CV including a list of publications as well as other achievements - Two reference letters from people who can be contacted by telephone or e-mail before or after the interview. Prospective candidates will be invited for interviews in person or by Skype in early January 2017. For more information please contact John Loehr +358-504151726 / john.loehr@helsinki.fi.

Our research team is greatly looking forward to your application!

John Loehr, Lammi Biological Station, University of Helsinki Mirkka Danielsbacka, University of Turku Virpi Lummaa, University of Turku Johanna Mappes, University of Jyväskylä Jenni Pettay, University of Turku Anna Rotkirch, Family Federation of Finland

"Loehr, John A" <john.loehr@helsinki.fi>

UWitwatersrand StripedMouseProject

Postdoctoral fellowship South Africa.

Success in an unpredictable habitat: geographic unpredictability and social flexibility

(University of the Witwatersrand, South Arica; Succulent Karoo Research Station; CNRS Strasbourg, France)

A 24 month postdoc position is available in the fields of Behavioral Ecology and Eco-Physiology in the Striped Mouse Research Group www.stripedmouse.com of Dr Neville Pillay https://www.wits.ac.za/apes and Dr Carsten Schradin http://www.iphc.cnrs.fr/-Carsten-Schradin-.html. The postdoc will be employed by the University of the Witwatersrand, South Africa, collect data in the Succulent Karoo Research Station and possibly do laboratory work at the Institut Pluridisciplinaire Hubert Curien, Departement d'Ecologie Physiologie et Ethologie (DEPE), France's largest eco-physiology laboratory.

Research topic. The striped mouse is well known for its social flexibility: it can live either in groups or solitarily. Previous long-term studies over 8 years revealed that the lower the population density, the more striped mice live solitarily. Now we want to test whether social flexibility, which is adaptive due to environmental variation over time, is also an adaptation to geographic variation.

In the Succulent Karoo, striped mice live in relatively small demes of several hundred to a few thousand individuals along dry riverbeds. These demes are isolated from each other via habitat that is uninhabitable for striped mice due to the lack of cover and food. Using genetic markers, we found that striped mice disperse over these unoccupied habitats to find other striped mouse demes several km away, travelling through hostile environments. However, they are unaware of the prevailing conditions in these different habitats. We know that it is mainly striped mice of below average body mass that disperse over these areas, possibly making the best of a bad job.

The postdoc will study 8 demes of striped mice (Rhabdomys pumilio) within the Goegap Nature Reserve in the Succulent Karoo of South Africa simultaneously during one breeding season, with the help of 8 research assistants. We expect to find significant differences between demes in 1) mean body mass of adult breeders; 2) population density; and 3) social organisation, especially the ratio of solitary vs. group-living individuals. The main field site is well established, and the population has been permanently monitored by a team at the research station for over a decade. Striped mice will be trapped, marked, and observed, and blood samples will be collected for hormone analyzes in Strasbourg.

Objectives

1. Relate geographic variation in population density to social flexibility.

2. Study the adaptive value of male dispersal.

3. Study the endocrine modulators of emigration and social flexibility, with a focus on testosterone and corticosterone levels.

4. Analyse and publish long-term data in the first year

Salary: This position is funded by the University of the Witwatersrand with a very competitive salary of R 198 432/ year, which allows for a comfortable standard of living in South Africa. In addition, medical aid is paid by the University as well as relocation costs of R10 000.

Starting date: July to November 2017 (variable).

Time schedule: The postdoc will first help with data collection in Goegap to become familiar with all field techniques. Up until April 2018, she/he will analysize and publish existing long-term data. The topic of this long term data will be discussed, but could be understanding the evolutionary, ecological and endocrine reasons for the occurrence of bachelor (all male) groups during some breeding seasons, or a project on sociogenetics, using a 8 years pedigree database. From May 2018 onwards, the different field sites will be prepared and research technicians trained. Main data collection will be from 1st July to 15th October 2018. Afterwards, data will be analysed and published.

Profile and requirements for the candidate:

- Must have obtained your PhD within the last 5 years

- Enthusiastic about field work with the willingness to spend 9 months /year in the field.

- Good organizational skills and the ability to work independently.

- Good personal skills and ability to lead a research team

- You can produce outstanding academic results!

- Strong background in eco-physiology and/or behavioral ecology.

- Very good writing skills proven by a good publication record.

- Good technical skills.

- Strong experimental, analytical and statistical skills.

Applicants should send a cover letter detailing their motivation and expectations of this position, a CV, and contact information of at least two referees combined into a single PDF to Neville Pillay (Neville.Pillay@wits.ac.za) and Carsten Schradin

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

WorkshopsCourses

Barcelona IntroPhylogenetics Jun26-30

Dear colleagues,

Registration is open for the course “Introduction to Phylogenetic Inference and its Applications”.

Dates: June 26th-30th, 2017.

Instructors: Dr. Miquel Arnedo (Universitat de Barcelona, Spain) y Dr. Salvador Carranza (Institut of Evolutionary Biology (CSIC-UPF, Spain).

PLACE: Facilities of the Centre de Restauració i Interpretació Paleontologica, Els Hostalets de Pierola, Barcelona (Spain).

During this course instructors will guide attenders and will provide training in conceptual and practical aspects of biological systematics. They will present the main methods of phylogenetic inference (parsimony, maximum likelihood and Bayesian inference), evolutionary models, data combinability, the estimation of divergence times and the use of quantitative approaches to species delimitation. Moreoverm in hands on computer sessions, we will introduce the most widely used computer programs for building alignments, selecting evolutionary models, inferring trees under alternative assumptions, estimating divergence times and delimiting species.

The participants are welcome to bring their own data and problems to be used during the practical sessions.

The course is aimed at advanced undergrads, PhD students, post-docs and faculty interested in the use of phylogenies for addressing evolutionary and ecological questions but with limited background in systematics and phylogenetic inference. All participants must bring their own personal laptop.

Registration and more info: http://www.transmittingscience.org/courses/phylogeny/introduction-phylogenetic-inference-applications/
PROGRAM: http://www.transmittingscience.org/courses/phylogeny/introduction-phylogenetic-inference-applications/#program This course is organized by Transmitting Science, the Institut Català de Paleontologia and the Centre de Restauració i Interpretació Paleontologica.

With best regards

Sole

Soledad De Esteban-Trivigno, PhD. Scientific Director Transmitting Science www.transmittingscience.org
soledad.esteban@transmittingscience.org

Berlin RNA-seqAnalysis Jun12-16

Using the Trinity Framework for De novo Transcriptome Assembly, Annotation, and Downstream Expression Studies

June 12-16, 2017, Berlin (Germany)

http://www.physalia-courses.org/courses/course11/ Instructors:

Brian Haas http://www.physalia-courses.org/instructors/t12/ (Senior Computational Biologist at the Broad Institute)

Timothy Tickle http://www.physalia-courses.org/instructors/t13/ (Senior Software Engineer at the Broad Institute)

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.

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.

Curriculum:

Day 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

Day 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

Day 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.

Day 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.

Day 5: Review and custom data analyses

Further information:

The cost is 530 euros (VAT included) including refreshments and course material. We also offer an all-inclusive option at 795 euros (VAT included), including course material, breakfast, lunch, dinner, refreshments, and accommodation.

Application deadline is the 12th of May 2017.

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

info@physalia-courses.org

http://www.physalia-courses.org/ Twitter: @physacourses

Carlo Pecoraro <info@physalia-courses.org>

Berlin ScientificWriting Mar28-29 2

Dear all,

we still have a few places available on our "Scientific Writing: organization and motivation booster" Workshop, 28-29 March 2017 in Berlin Germany

http://www.physalia-courses.org/courses/course7/ Instructor: Dr. Andrea Sanchini (Robert Koch Institut, Berlin)

Overview

Scientific writing is hard. Young students have difficulties in writing their articles or theses and at the same time carrying out their research projects. Supervisors and Professors have difficulties to train younger scientists in scientific writing. In addition, the standards for the publication of research articles and other scientific documents are increasing. This course is intended to be very pragmatic: we will develop a set of how-to information for writing research articles and for increasing writing productivity. The aim of this course is to give to participants the knowledge and the tools to change and improve their routine writing activities. At the end of the course the participants will became more organized and motivated in scientific writing.

Teaching format

The instructor provides lectures and tips from own writing experience. Participants will do writing exercises individually and in groups in order to apply the knowledge acquired during the lectures. The instructor provides also practical examples on how to use software useful for scientific writing. There will be enough time to share feedback and challenges in group discussions.

Preparing for the course

During the course, participants can draft part of their next writing project (one to two pages). This project can be a research article or a thesis.

Therefore participants are asked to decide in advance which writing task they want to do during the course.

Intended audience

The course is especially useful for PhD candidates of Natural, Life and Social Sciences faculties at any stage of their PhD. The course is also useful for young students such as Bachelor and Master Students of the same faculties in order to make them already familiar with the process of scientific writing. More experienced scientists and researchers can also take advantage of the course, since they can improve their writing skills and productivity.

Course Program

1st Day

Session 1: Challenges in scientific writing

In the first session of the course participants will get familiar with the basic principles of scientific writing. The instructor will show the common challenges and typical blocks regarding scientific writing. The instructor will also show misconceptions about scientific writing and wrong habits that lead to write slowly and to produce poor texts. The participants will then learn about the different stages of the writing process, and how to effectively organize their writing projects. At the end of the session participants will also explore the most common causes of unclear scientific writing.

Session 2: Structure of a research article

Here the instructor presents the main sections of a research articles: Introduction, Methods, Results, Discussion, References and Abstract. Particular importance will be given to the paragraph structure, which can be used as basic writing unit of a research article. The instructor will also present how to manage the flow of information in scientific writing.

2nd Day

Session 3: Figures and Tables

In this session the instructor will explain how to effectively present the scientific information in figures and tables in a clear and unambiguous way. In addition, information on how to write figure and table legends will also be provided.

Session 4: Writing productivity

Here the instructor shows the different types of writers and their respective advantages and disadvantages for scientific writing. The instructor will show several techniques, software and motivational tools to increase the writing productivity and remove writers' blocks. The aim is to show that writing productivity is a skill that can be learned and mastered with discipline and commitment.

Session 5: Self- and team-management of the writing process

In the last session the instructor will focus on the management part of scientific writing. Specifically the team work among co-authors and supervisors, how to organize the time effectively in order to reach the writing goals, how to plan the writing projects and how to increase efficiency through self-assessment.

Further information:

The cost is 350 euros (VAT included) including refreshments and course material. We also offer an all-inclusive package at 460 euros (VAT included), including course material, refreshments, accomodation and meals (breakfast, lunch, dinner).

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

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http://www.physalia-courses.org/ Twitter: @physacourses

mobile: +49 15771084054

Skype: carlo_pecoraro

ColoradoStateU GenomicsOfDiseaseInWildlife Jun3-7

Where: Colorado State University_Colorado What: Genomics of Disease in Wildlife Workshop When: June 3-11, 2017

Website for more information and application instructions: www.gdw2017workshop.colostate.edu Application Deadline: February 1, 2017

Email inquiries: CVMBS_genomics2017@mail.colostate.edu

Overview:

Title: Genomics of Disease in Wildlife: A Workshop

Location: Lory Conference Student Center, Colorado State University, Fort Collins, CO

Dates: June 3-11, 2017

Website: www.gdw2017workshop.colostate.edu Application deadline: February 1, 2017.

Wildlife biodiversity can be drastically affected by the outbreak and transmission of disease pathogens in both natural habitats and ex situ populations. Recent technological advances in genomic sciences and increasingly affordable Next Generation Sequencing (NGS) assay costs have coalesced to result in powerful tools to monitor, detect, and reconstruct the past, present and future role of pathogens within wildlife biodiversity. This short course will provide hands-on training for graduate level and above researchers in wildlife disease related disciplines seeking to incorporate genomic data into their projects. The course will be taught by a core group of experts in genome data analyses with invited faculty comprised of pre-eminent scientists performing cutting edge of research in host-pathogen genomics in wildlife.

Why is the course needed?

Advances in genomic technology now provide an extraordinary opportunity to rapidly assess the impact of disease in wildlife biodiversity, management, and conservation. Wildlife researchers are uniquely positioned to merge ecological, biological, and evolutionary studies with genomic technologies to generate unprecedented Big Data tools in disease research. The workshop will provide a venue to accomplish this goal, will provide networking opportunities for colleagues from intersecting interests, and will advance genomic tools in wildlife disease investigations.

How will the course address the need?

The course will provide essential training to wildlife biologists, veterinarians, conservation managers, and related experts to successfully incorporate NGS data in wildlife research. Attendees will conduct hands-on analyses of real world genomic data of both host and pathogen. The course will provide: (1) an overview of current bioinformatics developments and approaches; (2) guidance to implement genomic tools in study design; (3) NGS data analysis and interpretation; and, (4) opportunities for interaction with peers, core faculty, and invited experts.

Workshop Syllabus

The workshop will cover a typical workflow commonly used in NGS analyses starting with the initial raw sequence through the final stages of identifying host:pathogen variants linked with disease. Each of the eight days of the workshop will cover an essential component of the NGS workflow in succession.

Morning sessions will be a series of instructional lectures and demonstrations that will concisely present the purpose, justification and implementation of the specific workflow unit. Short and exciting flash talks presented by CSU faculty will present some of their ongoing investigations using genomic tools in wildlife disease. The afternoon sessions will be computer-intensive labs in which attendees will perform hands-on analyses with real-world genomic data for each workflow topic. Evening plenary lectures from invited faculty will conclude each days activities.

Teaching tools will include exercises using real-world NGS data from a range of pathogens and host species. Participants will learn the importance of integrating NGS data from both host and pathogen in order to better understand current epidemics in wildlife.

For the duration of the course, each attendee will be provided with a MacBook Pro computer and peripheral equipment, and prepared genome datasets from several host species and associated pathogens. These datasets will be organized into various files and formats prior to the course, demonstrate key concepts, and be the foundation for computer exercises and teaching tools.

Summary of Workshop Schedule

Day 1: Arrival, Registration and Opening Reception. The workshop begins in the evening of Sunday June 3, 2017 at the Lory Conference Center. A welcome session will introduce faculty and an overview of the workshop. An informal welcome reception follows with faculty, staff and participants.

Day 2: Optimizing NGS data and study design. Lectures and computer labs will introduce the different types of NGS data and how to best use these data in the study of disease in wildlife. Topics will include the latest advances in NGS technologies, NGS definitions, examples, applications, and experimental design. Computer lab will introduce host and pathogen datasets for the workshop, methods in genome mining, and navigating genome browsers.

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ErasmusMundus Program 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.

Being financed by the European Community, MEME has to satisfy the high quality standards imposed the prestigious Erasmus+ Program. 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: 15 August 2017

Application deadline: 1 February 2017

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)

Glasgow Bioinformatics Jul3-7

'Bioinformatics for geneticists and biologists (BIGB02)

Delivered by Dr. Nic Blouin and Dr Ian Misner

http://www.prstatistics.com/course/bioinformatics-for-geneticists-and-biologists-bigb02/ This course will run from 3rd - 7th July 2017 at SCENE Field Station, Loch Lomond, Glasgow

OVERVIEW The handling of large datasets has become intractable without some level of bioinformatic literacy. Many biologists find that there is a steep learning curve to develop the confidence required to explore their genomics datasets effectively. This bioinformatics short course includes a rich collection of hands-on instruction and lectures specifically intended to help novice users become comfortable with a range of tools currently used to analyse next-generation data.

INTENDED AUDIENCE The course is aimed at anyone interested in learning bioinformatics tools needed for handling large genomic datasets.

Course content is as follows

Monday 3rd - Classes from 09:00 to 17:00 Module 1: Linux. Linux is taught on the first day, this takes the entire day. Once you get through this portion you will be on your way to completing your own NGS analysis. We have created a workbook for this portion of the course. This is a step-by-step, or in the case, command-by-command, Linux guide. We complete each command as a class and discuss and review issues along the way.

Tuesday 4th - Classes from 09:00 to 17:00 Module 2: RNAseq. We will cover two of the more popular tools in this workshop, The Tuxedo package & Trinity. Outcomes; Confidence to design effective RNAseq experiments. Knowledge of NGS sequencing platforms and their differing applications, ability to analyze Illumina data for quality and contamination. Proficiency to implement the Tuxedo package to analyze an RNAseq dataset.Create publication ready graphics with cumeRbund and EdgeR.

Wednesday 5th - Classes from 09:00 to 17:00 Module 3: Assembly. Whether you have a reference genome or are working with de novo samples there are some basic tools and practices that we cover to help assist you in your genome project. In this module we will cover the basic metrics you should review when doing assembly as well as best practices to consider in your own project. Outcomes; Take raw reads through a complete assembly process. Working knowledge of different assembly issues/challenges. The effect of assembly settings on assembly outcomes.

Thursday 6th - Classes from 09:00 to 17:00 Module 4: Annotation. We will use MAKER and Blast2GO and annotate the genome we assembled in the assembly module. Outcomes; Understand the differences between functional and structural annotations. Train MAKER to improve structural annotations. Understand how MAKER improves with more evidence and training; visualize structural annotations. Apply functional annotations with Blast2GO.

Friday 7th - Classes from 09:00 to 16:00 Module 5: Python. Why Python? In truth it doesn't matter what coding language you learn but you should learn one. Python has a very straightforward syntax that is easy to understand.In this module we will utilise the clearly explained training examples from Python for Biologists. Outcomes; Understand Python language syntax. Create scripts to answer biological problems & parse and analyse BLAST outputs using custom Python code.

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

Upcoming courses - email for details oliverhooker@prstatistics.com

1. MODEL BASED MULTIVARIATE ANALYSIS OF ECOLOGICAL DATA USING R (January 2017) http://www.prstatistics.com/course/model-base-multivariate-analysis-of-abundance-data-using-r-mbmv01/ 2. ADVANCED PYTHON FOR BIOLOGISTS (February 2017) http://www.prstatistics.com/course/advanced-python-biologists-apyb01/ 3. STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR USING R (February 2017) http://www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm03/ 4. NETWORK ANAYLSIS FOR ECOLOGISTS USING R (March 2017) http://www.prstatistics.com/course/network-analysis-ecologists-ntwa01/ 5. ADVANCES IN MULTIVAIRAITE ANALYSIS OF SPATIAL ECO-

LOGICAL DATA (April 2017)

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Guarda Switzerland Evolution Jun17-24

It is my pleasure to announce the 2017 Guarda summer school in Evolutionary Biology for master and PhD students. The main aim of the course is to develop the skills to produce an independent research project in evolutionary biology.

The summer school takes place 17. - 24. June in the Swiss mountain village Guarda. Faculty includes Rosemary and Peter Grant (Princeton University, USA), Dolph Schluter (University of British Columbia, Canada), Sebastian Bonhoeffer (ETH-Zurich, Switzerland) and Dieter Ebert (Basel University, Switzerland; organizer).

The course is intended for master students and early PhD students with a keen interest in evolutionary biology.

The web page with all details:

http://www.evolution.unibas.ch/teaching/guarda/index.htm Application is open now. Deadline is 1. February 2017

Please communicate this information to interested students.

With best wishes,

dieter ebert

–

Dieter Ebert

University of Basel,

Zoological Institute,

Vesalgasse 1,

4051 Basel,

Switzerland

Tel. +41 (0)61 267 03 60

Email: dieter.ebert@unibas.ch

"dieter.ebert@unibas.ch" <dieter.ebert@unibas.ch>

LiveVideo NatSelectionGenomicData Dec16-18

VIDEO STREAMING of the workshop "Inferring natural selection from genomic data", will be available starting at 2PM (local time), December 16, 2016.

http://seatv.unife.it/ The workshop is held in Ferrara, Italy. See the web site http://www.sibe2016.it/ for the program.

Regards Giorgio Bertorelle

Giorgio Bertorelle Department of Life Sciences and Biotechnology University of Ferrara http://docente.unife.it/giorgio.bertorelle Phone +39 0532 455743 Fax: +39 0532 249761

Bertorelle Giorgio <ggb@unife.it>

MaxPlanckInst EvolBio OnePastHealth DeadlineDec21

This is a reminder for our workshop on zoonotic diseases, host-parasite coevolution and ancient DNA (aDNA). *Deadline is Dec 21 !!*

The Max Planck Institute for Evolutionary Biology and the Robert Koch Institute are organizing the workshop

One Past Health

- Understanding past zoonotic events to predict future ones -

from February 15th to 17th, 2017, at the Max Planck Institute for Evolutionary Biology in Ploen/Germany.

http://web.evolbio.mpg.de/OnePastHealth This workshop aims to foster the interdisciplinary dialog between medical, veterinary and biological sciences, bringing together empirical and theoretical researchers interested in disease ecology, epidemiology, host-pathogen coevolution, paleogenomics, and more. The resulting interactions will promote interdisciplinary scientific progress and may ultimately help uncovering ways to prevent future zoonotic events.

Synopsis: Many infectious diseases that are of high public health relevance today find their roots in past zoonotic events, e.g. the HIV-1 pandemics. Similarly, for these infectious diseases involving recurrent transmission from zoonotic reservoirs, most transmission events lie in the past, e.g. the historical pandemics of Yersinia pestis. These past events are an immense, precious and underexplored record of the processes leading to zoonotic emergence.

We have some tools to indirectly frame the context of zoonotic events. Historical outbreak records are such a tool but unfortunately often reveal a very unclear source of information. Over the last 2 decades, we took advantage of major advances in molecular biology, statistics and computational sciences to leverage the power of a natural record of the evolutionary history: the genetic diversity of present-day pathogens. This information was used to determine the origin in time and space as well as the later spread of Ebola viruses or HIV-1. But what if we could travel back in time and observe what really happened? We could then directly test the hypotheses we derive from present-day genetic diversity and catch evolution red-handed at crucial steps of the emergence process. Ancient DNA (aDNA) approaches are now ripe to simultaneously investigate the evolution of many pathogens (including zoonotic ones) and the evolution of the immune system of their hosts. This maturity nicely coincides with the development of modeling frameworks that allow us to make the most of heterochronous data and to describe individual pathogen trajectories in the context of the microbial communities they belong to.

Confirmed keynote speakers are:

Charlie Nunn, Duke University, USA Christian Drosten, Uni Bonn, Germany Frank Kirchhoff, Uni Ulm, Germany Simone Sommer, Uni Ulm, Germany Philippe Lemey, KU Leuven, Belgium Johannes Krause, MPI-SHH, Germany

Registration: There will be some slots for contributed talks as well as a poster session. Registration is on a first-come-first-serve basis. Deadline for registration is December 21st 2016. Please see the registration page on the workshop website for more details:

http://web.evolbio.mpg.de/OnePastHealth _Organizers:_ Sebastien Calvignac, Robert Koch Institute, Berlin Tobias Lenz, MPI for Evolutionary Biology, Ploen

Dr. Tobias Lenz, Group Leader Emmy Noether Group for Evolutionary Immunogenomics Department of Evolutionary Ecology Max Planck Institute for Evolutionary Biology August-Thienemann-Str. 2 24306 Ploen, Germany Tel: +49 4522 763-228 Fax: +49 4522 763-310 Email: lenz@evolbio.mpg.de http://www.evolbio.mpg.de/-EvolutionaryImmunogenomics "lenz@evolbio.mpg.de" <lenz@evolbio.mpg.de>

MNHN Paris DNABarcodesTaxonomy Mar13-17

The course "Integrative taxonomy and taxonomic expertise : DNA barcodes in the genomic era" will be from the 13th to the 17th of March, 2016 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 < https://sites.google.com/site/coursbarcode/ >) before the the 3rd of January, 2017.

If you have any question, please contact: Line Le Gall (legall@mnhn.fr) Nicolas Puillandre (puillandre@mnhn.fr) Sarah Samadi (sarah@mnhn.fr)

nicolaspuillandre@gmail.com

Naples EMBOPopulationGenomics May18-26

EMBO, in collaboration with the Elixir-ITA, Isita and the IGB-CNR, is pleased to inform you that the applications for the upcoming training course on "Population Genomics: background and tools" are now open.

IMPORTANT DATES for this Course: Deadline for applications: 24/02/2017 Latest notification of acceptance: 10/03/2017 Course date: 18-26/05/2017 Venue: National Research Council, Institute of Genetics and Biophysics, via P. Castellino 111, 80131 Naples, Italy

A maximum of 24 candidates will be selected based on their application. Notifications of acceptance will be sent shortly after the closing date of registration.

Full details, including the course programme and the application form, at: http://meetings.embo.org/event/-17-population-genomics Instructors: Aida Andres (Max

Planck Institute for Evolutionary Anthropology, Germany) Andrea Manica (University of Cambridge, UK) Andrew Clark (Cornell University, USA) Garrett Hellenthal (University College London, UK) Ida Moltke (University of Copenhagen, Denmark) Martin Sikora (Natural History Museum of Denmark, Denmark) Mathias Currat (Université de Genève, Switzerland) Olivier Delaneau (Université de Genève, Switzerland) Pascale Gerbault (University of Westminster, UK)

Course description Study methods in population genomics have been profoundly reshaped in the last few years thanks to the growing availability of complete genomic sequences at population level. The rapid and recent growth of data and methods calls for new approaches to become routine in evolutionary genomics laboratories. The objective of this EMBO Practical Course is to give an overview of state of the art methods in population genomics combining lecturing from outstanding experienced population geneticists and software developers. All conceptual innovation will be presented in lectures and applied in practice both individually and in group work. Practicals includes computer exercises supervised by lecturers and training assistants. After attending the course participants will be aware of up-to-date concepts in population genetics, capable of running analyses using software based on whole genome data sequences and able to deal with basic aspects of any population genomics project. This EMBO Practical Course aims at evolutionary biologists who already have bioinformatics skills. PhD students and Post-Doc researchers will benefit the most out of this course, but applications from all candidates will be evaluated in their context.

Thank you for your interest, The Organisers

Chiara Batini (University of Leicester, UK) Vincenza Colonna (CNR, Napoli, IT) Allegra Via (CNR, Bari, IT)

"cb334@leicester.ac.uk" <cb334@leicester.ac.uk>

NGSTraining

Have your say on Bioinformatics and NGS training

New to NGS? Struggling with bioinformatics? Looking for help?

University of Leicester's Bioinformatics and Biostatistics Analysis Support Hub (BBASH) offers courses in bioinformatics with an emphasis on next-generation sequencing.

To help us understand your training needs we invite you to fill out this survey:

https://goo.gl/forms/3L31QIvtswAsyNLL2 Your responses will help us to shape our courses to your needs.

Bioinformatics and Biostatistics Analysis Support Hub (BBASH) University of Leicester, University Road, Leicester, LE1 7RH, UK w: www.le.ac.uk/bbash e: ngstraining@leicester.ac.uk

ngstraining@leicester.ac.uk

Portugal EvolBiol Jan-Feb

Subject: Portugal-cE3c-Course: four advanced courses with deadlines January 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=8 Course Biodiversity and Plant Evolution organized by Helena Cotrim and Manuela Sim-Sim | January 23-27, 2017@ Lisbon, Portugal

Objectives: On completion of the course, the students shall have acquired the following knowledge and understanding: Describe the main evolutionary acquisitions on groups of the plant kingdom and its adaptive significance.

- Comprehend the modern plant phylogeny and its sources of information. - Explain the underlying evolutionary mechanisms of diversity and speciation in the plant kingdom. - Describe the variety of pollination syndromes, reproductive systems and population structures present in the plant kingdom, and explain the mechanisms underlying this diversity. - Explain and critically analyse how the genetic diversity and evolutionary potential of plant populations are influenced by phenomena like phenotypic plasticity, seed banks, hybridization, polyploidy and postglacial colonization history. - Formulate hypotheses and propose methods when studying evolutionary phenomena in wild plant species.

Course instructors Helena Cotrim (hmcotrim@fc.ul.pt) Assistant Professor at the Faculty of Sciences of the University of Lisbon, researcher at the

Centre for Ecology, Evolution and Environmental Changes (http://ce3c.ciencias.ulisboa.pt/member/-helena-maria-da-conceiccedilatildeo-cotrim)

And

Maria Manuela Sim-Sim (msimsim@fc.ul.pt) Assistant Professor at the Faculty of Sciences of the University of Lisbon, coordinator of the NHS research group at the Centre for Ecology, Evolution and Environmental Changes (http://ce3c.ciencias.ulisboa.pt/member/-maria-manuela-pinheiro-sim-sim)

Intended audience: This five days intensive course will be open to a maximum number of 10 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics.

Minimum formation: Bachelor in Biology or related area.

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: January 8th, 2017

Candidates should send a short CV and motivation letter to Helena Cotrim (email hmcotrim@fc.ul.pt)

For additional details about the course and to know how to register, click here: http://ce3c.ciencias.ulisboa.pt/-training/?cat=8 For more information about the course, please contact: Helena Cotrim (email hmcotrim@fc.ul.pt) or Maria Manuela Sim-Sim (email: msimsim@fc.ul.pt) Course Practical Course on Phylogenetics organized by Octavio Paulo| January 30 -February 3 2017 @ Lisbon, Portugal

Objectives: Phylogenetics is one of the scientific areas of Biology that has grown fast and evolved in methodological terms in the last years. Its applications go from the studies of the evolution of species and populations to the least expected, as the study of the origin of the AIDS virus or seasonal cycles of the flu. The course is aimed at students and professionals that intend to get started in phylogenetic analysis as well as researchers already with some experience wanting to deepen or update their knowledge in the field. The course consists of theoretical classes as well as hands-on practical sessions using software. Participants are encouraged to bring their own sequence data for analysis.

Course instructor Octavio Paulo (octavio.paulo@fc.ul.pt) Professor at the Faculty of Sciences of the University of Lisbon, researcher at the Centre for Ecology, Evolution and Environmental Changes (http://ce3c.ciencias.ulisboa.pt/member/-octaacutevio-s-paulo), Coordinator of the Computational Biology & Population Genomics Group (http://ce3c.ciencias.ulisboa.pt/team/COBIG2)

Intended audience: This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD or MSc students in Biology, Evolution, Genetics or related areas, and postdocs and other professionals working in related topics.

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Switzerland EvolBiol Jun17-23

Evolutionary Biology Workshop in the Alps

(The previous posting contained a typo in an invited professor's name, for which we apologize.)

The 2017 edition of the Evolutionary Biology Workshop in the Alps will take place on 17-23 June 2017 in Riederfurka, Switzerland.

Target participants are PhD students in early stages of PhD and advanced Master students.

The main goals of this annual workshop, based on a concept developed by Stephen Stearns and John Maynard Smith, are to develop the following skills: - developing your scientific ideas through discussions in groups; - thinking critically and expressing oneself clearly; - turning a general idea into a research project; - writing a research proposal and defending it.

Faculty: Lynda Delph (Indiana University) Curt Lively (Indiana University) Noah Whiteman (University of California Berkeley) Sergio Rasmann (University of Neuchatel) Tadeusz Kawecki (University of Lausanne)

It is you, the students, who will be in charge in this course. You will be divided in groups of 4-5 students. In those groups, you will work on your ideas. You, as a group, will decide what the important open questions in broadly defined evolutionary biology are, you will choose one, and attempt to develop a proposal for a research project that will address it. The faculty will visit the groups during the discussions to answer questions, provide coaching and give feedback on the projects, but they will generally take the back seat. Additionally, the faculty will give informal talks about their research and be available for informal discussions with individual students. At the end you will present your projects to other participants, and we will party.

The workshop will take place in Villa Cassel (http://www.pronatura-aletsch.ch/home-en), at 2000 m of altitude, in a 110 year old villa where Winston Churchill once stayed, amid the magnificent mountain landscape of a UNESCO World Heritage Site, and a walking distance from the largest glacier of the Alps. This isolated site will help you to concentrate on the course while giving you also the chance to enjoy the views and the alpine flora.

Fee: CHF 490.-

Participants will receive a course certificate for 3 ETCS credits.

To apply, send a single file (pdf or rtf) containing a short motivation letter including a brief summary of your research interest, a cv, and the name of your scientific advisor to Caroline Betto-Colliard <Caroline.Betto-Colliard@unil.ch>, with Cc to tadeusz.kawecki@unil.ch . Please put "Evolutionary workshop" in the subject. Application deadline: 29 January 2017.

"tadeusz.kawecki@unil.ch" <tadeusz.kawecki@unil.ch>

Venice EvoDevo Sep18-21

Summer School on Evolutionary Developmental Biology Conceptual and Methodological Foundations

5th Edition: Process Thinking for Evo-Devo

Venice, September 18th-21st 2017

Organizers: Alessandro Minelli, Gerd B. Müller and Giuseppe Fusco School director: Johannes Jaeger

School sponsors: Istituto Veneto di Scienze, Lettere ed Arti (IVSLA), Venice and Konrad Lorenz Institute for Evolution and Cognition Research (KLI), Vienna.

Location: Istituto Veneto di Scienze, Lettere ed Arti, Palazzo Franchetti, Venice

Taching panel: Johannes Jaeger (School Director, KLI Klosterneuburg, Austria), Scott Gilbert (Swarthmore College, Swarthmore, PA, U.S.A.), James DiFrisco (KLI Klosterneuburg, Austria), Nick Monk (University of Sheffield, U.K.), Berta Verd (KLI Klosterneuburg, Austria), Ron Jenner (Natural History Museum, London, U.K.), Graham Budd (University of Uppsala, Sweden), Stuart Kauffman (Institute for Systems Biology, Seattle, WA, U.S.A.)

Deadline for applications: May 30th 2017

For details, visit http://www.istitutoveneto.org/EDB2015/ Giuseppe Fusco Department of Biology University of Padova Via U. Bassi 58/B I-35131 Padova Italy tel. +39.049.827.6238 fax +39.049.827.6230 e-mail giuseppe.fusco@unipd.it webpage http://dept.bio.unipd.it/fusco

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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.