EvolDir

February 1, 2018

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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ArizonaStateU MutationRateEvolution Mar27-28

Mutation Rate Evolution Meeting

Date: March 27-28th, 2018 Location: Arizona State University, Tempe (AZ), USA

Join us on March 27-28th 2018 at Arizona State University's Center for Evolution and Medicine for the Mutation Rate Evolution Meeting. This meeting aims to bring together leading experts, early-career researchers, and trainees interested in studying mutation rates in different organisms. Students/Postdocs will have an opportunity to present their work, and to network with other colleagues in the field.

Keynote Speakers Oskar Hallatschek, University of California, Berkeley, US Kelley Harris, University of Washington, Seattle, US Peter Keightley, University of Edinburgh, Edinburgh, UK Michael Lynch, Arizona State University, Tempe, US Gil McVean, Oxford Big Data Institute, Oxford, UK Susanne Pfeifer, Arizona State University, Tempe, US Anna Selmecki, Creighton University Medical School, Omaha, US Anne Stone, Arizona State University, Tempe, US

Google Travel Awards In order to foster exchange between early-career women and leading research scientists in the field, Google is sponsoring a limited number of travel awards to support the participation of female undergraduate, graduate, and postdoctoral fellows.

Registration Registration is free of charge but mandatory. Breakfast, lunch, and coffee will be provided during the meeting. The meeting is limited to 50 participants and priority will be given to participants who are submitting an abstract to present their work at the meeting.

Registration and abstract submission is now open. Abstract submission deadline: January 31st 2018.

For more information, to register, or to submit an abstract, visit http://spfeiferlab.org/meeting spfeife1@asu.edu

Bangalore India ButterflyEcolEvol Jun11-14

8th International Conference on the Biology of Butterflies

Dates: 11-14 June 2018

Place: Bangalore, India

The 8th International Conference on the Biology of Butterflies conference will be held in Bangalore, India, from 11-14 June 2018. The International Conferences on the Biology of Butterflies are international gatherings, organized every four years, of primarily professional biologists who study evolutionary biology, behaviour, ecology, systematics, biogeography, genetics, developmental biology, and biodiversity conservation, with butterflies and moths as their focal study organisms. This is an excellent academic and professional forum for latest discoveries and to exchange news in these research areas.

Tourism: Visiting Bangalore for the conference will also provide a fantastic opportunity to for cultural and natural history tours. We are organizing a 1 day pre-conference field trip to Makalidurga near Bangalore, and will facilitate longer post-conference trips to some exciting places in the Western Ghats. The BoB website has more information. We encourage you to visit along with family and friends

Workshop: We will also have a 3 day post-conference workshop (19-21 June) intended primarily for students interested in butterfly biology. This will be held in Coorg, ca. 270 km from Bangalore.

Website: www.biologyofbutterflies.org Organisers: Krushnamegh Kunte (krushnamegh@ncbs.res.in) Ullasa Kodandaramaiah (ullasa@iisertvm.ac.in)

ullasa@iisertvm.ac.in

Florence SEBAnnualMeeting Jul3-6

Dear colleagues,

We are organising a session on âof the 'pace-of-life syndrome' concept: Is the idea of integrated syndromes supported by experimental data?' at the Society of Experimental Biology's Annual Meeting < www.sebiology.org/events/event/seb-florence-2018/-programme/animal-biology#paceoflife > in Florence (3-6 July 2018).

The programme has some great sessions covering animal, plant, cell biology and education. There is also the opportunity to submit your research to any of the sessions. Abstract submission is now open, < www.sebiology.org/-events/event/seb-florence-2018/abstracts >

Please see below the abstract and invited speakers for the âof the 'pace-of-life syndrome' concept: Is the idea of integrated syndromes supported by experimental data?" session. We hope to attract a wide range of talks and posters focussed on this topic!

Best wishes, Jenni Prokkola, University of Liverpool Tommy Norin, University of Glasgow Neil Metcalfe, University of Glasgow Anssi Vainikka, University of Eastern Finland Petri Niemelä, LMU-München

âof the 'pace-of-life syndrome' concept: Is the idea of integrated syndromes supported by experimental data?' < www.sebiology.org/events/event/seb-florence-2018/-programme/animal-biology#paceoflife >

Denis Réale (Université Du Québec Ã€Montréal, Canada) - The pace-of-life syndrome hypothesis: life-history roots, mixed support, and future directions

Anne Bronikowski (Iowa State University, USA) - Empirical evaluation of the pace-of-life syndrome at genetic, physiological, and population levels of organization in the garter snake, Thamnophis elegans

Joacim Näslund (University of South Bohemia In Äeské BudÄjovice, Czech Republic) - The complex pace-of-life syndrome of trout: state-dependence, behavioural types, and territoriality

Kate Laskowski (Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Germany) - Individual behaviour, foraging specializations and life-history strategies as integrated phenotypes in a wild pike population

Animal life-history is characterised along a slow-fast continuum: "slow" species, populations, or individuals exhibit slow developmental rates, low and delayed reproductive outputs, and long life spans, whereas those on the "fast" track express the opposite traits. This continuum is captured by the 'pace-of-life syndrome' (POLS) concept according to which certain combinations of life-history, behavioural, and physiological traits (i.e. syndromes) may yield higher fitness than others, depending on the environment. The POLS concept is appealing to multiple research disciplines due to its capacity to predict relationships among diverse traits. However, empirical studies provide mixed support for POLS. This session is aimed at examining the generality of the POLS concept. We welcome all submissions (talks and posters) related to the POLS concept but especially encourage studies investigating (1) which combinations of traits are (or are not) consistently linked, (2) if links between traits persist across environmental gradients, stress gradients, or time, and (3) which proximate mechanisms facilitate or constrain trait (co)variation. The aim of the session is to establish an overview of the current state of research on POLS, and help bridge a gap between physiologists and evolutionary, behavioural, and molecular ecologists in order to further understand the importance of POL

jmprok@utu.fi jmprok@utu.fi

Galway Ireland EvolutionOfRegeneration Jun26-29

Dear all,

We are pleased to announce our symposium "Evolution of Regeneration in Metazoa" as part of the 7th Euro Evo Devo meeting in Galway, Ireland, 26th-29nd june next year (2018) http://www.evodevo2018.eu/ehome/-evodevo2018/Welcome/ . SYNOPSIS.This symposium is dedicated to the re-emerging field of regeneration, a widespread phenomenon in animals. Using a large variety of metazoans species and modern techniques, we intend to get a general view of the evolution of animal regeneration as well as to test the presence of general principles and/or shared genetic programs that underlie this intriguing phenomenon. A specific attention will be given to the identity, plasticity and differentiation potential of the cells required for the regeneration processes.

Our Invited speakers are Dr Maja Adamska (Australian National University, Canberra, Australia), Dr Karen Echeverri (University of Minnesota, USA), Dr Uri Frank (National University of Ireland, Galway, Ireland) and Dr Jochen Rink EMBO Young Investigator Lecture (Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany).

We invite you to submit an abstract following the online instructions on the Congress website (http://www.evodevo2018.eu/ehome/evodevo2018/-Registration/). Deadline for abstract submission (+ registration required) is 16th February 2018. Deadline for early Bird Registration Fee is 13th April 2018.

Sincerely,

Dr Eric Röttinger and Dr Eve Gazave

– Eve Gazave, PhD Chargée de Recherche CR2 Ãquipe Cellules Souches, Développement et Evolution Institut Jacques Monod , CNRS UMR 7592 Université Paris-Diderot ; Paris 7 Bâtiment Buffon. 1e étage; pièce 156b 15 rue Hélène Brion 75205 Paris cedex 13 France E-mail: eve.gazave@ijm.fr Tel (33) 1 57 27 80 03 Fax (33) 1 57 27 80 87

http://www.ijm.fr/recherche/equipes/cellules-souches-developpement-et-evolution/ https://-stemdevevo.wordpress.com/ ATTENTION : new email eve.gazave@ijm.fr

Eve Gazave <eve.gazave@ijm.fr>

Hawaii OriginsAdaptiveRadiation Jul22-25

Registration is now open for the American Genetic Association Symposium, "Origins of Adaptive Radiation", July 22-25 in Waimea, Hawaii.

The meeting will explore processes at the early stages of adaptive diversification – allopatry vs sympatry in fostering initial divergence interplay between isolation and mixing in divergence and adaptation plasticity in facilitating adaptation hybridization and admixture repeated evolution of similar forms conditions that facilitate adaptive radiation

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

We encourage all those who are interested to submit abstracts for posters. A small number of abstracts will be selected for oral presentations and associated travel compensation.

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

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

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

For all details, visit http://www.theaga.org . Best wishes,

Rosemary Gillespie, AGA President

Speakers: Key Distinguished Lecturer: Ole Seehausen, Eawag Center, Switzerland

Gordon Bennett, University of California, Merced Louis Bernatchez, University of Laval, Canada Brian Bowen, Hawaii Institute of Marine Biology

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

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

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

Karin Pfennig, University of North Carolina at Chapel Hill Dan Rubinoff, University of Hawaii, Manoa Dolph Schluter, University of British Columbia, Canada

Kerry Shaw, Cornell University Elizabeth Stacy, University of Hawaii, Hilo Katie Wagner, University of Wyoming

contact: Anjanette Baker <theaga@theaga.org>

Anjanette Baker <theaga@theaga.org>

Hinxton EvolSystemsBiol Apr11-13 DeadlineJan16

Dear all,

The early bird registration for the 2nd Evolutionary System Biology Conference in Hinxton is next week. The conference will provide a forum for scientists interested in applying systems and mechanistic approaches to understand evolution. https://coursesandconferences.wellcomegenomecampus.org/events/item.aspx?e=681 We will explore the evolution of biological systems at different levels: from genes and molecules to organism development and physiology. Particular emphasis will be placed on understanding evolution through mechanistic biology.

The programme is of particular interest to those working at the interface of evolution, quantitative genetics, and systems biology. We welcome abstracts from all areas relevant to the main themes of the meeting, for both oral and poster presentations. Several oral presentations will be chosen from the abstracts submitted.

The scientific programme committee, Ben Lehner Marie-Anne Félix Patricia Wittkopp

DEADLINES Early bird discount: 16 January Bursary deadline: 30 January Abstract deadline: 13 February Registration deadline: 13 March

KEYNOTE SPEAKERS * **Caroline Dean * John Innes Centre, UK * **Stan Leibler* The Rockefeller University, USA

CONFIRMED SPEAKERS * **Christina Burch* University of North Carolina at Chapel Hill, USA

Juliette De Meaux University of Münster, Germany * **Angela DePace* Harvard Medical School, USA

Fyodor Kondrashov Centre for Genomic Regulation Barcelona, Spain

Christian Landry Laval University, Canada

Eric Meyer Ãcole Normale Supérieure, France

Patrick Phillips University of Oregon, USA

Matt Rockman New York University, USA

Mark Siegal New York University, USA

Aleksandra Walczak Ecole Normale Supérieure, France

Daniel Weinreich Brown University, USA * **Gaël Yvert *

Ãcole Normale Supérieure de Lyon, France

– Marie-Anne Felix Institute of Biology of the Ecole Normale Supérieure (IBENS) 46 rue d'Ulm, 75230 Paris cedex 05, France 8th floor. Office: Room 801. Lab: Room 817. mail:felix@biologie.ens.fr Tel: +33-1-44-32-39-44 http://www.ibens.ens.fr/?rubrique29&lang=en STRAINS:http://www.justbio.com/worms/index.php Marie Anne Felix <felix@biologie.ens.fr>

Manchester MolGenomeEvolution Mar5

Manchester's Molecular and Genome Evolution Symposium (#MaGE2018) is back again this year on Monday 5th March! Registration and abstract submission are now open.

MaGE encompasses all aspects of molecular and genome evolution, ranging from genomic analyses or computational algorithm development, to molecular ecology, population genetics, and experimental evolution.

MaGE 2018 will be a day-long event in Manchester's Michael Smith Building, including a plenary lecture from Mike Brockhurst alongside a series of contributed talks, and a poster session. The full programme is currently being put together, but past programmes can be viewed at the URL below.

MaGE is free to attend, but places are limited so please register at the URL below, and submit a title if you would like to present a talk or poster. We are particularly keen to give PhD students and post-docs a chance to present their work. All contributed talks and posters will also be considered for a prize, presented at the drinks reception following the symposium.

Hope to see you in March!

For full details, including registration and abstract submission deadlines, see: https://manchestermage.wordpress.com/ Danna Gifford, Chris Knight and Sam Griffiths-Jones

dannagifford@gmail.com

Marseilles EvolBiol Sep25-28 EarlyDeadline

Dear all, Please note that the early dead line for the next evolutionary biology meeting at Marseilles is January 31 the meeting Will take place on September 25-28 2018 in Marseilles (South of France) more info : aeeb.fr

The following subjects will be discussed:

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

contact Marie-Hélène Rome marie-helene-rome@univ-amu.fr best regards Pierre

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

Marseilles Evolution Sept25-28

Dear all , the organisers of the evolutionary biology meeting "at" Marseilles publish in collaboration with Springer Nature a book since 2008 see for more info: http://aeeb.fr/18th-ebm-2/books/ Please note that the early dead line is January 31 The date of the meeting are september 25-28 (followed by 2 days of the visit of the city) The following subjects will be discussed: - Evolutionary biology concepts and modelisations for biological annotation; - Biodiversity and Systematics; - Comparative genomics and post-genomics (at all taxonomic levels); - Functional phylogeny; -Transposon evolution; - Convergent evolution; - Environment and biological evolution; - Origin of Life and exobiology; - Self non - self evolution; - Non-adaptative versus adaptative evolution; - The ≪ minor ≫ phyla: their usefulness in evolutionary biology knowledge.

see

aeeb.fr

best regards Pierre

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

Minneapolis BehaviouralEvolution Aug11-16

Hi, I would like to place the following announcement in EvolDir: We invite you to attend ISBE 2018, the next meeting of the International Society for Behavioral Ecology. The meeting will be held at the Convention Center in Minneapolis, Minnesota, U.S.A., from 11-16 August, 2018. We hope to have a diverse representation of behavioral ecologists on hand for an outstanding lineup of invited speakers from all over the world, as well as the usual contributed talks and poster sessions and, of course, the traditional soccer match. In addition to the fantastic science, there are lots of reasons to attend ISBE 2018. The city of Minneapolis, and its nearby sister city of St. Paul, create a vibrant cosmopolitan area (the "Twin Cities") with much to offer, and "the Land of 10,000 Lakes" (i.e., the State of Minnesota) has unmatched opportunities for outdoor activities ranging from canoeing to hiking and backpacking. Check out our excursions and attractions page for some ideas on things to do before, during, and after your visit. In the meantime, to receive periodic updates you can follow us on facebook and twitter using the "Follow" link above. We look forward to seeing you in the Twin Cities in August!

- The ISBE 2018 Local Organizers

Marlene Zuk Professor, Department of Ecology, Evolution and Behavior Associate Dean for Faculty, College of Biological Sciences University of Minnesota St. Paul, MN 55108 USA http://www.cbs.umn.edu/explore/-departments/eeb/faculty-research/directo ry/marlene-zuk Phone: 612-625-5727 mzuk@umn.edu

Marlene Zuk <mzuk@umn.edu>

Montpellier Evol2018 Aug18-22 Maladaptation

Dear Colleagues:

We are excited to announce that there will be a symposium on the topic of maladaptation at the 2018 Evolution meeting in Montpelier, France. Please see the symposium information below and consider applying and/or sharing this announcement with colleagues who may be interested.

The submission deadline is January 15th. Those interested in speaking in this symposium can submit abstracts for consideration here: http://-evolutionmontpellier2018.org/call-abstracts Symposium 58. Causes of maladaptation: environmental change, demography, inbreeding and genetic constraints

Organizers: Steven Brady, Daniel Bolnick, Anne-Laure Ferchaud, Charles Perrier, Donald Waller

Evolutionists seek to understand how populations adapt to environmental change and to predict the consequences. Selection that lags the pace of environmental change and inbreeding resulting from habitat loss and fragmentation both act to diminish the degree to which populations are adapted to their environments. Genetic drift in smaller populations also acts to constrain responses to positive and purifying selection. This will tend to increase the fixation of deleterious alleles, reducing population-wide fitness. These non-adaptive forces could eventually overwhelm adaptive ones, limiting adaptive potential of populations. Advances in genomics now empower us to detect and map adaptive and mal-adaptive variation across the genome. We welcome theoretical, methodological and empirical contributions that: (1) assess mal-adaptation and accumulated genetic load; (2) examine the role of inbreeding and other demographic processes in maladaptation; (3) describe the genetic causes of mal-adaptation including the effects of dominance, linkage and identity disequilibria, epistasis, and gene flow; (4) enhance theory on the extent of genetic change needed to rapidly adapt to rapidly changing environments, and (5) evaluate opportunities for genetic rescue versus the risk of extinction.

Invited speaker: Andrew Hendry Rethinking maladaptation

Steven Brady Assistant Professor | Southern Connecticut State University stevenpbrady.weebly.com Office: 203-392-7206 | Jennings Rm 215A

brady.steven@gmail.com

Montpellier Evol2018 Aug19-22 AdaptationAncientDNA

Dear colleagues,

Happy new year.

We are happy to invite abstract submission to our symposium on Ancient DNA studies of adaptive processes through time (S43) at the Evolution 2018 conference in Montpellier, France (http://evolutionmontpellier2018.org/symposia).

Abstract submission is open until 15 january 2018, see: http://evolutionmontpellier2018.org/call-abstracts Long-term time series data have the benefit of being able to estimate effective population size through time using neutral markers and identify the timing of demographic change relative to ecological change; and to quantify the tempo and chronology of changes in allele frequencies and sites known to be the targets of natural selection during ecological shifts. Given the temporal aspect of adaptation and speciation, ancient DNA (aDNA) techniques are an obvious and promising tool with which to track the progress of natural selection's effect upon the genome using time-series data. However, the emerging field of palaeogenomics has been under-exploited in studying this temporal component of adaptation and speciation. Here we propose to take the field a further step forward by utilising palaeogenomics to bridge this gap, allowing multi-locus adaptation, speciation and multi-species adaptive radiation to be investigated along the evolutionary continuum, from inception to completion.

Organizers: Andrew Foote, Eline Lorenzen

Best wishes, Andy

– Dr Andrew Foote Molecular Ecology Fisheries Genetics Lab, School of Biological Sciences, Bangor University, Bangor, Wales

footead@gmail.com

Montpellier Evol2018 Aug19-22 BalancedPolymorphism

Dear Colleagues,

We are pleased to invite abstract submissions to our symposium "Ecological and genetic mechanisms underlying balanced polymorphisms", at the joint ESEB-SSE Congress in Montpellier, France (19-22 Aug. 2018).

The aim of this symposium is to integrate the many facets of our knowledge of balanced polymorphisms and foster cross-talk between research on the genetics of polymorphic traits, and research on the ecology of selection explaining the maintenance of those polymorphisms.

We are also interested in research on the evolutionary paths to the formation of differentiated polymorphisms, composed of several characters with epistatic interactions.

Our invited speaker will be Clemens Kupper from the Max Plack Institute for Ornithology in Seewiesen, Germany, who will be speaking on "The genetics and evolution of elaborate mating behaviours in birds".

NOTE: ***The deadline for submissions is January 15th 2018***.

Abstracts may be submitted at: http://evolutionmontpellier2018.org/call-abstracts Our symposium abstract: This symposium will explore how balanced polymorphisms evolve, and how multiple complex strategies arise and are maintained within populations. Sometimes called syndromes, complex polymorphisms typically coordinate variations in morphology, behaviour, and/or life history traits. Classic examples include distinct sexual tactics in birds, alternative pollination strategies in plants, coexisting colony types in ants, mimicry polymorphisms in butterflies.

Contributions will address how polymorphisms that require the appropriate segregation of multiple underlying mutations are generated and maintained. We welcome contributions from empirical and theoretical perspective, and aim to highlight the considerable progress that can be driven by the combination of ecology, genetics and genomics. While some approaches clarify the genetic basis and the recombination landscape underlying the co-segregation of multiple traits (e.g. inversion polymorphisms, large structural variants, supergenes), other approaches focus on the fitness landscapes associated with stable polymorphisms (sexual antagonism, self-incompatibility, frequency-dependent selection, heterozygote advantage). Combining those facets, a clearer picture emerges of how and why genes and their associated characters co-vary in linkage disequilibrium. A third facet to our understanding of complex polymorphisms is to address the apparent paradox of how differentiated haplotypes are formed in the first place, and how new combinations of epistatic characters may be picked by selection.

Organisers: Mathieu Joron, CNRS, Montpellier, France (mathieu.joron@cefe.cnrs.fr), and Annabel Whibley, John Innes Centre, Norwich, UK (annabel.whibley@jic.ac.uk).

We look forward to seeing you in Montpellier! Mathieu Joron Centre d'Ecologie Fonctionnelle et Evolutive CNRS, 1919 route de Mende, 34293 Montpellier 5, France

Mathieu Joron <mathieu.joron@cefe.cnrs.fr>

Montpellier Evol2018 Aug19-22 DeadlineJan15

Reminder: the call for abstracts for the Joint Congress on Evolutionary Biology will soon be closed (January 15th 2018). This is the last call!

Submit now! 'V http://evolutionmontpellier2018.org/call-abstracts We are happy to inform you that abstract submission is now open for next year's 2^nd Joint Congress on Evolutionary Biology in Montpellier, France (18-22 August 2018). Joint Congresses take place every six years and bring together four of the world's largest academic societies in the field of evolutionary biology: the European Society for Evolutionary Biology < http://eseb.org >, the American Society of Naturalists < http://www.amnat.org/ >, the Society for the Study of Evolution < http://www.evolutionsociety.org/ > and the Society of Systematic Biologists < http://www.systbio.org/ >.

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

The list of symposia is available at:

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

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

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

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

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

November 6^th 2017: Call for abstracts opens

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

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

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

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

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

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

Montpellier Evol2018 Aug19-22 EvolutionaryImmunology

We welcome abstracts submitted for our symposium “Evolutionary immunology: tradeoffs and mechanisms” (S15) at the 2018 Joint Congress on Evolutionary Biology in Montpellier, France, (August 19th-22nd) with Scott Edwards as the keynote speaker.

The deadline for abstract submission is January 15, 2018. For further information please see http://-evolutionmontpellier2018.org/symposia Submissions are encouraged from scientists from diverse backgrounds with the goal of exploring how studies of disease can advance evolutionary biology and encourage evolutionary applications in medicine.

Sincerely,

Jamie Winternitz, Jessie Abbate, Randolph Nesse, Frank RÂÂ^{1}hli (organizers)

SYNOPSIS: There is growing interest in the role of trade-offs on the evolution of host defense strategies, such as competition between resistance vs. tolerance mechanisms, protection against a diversity of foreign invaders vs. vulnerability to autoimmune and inflammatory disorders, or exposure to multiple coevolving pathogens. Excitingly, advances in high-throughput sequencing technologies present the opportunity to move beyond candidate gene approaches to study host resistance using unbiased whole-genome approaches of both the host and pathogen. In addition, genome-wide association study (GWAS) approaches could also reveal the relative importance of select genes of large effect versus many genes of small effect across the genome for disease resistance. Thus, GWAS offer the potential to reveal new insights into the genetic basis of parasite-mediated selection on host and pathogen genetic diversity. This symposium will also explore how co-evolution shapes asymmetric fitness landscapes that result in apparent suboptimal immune function. Given the recent explosion of autoimmune disorders in recent decades, we especially encourage presentations that investigate this pattern through evolutionary immunological studies of trade-offs between resistance and autoimmune diseases.

Randolph Nesse <nesse@asu.edu>

Montpellier Evol2018 Aug19-22 FloralEvolution

Dear colleagues,

A reminder that the deadline for submitting abstracts to the ESEB-SSE joint meeting is only a few days away, on Monday January 15. The meeting will take place August 19-22 in Montpellier, France. We encourage you to submit an abstract to our symposium on Floral Evolution.

Our symposium is S70 : Floral evolution: breeding systems, pollinators, and beyond. Dr. Nina Sletvold, from the University of Uppsala, Sweden, is the invited speaker. Her talk is entitled “Abiotic factors, biotic context (antagonists, community) and pollinator-mediated selection”.

Abstracts can be submitted at http://-evolutionmontpellier2018.org/call-abstracts . Talks and posters of this symposium (S70) will be invited to submit for publication in a special issue of the International Journal of Plant Sciences. With your contributions, we are looking forward to a great symposium and an excellent special issue.

Symposium abstract: Pollinator-mediated selection is the major paradigm dominating the theory of floral evolution. It has been proposed as the major force directing floral trait evolution, from flower colour to phenology and floral shape. But some recent studies have raised questions about the relative importance of pollinators as selective agents on floral traits. Herbivores and abiotic stresses may counterbalance and mask pollinator-mediated selection. In addition, a plant breeding system can affect pollinator attraction and impact floral evolution. These processes can all be influenced by anthropogenic changes such as habitat loss and global warming. Finally, the genetic architecture of floral traits may constrain floral evolution and despite the major impact of floral shape on plant reproductive success, the quantitative exploration of floral shape, its evolution and diversity, and its molecular basis have received little attention. In this symposium, we intend to broaden the scope of pollination ecology in order to enhance our ability to detect the evolutionary consequences of plant-pollinator interactions. We propose to bring together new and exciting studies that shed light on evolutionary processes that shape flowers and reproductive organs in plants. Emphasis will be given to factors beyond pollination and factors that interact with pollination, from co-acting selective agents to the genetic basis of floral traits. The proposed symposium will emphasize the multifaceted process of natural selection and reexamine established paradigms in the light of new findings.

Organizers: Johanne Brunet, USDA-ARS; University of Wisconsin-Madison, USA. Diane Byers, Illinois State University, USA. Eric Imbert, University of Montpellier, France. Yuval Sapir, Tel Aviv University, Israel. Jürg Schönenberger and Yannick Staedler, University of Vienna, Austria.

Thank you and looking forward to reading your abstracts!

Johanne Brunet

Madison, WI, USA

Johanne Brunet <jbrunet@wisc.edu>

Montpellier Evol2018 Aug19-22 GlobalChange

Dear Colleagues,

We welcome abstract submissions to the symposium on: "Rapid Evolutionary Responses to Global Change," for the 2018 Joint SSE+ESEB Congress in Montpellier, France.

The deadline for submissions is January 15th 2018. Abstracts may be submitted at: http://evolutionmontpellier2018.org/call-abstracts Title of the Symposium: Rapid Evolutionary Responses to Global Change

Global climate change ranks among the greatest threats facing humanity, and evolutionary responses will be most certainly needed for many species to avoid extinction. While there is mounting evidence for species responses to global change, we still lack the ability to predict whether and the extent to which populations could respond to this change. This Symposium attempts to consolidate state-of-the-art knowledge on evolutionary responses and enhance our capacity to make predictions about adaptation and extinction to global change. Specifically, we need to increase our understanding of what role evolutionary processes play in species range shifts, what types and number of genetic mutations are most likely to be adaptive, or what is the importance of genetic adaptive evolution vs phenotypic plasticity. These questions need to be explored in a variety of biotic and abiotic stresses as they might have dramatically different natures, namely temperature rises, severe droughts, acidification and salinity decline of the seas, or new pests. We invite work on wild populations, experimental evolution, quantitative genetic experiments, and theoretical population genetic models, and we encourage participants to discuss from such diverse angles the question of rapid evolution and adaptation. We plan to use this symposium as a launching point to integrate knowledge across disciplines and stimulate discussion on areas that require further investigation, so that we could gain fundamental insights.

Invited Speaker: Dmitri Petrov, Stanford University Organizers: Carol Lee, Moises Exposito-Alonso, Johannes Scheepens, François Vasseur, Thorsten Reusch

Carol Eunmi Lee, Ph.D. Professor Center of Rapid Evolution (CORE) and Department of Integrative Biology

430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

http://carollee.labs.wisc.edu carollee@wisc.edu

Montpellier Evol2018 Aug19-22 MatePreferenceMatingSystems

Dear colleagues,

We are pleased to invite abstract submissions to our symposium, Understanding mate preferences and mating systems: from genetics to behavior (S74), during the upcoming Joint Congress on Evolutionary Biology in Montpellier, France, August 19-22, 2018. (Deadline coming soon! Jan. 15th.) It will be an exciting symposium bringing together speakers from multiple backgrounds to explore what new genetic and genomics tools are bringing to our understanding of mating systems and mate preferences (see abstract below). . Abstracts for oral presentations and posters will be accepted through 15 January). We look forward to your submissions. Symposium Abstract: As a critical component of speciation and sexual selection, mating behavior has long been an area of study in evolutionary biology. In an attempt to investigate its mechanisms, we have gained abundant insight into the sensory, neural and physiological processes behind mating behavior. With the advent of increasingly refined tools and their application to many diverse organisms, we now have a better understanding of the mechanisms underlying the evolution of mate preference, mating behavior and more generally sexual selection. This symposium will integrate what we have learned about the various components of mating behavior, including sensory systems, mate preferences as well as mating systems and reproductive behavior. Our goals are to (i) highlight recent studies from diverse fields and organisms, with an emphasis on genetic and genomic approaches, in order to provide a synthetic understanding of the evolution of mate preference and mating behavior; and to (ii) provide a platform to generate a roadmap for future research in these areas.

Invited speaker: Molly E. Cummings The neurogenomics of mate preference and the cognition connection

Organizers: Natasha Bloch (n.bloch@ucl.ac.uk), Iulia Darolti (iulia.darolti.15@ucl.ac.uk).

Natasha Bloch, PhD NSF Post-doctoral Fellow in Biology Marie Curie research fellow Department of Genetics, Evolution and the Environment University College London

The Darwin Building Gower Street, London WC1E 6BT Tel: 020 7679 2170 (ext. 32170) E-mail: n.bloch@ucl.ac.uk http://home.uchicago.edu/~nbloch "Bloch, Natasha" <n.bloch@ucl.ac.uk>

Montpellier Evol2018 Aug19-22 RecombinationEvolution

Dear colleagues,

We are pleased to invite abstract submissions for our symposium at the Joint Congress on Evolutionary Biology to be held in Montpellier, France in August 2018. Please see information below, and submit an abstract at http://evolutionmontpellier2018.org/call-abstracts by January 15.

We hope to feature a diverse collection of enthusiastic speakers.

Title: Causes and Consequences of Recombination Rate Evolution

Invited Speaker: Mohamed Noor

Is Variation in Recombination Rate Adaptive?

Summary:

Meiotic recombination plays fundamental roles in evolution and genetics. By controlling linkage between loci, recombination mediates the efficiency and effects of natural selection on both beneficial and deleterious mutations. Recombination shapes the evolution of DNA sequence composition via biased gene conversion and drives fluctuations in genealogical history along chromosomes. In many species, recombination also ensures the correct segregation of homologous chromosomes at meiosis and is essential for the maintenance of genome integrity. Despite its central biological significance, recombination rate varies among individuals, between species, and across genomes. Our symposium will highlight recent discoveries about the causes and consequences of variation in recombination rates. We intend to showcase research that cuts across genomic and evolutionary scales - from recombination hotspots to whole genomes, and from individuals to clades. We expect our symposium will unite the perspectives of empiricists and theoreticians whose work on recombination rate evolution remains disconnected.

Organizers: Marie Cariou, Beth Dumont, Bret Payseur, Fanny Pouyet

Bret Payseur <bret.payseur@wisc.edu>

Montpellier Evol2018 Aug19-22 SexualConflict

Dear Colleagues,

We are excited to announce our symposium on the 'Manifestation and resolution of sexual conflict' (S56) at the 2018 Evolution conference in Montpelier, France.

Abstract submission is open until 15th January 2018 at http:// evolutionmontpellier2018.org/call-abstracts

The invited speaker to our symposium is Craig Primmer (University of Helsinki) who will be talking about his work on sex dependent dominance and sexual conflict resolution in salmon.

Males and females are often subject to contrasting selection pressures, which can generate significant amounts of sexual conflict when traits have a shared genetic basis between the sexes. Sexual conflict has the potential to substantially increase standing genetic diversity in populations and thereby act as an important force in adaptation. However, the causes of sexual conflict, and the mechanisms by which it can be resolved, remain hotly debated. Recent studies have begun to combine phenotypic studies, population genetic methods, and genome wide sequence data to identify targets of sexual conflict. Now is a pertinent time to: i) synthesize the population genetic signatures arising from sexual conflict, and how they vary according to the type of sexual conflict; ii) highlight our understanding of the consequences of conflict; including the role of balancing selection in maintaining population genetic diversity; and iii) develop a cohesive understanding of the potential genomic mechanisms leading to the resolution of sexual conflict, including the relative roles of gene expression, alternative splicing, imprinting and sex-linkage. Organisers: Katie Peichel and Alison Wright

– Dr Alison Wright

NERC Independent Research Fellow Dept. of Animal and Plant Sciences, University of Sheffield Sheffield, S10 2TN

Twitter: @alielw Lab webpage < http://www.alisonewright.co.uk > Departmental webpage < http://www.sheffield.ac.uk/aps/staff-and-students/acadstaff/wright >

“a.e.wright@sheffield.ac.uk”
<a.e.wright@sheffield.ac.uk>

Montpellier Evol2018 Aug19-22 SocialBehaviorOmics

Dear colleagues,

We welcome abstract submission to our symposium, “Social behavior and evolution in the omics era”, part of the Joint Congress on Evolutionary Biology in Montpellier, France, August 19-22, 2018. (Details below.) We aim to attract a diverse group of speakers to participate in an exciting symposium at an outstanding international conference. Abstracts for oral presentations and posters will be accepted through 15 January (http://evolutionmontpellier2018.org/call-abstracts). We look forward to your submissions and hope to see you this August!

Symposium S8: Social behavior and evolution in the omics era

Symposium Abstract:

>From genes cooperating to form organisms to animals cooperating to form societies, all of life is social. Social behaviours, including cooperation, aggression, mating, and parenting, have historically been confined to studies of organismal- or population-level phenotypes. Thanks to the -omics revolution, it is now possible to dissect the evolution of these behaviours to the genotypic level. Furthermore, in the study of mutualisms, genomics have been used to unveil previously hidden microsymbionts, while transcriptomics, metabolomics and proteomics have identified which genetic and metabolic pathways are used and therefore how individuals are interacting. Omics methodologies can be used to identify social cheats and infer evolutionary dynamics in natural populations, and will be central to examining the consequences of social behaviours for genome evolution and gene expression, both within and between species. This symposium will bring together researchers using omic approaches to clarify fundamental aspects of sociobiology and behavioural ecology including who is interacting and how, and those attempting to link the occurrence of social behaviours with variation across the genome, transcriptome and metabolome.

Invited speaker: Sandra B. Andersen, “Long-term social dynamics drive loss of function in pathogenic bacteria

Organizing committee: John Bruce, Melanie Ghoul, Jaime Grace, and Philip Johns

Best, Jaime

Jaime Leigh Grace, Ph.D. Assistant Professor Department of Biology Bradley University 1501 W. Bradley Ave. Peoria, IL 61625 USA +1 309 677 3014 <(309)%20677-3014> jgrace@bradley.edu

jgrace@fsmail.bradley.edu

Montpellier Evol2018 Aug19-22 StructuralVariants

Dear Colleagues,

We are glad to invite you to participate and submit an abstract (before Jan 15th) to our symposium “S27. Moving beyond point mutations: the role of structural genomic variation in adaptation and novelty” at the 2018 Evolution meeting in Montpellier, France (August 19th-22nd).

We hope this symposium will be the opportunity to discuss recent research on the role of structural variants (inversions, duplications, etc..) in evolution, from the apparition of novelty (*de novo *genes...) to adaptation or speciation. We'd like to gather scientist with diverse backgrounds and using complementary methods (experimental, computational, genomic,etc...)

Please find below the detailled summary of the symposium. You may submit your abstract through this website http://evolutionmontpellier2018.org/call-abstracts . S27. Moving beyond point mutations: the role of structural genomic variation in adaptation and novelty

Abstract: One of the key challenges in evolutionary biology is to understand how novelty arises. Genomic structural variants, such as large indels, translocations, duplications and inversions, are ubiquitous in nature. However, their role in adaptation and diversification remains largely unknown compared to single-nucleotide mutations. Recent advances in genomics, notably single-molecule long read sequencing combined with novel assembly algorithms, have now empowered researchers to systematically discover and characterize these complex variants for the first time. But how exactly do structural variants contribute to novelty at the molecular level? Remarkably, structural variants have been linked to the spread and evolution of selfish genetic elements (transposons, meiotic drivers and post-segregation distorters) as well as the birth and diversification of gene families (gene duplication and de novo gene evolution). Furthermore, transcriptomic and pedigree analyses suggest that structural variants are frequently associated with QTLs or neo-functionalization. With this symposium, we aim to bring together researchers who apply experimental and computational approaches to: 1) characterize structural variants, 2) test the role of structural variants in adaptation and diversification, including studies with an emphasis on selfish genetic elements and de novo gene evolution, and 3) document the ecological determinants of that govern the distribution of structural variants in wild populations.

Organizers: Eyal Ben-David, Emma Berdan, Alejandro Burga, Claire Merot, Maren Wellenreuther

Invited speaker: Aoife McLysaght "Open questions in the study of de novo genes: what, how and why"

On behalf of the organizers, Best regards,

Claire Mérot

Post-doctoral FRQS fellow Bernatchez lab Institut Biologie Integrative des Systemes Université Laval Québec, Canada

< https://www.avast.com/sig-email?utm_medium=email&utm_source=link&utm_campaign=sig-email&utm_content=webmail > Garanti sans virus. www.avast.com < https://www.avast.com/sig-email?utm_medium=email&utm_source=link&utm_campaign=sig-email&utm_content=webmail > <#DAB4FAD8-2DD7-40BB-A1B8-4E2AA1F9FDF2>

Claire Mérot <claire.merot@gmail.com>

Montpellier Evol2018 Aug19-22 UrbanEvolution

Dear Colleagues,

We are happy to invite you and submit an abstract to the symposium "/Evolution in an urbanizing world/" (S.63) at the joint ESEB-SSE Evolution congress in Montpellier (August 19-22 2018). Deadline for abstract submission is on January 15.

S63. Evolution in an urbanizing world

Organizers: Anne Charmantier, Adrien Frantz, Julien Gasparini, Marc Johnson

Cities are rapidly expanding environments with original combinations of abiotic, biotic, and human social factors. The replication and global distribution of cities offer a unique opportunity to investigate how environmental changes affect phenotypic (morphological, physiological, behavioural, and life history) and genomic evolution. In particular, it is crucial to determine whether divergence in phenotypes across urbanization gradients is the expression of either ecotypes adapted to urban conditions, phenotypic plasticity, or non-adaptive evolution. Recent projects have provided a small but growing number of spectacular cases of rapid evolution and local adaptation to the urban environment, and have also revealed a promising potential to address eco-evolutionary dynamics in this context. They have finally provided unique scope to integrate evolutionary ecology in a conservation context. In the last five years, the field of urban evolution has budded from the strongly established field of urban ecology, and blossomed into a vibrant and dynamic multi-disciplinary area of study. This symposium offers to synthesize results from this burgeoning field, and simultaneously bridge biological conservation, ecosystem function, ecological genomics and behavioural ecology. We particularly encourage submissions of abstracts that create bridges between these fields in all taxa, approaches and spatio-temporal scales.

Invited speaker: Marta Szulkin "/Testing for urban versus forest ecotypes in a wild bird across multiple urbanization gradients/".

Looking forward to reading your contributions!

Thank you all, Anne Charmantier, Julien Gasparini, Marc Johnson, Adrien Frantz

"adrien.frantz@upmc.fr" <adrien.frantz@upmc.fr>

Roscoff France EvolutionReproductiveSystems DeadlineJan16

Dear Colleagues, the deadline for abstract submission to our upcoming Jacques Monod conference on reproductive systems evolution is next week (Jan 16). Please visit our website for general informations and instructions on how to register: http://www.cnrs.fr/insb/cjm/-2018/Schwander_e.html Hoping to see you there, Tanja Schwander, Thomas Lenormand & Denis Roze

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

SEX UNCOVERED, THE EVOLUTIONARY BIOLOGY OF REPRODUCTIVE SYSTEMS

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

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

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

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

We hope to see you there

Tanja Schwander, Thomas Lenormand & Denis Roze

Denis Roze <roze@sb-roscoff.fr>

Shenzhen AsiaEvo Apr18-20

Hi

We would like to draw your attention to the following symposia to be held at the 1st AsiaEvo conference in Shenzhen, China; April 18th-20th 2018 (http://www.asianevo.org/).

The deadline for abstract submission is January 20th 2018. There are 5 student and 5 postdoc travel awards available (http://www.asianevo.org/-programme/student_awards.html).

Symposium #25: The evolution of behavioural responses in biological invasions Organizer: Kit Magellan (University of Hong Kong)

Invited speakers: Jaimie Dick (Queens University, Belfast); Martin Reichard (Czech Academy of Sciences), Gudbjorg Asta Olafsdottir (University of Iceland)

Abstract: One of the greatest pressures on ecosystems and biodiversity is biotic invasions. However, invasions also provide a rare opportunity to observe and quantify evolution in action: both invasives and natives must adapt to species with which they have no evolutionary history in order to survive. A key attribute of successful invasive species is behavioral flexibility. Conversely, a likely immediate effect of invasions is disruption of native species behaviour. These individual level effects will translate to changes in population level parameters and will influence selection pressures on both native and invasive species. Moreover, anthropogenic influences such as urbanization and climate change may facilitate or oppose adaptation. Assessing the evolutionary interactions between behaviour and biotic invasions is therefore of critical global importance in the modern world and for future generations.

Symposium #1: Rapid microevolution of invasive species Organizer: Aibin Zhan (Chinese Academy of Sciences)

Invited speakers: Hugh MacIsaac (University of Windsor), Carol Lee (University of Wisconsin), Carolyn Tepolt (Woods Hole Oceanographic Institution), Elizabeta Briski (GEOMAR)

Abstract: The introductions and spread of invasive species globally have caused enormous costs to the economy (~ $1 trillion per annum in lost goods and services). Such economic loss is particularly severe in countries that have been highly impacted by invasive species, with estimates for the UK, US and China of US $1 billion, 120 billion and 15 billion, respectively. Alarmingly, however, rates of biological invasions continue to accelerate, thus posing growing and urgent threats to the global environment and economy.

The study of microevolutionary processes in the wild represents one of the major challenges in ecological and evolutionary studies, especially those aiming to reveal genetic bases of microevolution using wild populations. Biological invasions provide good "natural experiments" to deeply dissect processes and mechanisms of rapid microevolution, as invasive species are transported into and subsequently survive different local environments in a short period of time. Consequently, natural selection associated with rapid and/or sudden environmental changes may drive rapid microevolution in different directions during the process of biological invasions.

This proposed section will focus on recent research directions and progress, as well as future perspectives, in the field of microevolution using invasive species as a model. The proposed internationally recognized well-known experts will focus on different angles of rapid microevolution at different levels, including ecosystem, population and gene levels.

With best regards Kit Magellan and Aibin Zhan

Dr Kit MAGELLAN Research Fellow School of Biological Sciences Kadoorie Biological Sciences Building University of Hong Kong Pokfulam Road Hong Kong

magellan <magellan@hku.hk>

ShenZhen AsiaEvo Apr18-20

First AsianEvo Conference in Shenzhen, China, April 18-20, 2018

http://www.asianevo.org We are pleased to announce the call for abstracts for a symposium on:

Human Evolution and Adaptation (Session 41)

Invited speakers:

Rasmus Nielsen, University of California, Berkeley, USA

Shuhua Xu, Chinese Academy of Science and Max Planck Germany (CAS-MPG) Partnered Institute for Computational Biology, China

Charleston Chiang, University of Southern California, USA

Humans represent an excellent model system for understanding a key question in evolutionary biology: the evolution and adaptation of a species. Broadly speaking, two interwoven evolutionary forces have shaped the human genome and molded present day genotype-phenotype relationships: the demographic history of the population and natural selection due to our past interactions with a changing environment. Combining an abundance of contemporary whole genome datasets from diverse populations with the emergence of ancient genomic data has already illuminated details of our past evolutionary processes. With the underlying demographic history in hand, increased understanding of the role of natural selection in the evolution of modern humans is possible, forming a basis for evolutionary medicine that could revolutionize how medicine is practiced. The success of domestication in many human populations may have intensified selection pressure in the past ~10,000 years owing to the change of life style and dramatic growth of population size (e.g., selection for lactose persistence and on many erythrocyte-related genes against malaria). Consequently, many adaptively evolving variants may have very recent origins and likely segregate at low frequencies in a population (recent selection). However, most statistical methods for detecting selection have limited power of detecting low-frequency selected alleles. Recently, the promise of precision medicine has led to the development of population-based human genome projects (usually >100,000 individuals) in many countries in a high hope of making a complete list of genetic variants underlying disease susceptibility. Such a gigantic dataset also provides us a great opportunity to study patterns of genetic variation and detect signatures of selection for low-frequency variants from a very large sample size. Therefore, this symposium welcomes authors to present their work in understanding human evolution in diverse populations through the lens of demographic history and/or actions of natural selections. These could include, but are not limited to, either theoretical or empirical approaches, utilizing both modern and ancient DNA samples. Moreover, interdisciplinary frameworks integrating insights from linguistics, anthropology, medicine, or genetics studies of domesticated animals or crop to address human evolutionary questions will also be welcomed.

Deadline for abstracts has been extended: January 20, 2018

http://www.asianevo.org/programme/abstract.html Travel awards are available for 5 students and 5 postdocs:

http://www.asianevo.org/programme/-student_awards.html Symposium organizers:

Charleston Chiang, University of Southern California, charleston.chiang@med.usc.edu

Qiaomei Fu, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Science, fuqiaomei@ivpp.ac.cn

Wen-Ya Ko, National Yang Ming University, wenko@ym.edu.tw

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Charleston W. K. Chiang, Ph.D.

Assistant Professor of Preventive Medicine

Center for Genetic Epidemiology

Keck School of Medicine, USC

http://chianglab.usc.edu Charleston Chiang <charleston.chiang@med.usc.edu>

StAndrews BESMacro Jul10-11

Registration for BES Macro 2018 is now open: https://www.eventbrite.co.uk/e/bes-macro-2018-tickets-42497024745 BES Macro 2018 is the annual meeting of the British Ecological Society Macroecology (and macroevolution) Special Interest Group, and we hope you'll join us for two days of macro-fun!

This year's conference is 10-11 July at the University of St Andrews, Scotland, UK. We've got a great line up of plenary speakers highlighting all kinds of macro-scale research as well as our annual student plenary, contributed talks, posters, and workshops. The registration deadline is April 30.

Keynote speakers:

* Brian McGill (University of Maine) * Nathalie Pettorelli (Zoological Society of London) * Bob O'Hara (Norwegian University of Science and Technology) * Anne Magurran (University of St Andrews)

Hope to see you there!

The BES Macro committee

Catherine Sheard <ces29@st-andrews.ac.uk>

StJohns Newfoundland AnimalFormFunction May7-11

The Comparative Morphology & Development (CMD) section of the Canadian Society of Zoologists (CSZ) invites you to attend the following symposium at the annual CSZ meeting:

———— May 7 - 11, 2018, on "The Rock" – ST. JOHN'S, NEWFOUNDLAND

MAIN SYMPOSIUM:— "Understanding morphology: Diverse approaches to deciphering animal form and function"

CAMPBELL ROLIAN (Calgary) Linking development, morphology and function in skeletal evolution

RAJEE RAJAKUMAR (Harvard) >From microworkers to supersoldiers:— Integrating social, developmental, and epigenetic processes to understand caste evolution in ants

TAMARA FRANZ ODENDAAL (Mount Saint Vincent) Developmental patterning and variation of the ocular skeleton

[Organized by Heather Jamniczky (Calgary)]

FOR MORE DETAILS ABOUT THIS SYMPOSIUM, SEE:

http://www.biology.ualberta.ca/CMD/home.htm TO REGISTER, OR TO LEARN MORE ABOUT THE CSZ ANNUAL MEETING, SEE:

http://www.csz-scz2018.com/ CONTRIBUTED PAPERS:— Spaces are also available for contributed papers in sessions organized by the CMD section.

ABSTRACT SUBMISSION DEADLINE:— Friday, March 1, 2018

"EARLY-BIRD" REGISTRATION DEADLINE:—— Friday, March 1, 2018

FINAL REGISTRATION DEADLINE:—— Sunday, April 23, 2018

Regards, Rich Palmer

–

A. Richard Palmer, FRSC Systematics and Evolution Group Department of Biological Sciences University of Alberta Edmonton, Alberta T6G 2E9 CANADA email:rich.palmer@ualberta.ca phone: (780) 492-3633 message: (780) 492-3308 FAX: (780) 492-9234 http://www.biology.ualberta.ca/palmer.hp/palmer.html Secretary-General Comparative Morphology & Development section Canadian Society of Zoologists: http://www.biology.ualberta.ca/CMD/home.htm Rich Palmer <rich.palmer@ualberta.ca>

Sweden SexInTheOceans May

Dear all, There is only one week left to submit abstracts to our forthcoming session "Sex in the oceans: from molecules to macroevolution": Please use the link: https://cemeb.science.gu.se/activities/marine-evolution-2018/registration and circulate among potentially interested folks. Closing date: Thursday, Feb. 1st

We remind that a collection of the best contribution will feature in a Special Issue of Evolutionary Applications, provisionally entitled "Complex reproductive strategies at sea: from evolutionary mechanisms to management implications".

We look forward to meeting you in bright Strömstad, as the luminous Scandinavian summer approaches!

Best wishes,

Stefano.

"S.Mariani@salford.ac.uk" <S.Mariani@salford.ac.uk>

Toronto AGA WildQuantGen Mar23-25

Register while there is still room!

The American Genetic Association President's Symposium, "Evolutionary Quantitative Genetics in the Wild", is getting full. We have received an international response from both students and established scientists, and look forward to a dynamic weekend event.

AGA symposia are small, friendly gatherings, and provide wonderful opportunities for researchers to engage with one another and share their science. This spring's meeting will take place March 23-25, at the beautiful Hart House on the University of Toronto campus. Invited talks and contributed posters are focused on quantitative genetics of fitness-related traits in an evolutionary context across diverse species.

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

Registration includes receptions, meals, and a complimentary 3-YEAR membership in the American Genetic Association, including subscription to Journal of Heredity.

For all details, visit https://www.theaga.org/program-genetic-arch.htm Best wishes,

Anne Bronikowski, 2017 AGA President John Stinchcombe, Local Host and Co-Organizer ________ Speakers:

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

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

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

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

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

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

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

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

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

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

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

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

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

Jon Slate, U. Sheffied ˜ "Recent natural selection causes adaptive evolution of an avian polygenic trait"

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

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

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

Christina Zakas, New York U. ˜ "The genetic basis of evolutionary transitions in development using a polychaete model"

Anjanette Baker <theaga@theaga.org>

UCambridge EvolutionaryGenetics Mar20

Dear Colleagues,

The annual Evolutionary Genetics and Genomics Symposium (EGGS) will take place on Tuesday 20th March 2018 at the University of Cambridge. This Genetics Society meeting attracts participants from across Europe and is a friendly and informal way to meet researchers in the field and listen to interesting talks. We aim to bring together participants from a range of backgrounds, with a particular focus on genomics and evolutionary biology.

EGGS 2018 will feature a keynote from Katie Peichel (University of Bern).

Registration is now open and costs just 5. Please register at https://goo.gl/wuW5iq Abstract submission is now open and the deadline has been extended to 10/2/2018. If you would be interested in presenting a talk please submit your abstract via this link:

https://goo.gl/K6RmSF With best wishes,

The organising committee.

Arunkumar Ramesh <ar885@cam.ac.uk>

UGothenburg MarineEvolution May15-17

Dear colleagues,

Here is a friendly reminder that early bird registration and abstract submission deadline for Marine Evolution 2018 in Sweden is on February first.

So, do not wait any longer, submit your abstracts now!

Registration and abstract submission can be done here: http://cemeb.science.gu.se/activities/marine-evolution-2018/registration Marine Evolution 2018 invites students and researchers in the field of Marine Evolutionary Biology. The program will contain plenary presentations by six renowned speakers, followed by 9 sessions on relevant topics. A list of sessions can be found here: http://cemeb.science.gu.se/activities/-

marine-evolution-2018/sessions The conference will take place over three days in the beautiful Bohuslän region, listed as one of the "ten last great wildernesses in the world" by CNN. It is situated on the Swedish West Coast, strategically located between major international airports in Oslo, Norway and Gothenburg, Sweden. Above the scientific program, the conference will also host excursion events, evening performances and time for discussions and relaxation. The venue is the Strömstad Spa, a modern conference infrastructure with pool and gym facilities. The conference fee is 3600 SEK (1600 SEK for PhD students), excl. VAT.

All the best, The Marine Evolution 2018 organizing committee

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

Pierre de Wit <pierre.de_wit@marine.gu.se>

ULiverpool InsectEvolution Mar21-22

Dear Colleagues,

Please see below information detailing the upcoming symposia "Insect Endosymbiont" and "Insect Infection & Immunity" to be held in Liverpool, UK, on March 21st and 22nd 2018.

These meetings are sponsored by the Royal Entomological Society and aim to bring together people working on different facets of insect symbioses and infection or immunity. We are running them alongside each other as it makes sense to consider these interactions together: symbionts can comprise part of the defence system of the host, and can alter vector competence. Reciprocally, the defence system of the host needs to discriminate between friends and foe. We hope you can come to both.

The Wednesday meeting will focus on specificity of symbiotic interactions, from functional aspects through to evolutionary ecology. The Thursday meeting will include immunity, defence, vector biology, evolution, biochemistry and ecology.

On Wednesday the invited speaker will be Prof Martin Kaltenpoth (http://www.bio.uni-mainz.de/zoo/oekologie/58_ENG_HTML.php), who is best known for his work on the beewolf-Streptomyces symbiosis in which Streptomyces produce antimicrobials that are used by the wasp to protect their offspring. In this meeting, he will be talking about more recent work "Symbiont-provided defense and nutrition in herbivorous beetles."

On Thursday our invited speaker will be Dr Lena Wilfert (http://biosciences.exeter.ac.uk/staff/index.php?web_id=Lena_Wilfert), who has worked on a range of pathogen/host interactions in insects, and is currently working on pollinator disease ecology and evolution. In this meeting, she will be talking about "Man-made epidemics: the evolutionary ecology of multi-host bee pathogens."

Both meetings will be small and informal, and short talks or posters are welcome from everyone at any career level. We would love people to attend both meetings, as that way we can gain insights from each other.

Please register for both events separately here: https://www.royensoc.co.uk/events The cost for each separate event is 10 for members, 15 for non-members, which covers lunch and two tea breaks.

Please send abstracts for both symposia to symbiont2018@gmail.com, by no later than 23:59 on Monday 5th February. Please specify if you would like to present a talk or poster and for which symposium. Please note that the poster session for both symposia will be held on Wednesday early evening.

For accommodation, https://www.hallmarkhotels.co.uk/hotels/hallmark-inn-liverpool/ is a budget but OK hotel (40 per room per night at the moment); for cheaper dorm beds, https://hattershostels.com/liverpool-hostel/ (15 per night at the moment in four bed dorm) are two places near the University. For those liking nicer sleeps, The Liner is mid-price, and Hope Street Hotel is in the more luxury bracket; all are within walking distance of Uni. It is a little advisable to book accommodation ahead to insure against the unlikely event that Liverpool make it through the Champion's League and are playing that night (at which point, accommodation becomes hard to find and expensive).

We look forward to seeing you in Liverpool in March, and please forward to any interested parties.

Kind Regards,

The organising committee:

Greg Hurst

Joanne Griffin

Michael Gerth

Georgia Drew

"Griffin, Joanne" <J.Griffin@liverpool.ac.uk>

Victoria BC ClimateAdaptation Jun10-15

Dear colleagues,

We are organising a special session at the upcoming ASLO meeting in Victoria, BC, Canada (10-15 June 2018: https://aslo.org/page/aslo-2018-summer-meeting). Our session is entitled: LIVING IN A VARIABLE WORLD: STUDYING THE ROLE AND CONSEQUENCE OF VARIANCE, COVARIANCE, AND EXTREMES IN AQUATIC ECOSYSTEMS. You can find the abstract below. Brian Helmuth and Mark Denny will be our keynote speakers.

We hope this session is of interest for you. Please forward this message to your lab group/network. Please note that the deadline for early registration and abstract submission is *16 February 2018*.

Looking forward to meet you at the ASLO meeting!

Apostolos Koussoroplis, Alexander Wacker & Sylvain Pincebourde

Abstract

In the last two decades, the importance of higher order statistical moments (e.g., variance, co-variance, skewness and kurtosis) in biotic and abiotic factors slowly made its way in ecology, traditionally a science of means and averages. For instance, we know now that considering the variance around the mean temperature will be essential for understanding the physiological, ecological and evolutionary consequences of climate change. Yet, many challenges still hold in this flourishing research topic, which remains relatively under-explored in aquatic ecology. In a multifactorial world, how variable are the major ecological drivers compared to temperature - by far the most studied factor? What are the covariance patterns of environmental stresses and extremes, and at which spatio-temporal scales do they occur? How do aquatic organisms perceive and deal with such variability? What are the consequences of ecological variance and extremes scaling from the organismal to the population and the community level? This session welcomes theoretical and experimental studies on such questions conducted at any temporal and spatial scale, regardless if the variance is driven by physiological changes, behavioural movements, environmental gradients or seasonally driven successions of species.

https://aslo.org/page/aslo-2018-summer-meeting –

Sylvain Pincebourde Chargé de Recherche CNRS www.sylvainpincebourde.wordpress.com Institut de Recherche sur la Biologie de l'Insecte (IRBI) Université François Rabelais, CNRS, UMR 7261 Parc Grandmont 37200 Tours France

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Sylvain Pincebourde <sylvain.pincebourde@univ-tours.fr>

WashingtonDC CrustaceanAdaptation May22-25

Hi All, As the organizers of the special symposium on "Adaptations to Life in the Deep Sea and Caves", we wanted to remind anyone interested in participating in this session (and the rest of the International Crustacean Congress) that the early registration deadline (reduced registration fee) is fast approaching — Jan. 15th.

We are inviting any crustacean or related researchers working on topics of adaptations to life in the deep sea and cave (see description below) to submit abstracts to this symposium. Abstracts will be reviewed shortly after the March 1st submission deadline and you will be notified shortly after that about inclusion in this special session.

To register go to http://www.birenheide.com/ICC2018/- or http://crustaceansociety.org/upcoming-meetings . Adaptations to Life in the Deep Sea and Caves Special Session, 9th International Crustacean Congress, Washington, DC, USA, 22-25 May 2018

Animals living in the deep sea exhibit many adaptations to the unique combination of challenges in the harsh and poorly known habitats of the deep sea. Studies of the morphology, physiology, behavior and ecology of crustaceans living in the deep-sea pelagic and benthic environments provide insight into the selective pressures animals here face, as well as a better understanding of the nature of the habitats themselves. Elaborations of sensory systems, locomotory and buoyancy mechanisms, and respiratory, reproductive and feeding strategies have all been documented in deep-sea crustaceans.

Many of the adaptations that we see in the deep sea are directly related to the lack of light in the habitat and the complex of resulting traits has been termed the "Darkness Syndrome" (Danielopol et al. 1996). We would like to bring together researchers working in any dark habitat for a portion of this session and welcome talks from biologists working in caves and other dark habitats. Please indicate along with your abstract submission that you would like to be included in the Darkness Syndrome portion of the session.

This session welcomes contributions from taxonomically and methodologically diverse backgrounds, including theoretical, taxonomic, morphological, physiological, behavioral, ecological, genetic and genomic, biomechanical, neurological and developmental biology. Integrative approaches are particularly welcome.

We do not plan to publish a special issue. We do not plan to apply for funding to recruit specific speakers. The session will accept as many talk proposals as appropriate based on submitted abstracts.

For any questions regarding the special session, please contact any of the Co-Coordinators: Tammy Frank, NOVA Southeastern University, tfrank1@nova.edu Karen Osborn, Smithsonian National Museum of Natural History, osbornk@si.edu Megan Porter, University of Hawaii, mlporter@hawaii.edu

Happy 2018, Karen

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

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

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

“Osborn, Karen” <OsbornK@si.edu>

WashingtonDC CrustaceanGenomics May22-25

Dear colleagues,

My co-organizer, Heather Bracken-Grissom, and I would like to invite you to present your research in the session Molecular Insights: The Genomic Revolution in Crustacean Biology at the upcoming International Crustacean Congress IX to be held May 22-25th 2018 in Washington DC. The deadline for early bird registration is fast approaching, *January 15, 2018.*

This conference is hosted by the Smithsonian Institution and Renaissance Hotel. We hope this session will provide a platform to share and discuss studies incorporating crustacean genetics and/or genomics. We encourage submissions that cover any crustacean taxa and we are particularly interested in phylogenetics/omics, transcriptomics, gene expression studies, tree of life studies, and population genomics. Graduate Students, Postdoctoral Scholars and Professors (at all levels) are encouraged to participate!

If you are interested in participating please reach out to Heather Bracken-Grissom at hbracken@fiu.edu or Joanna “Jo” Wolfe at jowolfe@mit.edu as we expect the session spots to fill quickly.

The deadline for abstract submissions is *March 1st 2018.*

More information on the conference can be found here detailing registration and abstract due dates and logistics: http://www.birenheide.com/ICC2018/ *Session details*:

*Molecular Insights: The Genomic Revolution in Crustacean Biology *

Co-Coordinators: Heather Bracken-Grissom, Florida International University, hbracken@fiu.edu Joanna Wolfe, Massachusetts Institute of Technology, jowolfe@mit.edu The field of crustacean genetics has undergone an exciting revolution in recent years. The advancement of sequencing technologies and methods has transformed the way carcinologists ask questions and collect data, especially for non-model organisms that lack genomic references. For several groups within Crustacea, this genomic revolution is still in its infancy. The potential to capitalize on recent technology is great, and findings from these studies will lead to unprecedented insights into the fields of evolutionary biology and molecular ecology.

For this session, we would like to invite researchers working in the field of crustacean genetics/genomics. We welcome contributions from phylogenetics/omics, population genomics, transcriptomics, among others. In addition to the abovementioned, theoretical and methodological talks will be considered.

We hope to highlight a diverse group of organisms that span various fields of crustacean biology. Please indicate that you would like to be included in the Molecular Insights session.

We do not plan to publish a special issue.

We do not plan to apply for funding to recruit specific speakers.

The session will accept as many talk proposals as appropriate based on submitted abstracts.

We look forward to seeing you in DC!

Kind regards,

Heather Bracken-Grissom and Jo Wolfe

– Jo Wolfe, Ph.D. Postdoctoral Associate Department of Earth, Atmospheric & Planetary Sciences Massachusetts Institute of Technology 77 Massachusetts Ave Cambridge, MA 02139

Jo Wolfe <jowolfe@mit.edu>

Yokohama SMBE2018VirusGenomeEvolution Jul8-12

Dear Colleagues,

We are pleased to invite abstract submission to our symposium "Virus genome evolution" at SMBE2018 in Yokohama, Japan. Abstracts may be submitted at http://smbe2018.jp/ by January 25.

Symposium 34. Virus genome evolution

Viruses exhibit a unique parasitic situation that shapes the evolution of their genomes. They evolved an extensive amount of genomic diversity with a wide range of complex life, reproduction, and inheritance strategies, including the use of different genetic materials, genome sizes, and a wide range of mutation rates. Virus evolution has had a strong influence on the evolution of other life forms, acting as source of novel genes, facilitating horizontal transfer, eliciting genomic alterations caused by virus integration, and creating potent coevolutionary selective pressure. The evolutionary process is also explicitly involved in many processes with medical implications, such as host switching, immune avoidance, and the development of drug resistance. The study of virus evolution has proven critical for the study of disease emergence and spread, exemplified by the recent Ebola and Zika outbreaks. The use of genomic approaches has transformed the field of virology, enabling these and other issues to be answered with ever more depth and precision. This symposium will highlight recent advances on virus genome evolution and will bring together different approaches on prokaryotic and eukaryotic virus evolution; how these viruses originated, diversified, and spread, how they change and adapt, and how they co-evolve with their hosts.

Invited Speakers: Adi Stern, Marcia F. Marston Organizers: Anne Kupczok, Marina Escalera Zamudio, Richard Goldstein

Anne Kupczok <akupczok@ifam.uni-kiel.de>

Yokohama SMBE Jul8-12

We invite submission of abstracts to our SMBE 2018 symposium: Improving inference frameworks by accounting for population structure Invited speakers: Sohini Ramachandran and Amy Goldberg Population structure encompasses a broad range of departures from panmixis, including sex, mating system, geographical subdivision, and admixture. A growing number of empirical studies support the view that population structure constitutes a significant and pervasive feature across the tree of life. Population structure can bias or invalidate a host of inferences, including patterns of gene flow, dates of admixture events, or signatures of selection. Such findings constitute a challenge to develop methods that directly confront population structure and exploit rather than avoid the higher-level associations it generates. For example, some studies for the mapping of disease genes in humans attempt to minimize the effects of population structure by restricting consideration to samples from groups believed to have low admixture. The development of methods that can accommodate population structure not only promotes better inference in all groups but also facilitates research with direct implications for human health in groups that are understudied because of a history of admixture.

This symposium also seeks to encourage the study of the extent to which population structure can mimic signatures of selection or changes in effective number.

Please submit online at http://smbe2018.jp/-cf_abstract.html by 25 January 2018 (23:59 PM, JST).

Looking forward to seeing you in Yokohama, 8-12 July 2018!

Emilia Huerta Sanchez Marcy Uyenoyama

"Marcy Uyenoyama, Ph.D." <marcy@duke.edu>

Yokohama SMBE Jul8-12 AbstrSubmission

Dear All,

We are delighted to announce that the abstract submission system for the Annual Meeting of the Society for Molecular Biology and Evolution 2018 is now open! We are accepting abstracts via the official SMBE 2018 website. Just follow the links below to find out more. SMBE 2018 also call for applications for a number of awards for students and postdoctoral researchers. The applications for these awards can be submitted via the abstract submission system.

The deadline for abstract submission and award application is January 25th, 2018. Taking place from July 8th 12th, 2018, in Yokohama, Japan, SMBE 2018 is an opportunity to join your colleagues and present your work internationally to world leaders and experts.

Registration for SMBE 2018 is currently open and early bird registration will end on April 16th.

SMBE 2018 Website < http://smbe2018.jp >

< http://smbe2018.jp/cf_abstract.html > | Call for Abstracts < http://smbe2018.jp/awards.html > | Award < http://smbe2018.jp/registration.html > | Registration

Professor Koichiro Tamura

Chair, Local Organizing Committee, SMBE 2018

SMBE 2018 <smbe2018-p@jtbcom.co.jp>

"takezaki@med.kagawa-u.ac.jp" <takezaki@med.kagawa-u.ac.jp>

Yokohama SMBE Jul8-12 DeadlineExtended

SMBE Undergraduate Travel and Mentoring Awards - Deadline extended

The Society for Molecular Biology and Evolution offers travel awards for undergraduate students to attend their annual meeting and recent mentoring there, this year in Yokohama, Japan (http://smbe2018.jp). Eligibility includes Masters students under a 3+2 system. Eligibility is based on status at the time of application.

Awardees will receive 1500-2000 USD ($) toward travel and registration fees (the larger amount is for long-haul travel, the smaller for within Australasia). You will also be assigned a mentor at the meeting to advise you and to introduce you to potential collaborators, PhD supervisors, etc. You will also participate in the meeting's poster session with a poster you will prepare on your research.

In order to apply, you need to prepare the following:

1. an abstract describing your research (<250 words)

2. a short explanation of why you want to attend this meeting, including mention of whether you fall into a group traditionally underrepresented at SMBE, such as enrolling in university later in life or being the first in your family to attend university (<250 words)

3. a short letter of support from your academic supervisor, confirming that the research is your own (<250 words)

4. a scan or photo of your student ID to confirm eligibility

Applications can be made through the SMBE abstract submission system at http://smbe2018.jp/-cf_abstract.html, which has been extended to accept submissions until Feb 1. You can either submit all components there, or you can have your advisor email their support letter to Joanna Masel masel@email.arizona.edu. If you have already submitted your abstract but have not yet applied for the award, you can email in your award materials. The deadline for receiving award materials by email (conditional on having submitted an abstract) is Feb 8.

You can find more information on the travel awards at http://www.smbe.org/smbe/AWARDS/-AnnualMeetingTravelAwards/ UndergraduateTravelandMentoringAward.aspx or send an email to Joanna Masel masel@email.arizona.edu.

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

Yokohama SMBE Jul8-12 DeadlineFeb1

SMBE 2018 Abstract Submission closing date now February 1

We are glad to have received numerous abstract submissions for SMBE 2018. Appreciating the strong interest, the deadline has been extended!

Final abstract submission closing date: Thursday, February 1, 2018

Don't miss this opportunity - be involved in the meeting' scientific program by submitting your abstract here. Please email us at <smbe2018-p@jtbcom.co.jp> for any questions.

Please submit your Abstract here: http://smbe2018.jp/-cf_abstract.html Dr Lulu Stader Executive Administrator, Society for Molecular Biology and Evolution smbe.contact@gmail.com

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

Yokohama SMBE Jul8-12 SatelliteRegionalMeetings

SMBE Satellite and Regional Meeting Call for Proposals

SMBE is now calling for proposals for workshops/satellite meetings. They are also calling for proposals for "interdisciplinary and regional actions". The proposed meeting or event should be held between Sep 1 2018 and Dec 31 2019. Funds will be awarded on a competitive basis to members of the molecular evolution research community, and the deadline for submission of proposals is April 1, 2018.

Satellite meeting/workshop proposals should be sent by email to the Chair of the SMBE Satellite Workshop Committee Joanna Masel (masel@u.arizona.edu). Interdisciplinary and Regional Actions proposals should be sent by email to the Chair of the SMBE Interdisciplinary Regional Actions Committee Maud Tenaillon (maud.tenaillon@inra.fr).

See http://www.smbe.org/smbe/MEETINGS/-SatelliteandRegionalMeetingGui delines.aspx for more detailed information.

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

Yokohama SMBE Jul8-12 TimingMethods

Dear Colleagues,

We are pleased to invite submission of abstracts to the SMBE 2018 symposium "Timing methodologies and applications".

Abstracts may be submitted at http://smbe2018.jp/-cf_abstract.html by January 25.

*** Symposium 46: Timing methodologies and applications ***

Timing of species and gene divergences is a primary outcome of many evolutionary analyses. The widespread application of molecular clocks to a variety of datasets and evolutionary histories has driven the diversification of these methods into many different approaches that often produce discordant timelines. Despite many efforts, generally applicable rules to reconcile these disagreements are still elusive leaving researchers with the difficult task of selecting most appropriate methods and parameters based on limited information or requiring complex comparative evaluations of multiple methods. Unfortunately, many of these current approaches that require multiple hypotheses testing are difficult to apply to large phylogenomic datasets, thus exacerbating the uncertainty in produced timelines. Participants in this symposium will explore the diversity of molecular clock methods and discuss their applications to simulated and empirical sequences from methodological and applied perspectives. The goal is to have an open discussion on the strengths and weaknesses of each method and identify best practices to reconcile different timelines. The research studies showcased in this symposium will explore the application of molecular clocks to species and gene divergences in an effort to shed light on the evolution of life through time.

Invited Speakers: Lindell Bromham, S. Blair Hedges Organizers: Fabia U. Battistuzzi, Beatriz Mello

***

We look forward to seeing you in Yokohama!

Fabia U. Battistuzzi (battistu@oakland.edu) Beatriz Mello (beatrizmello@ufrj.br)

Beatriz Mello <biaumello@gmail.com>

Yokohama SMBE Jul8-12 TravelDeadlineExt

Society for Molecular Biology & Evolution

SMBE Undergraduate Travel and Mentoring Awards - Deadline extended

The Society for Molecular Biology and Evolution offers travel awards for undergraduate students to attend their annual meeting and recent mentoring there, this year in Yokohama, Japan (http://smbe2018.jp). Eligibility includes Masters students under a 3+2 system. Eligibility is based on status at the time of application.

Awardees will receive 1500-2000 USD ($) toward travel and registration fees (the larger amount is for long-haul travel, the smaller for within Australasia). You will also be assigned a mentor at the meeting to advise you and to introduce you to potential collaborators, PhD supervisors, etc. You will also participate in the meeting's poster session with a poster you will prepare on your research.

In order to apply, you need to prepare the following: 1. an abstract describing your research (<250 words) 2. a short explanation of why you want to attend this meeting, including mention of whether you fall into a group traditionally underrepresented at SMBE, such as enrolling in university later in life or being the first in your family to attend university (<250 words) 3. a short letter of support from your academic supervisor, confirming that the research is your own (<250 words) 4. a scan or photo of your student ID to confirm eligibility

Applications can be made through the SMBE abstract submission system at http://smbe2018.jp/-cf_abstract.html, which has been extended to accept submissions until February 1. You can either submit all components there, or you can have your advisor email their support letter to Joanna Masel masel@email.arizona.edu.

If you have already submitted your abstract but have not yet applied for the award, you can email in your award materials. The deadline for receiving award materials by email (conditional on having submitted an abstract) is February 8.

You can find more information on the travel awards at http://www.smbe.org/smbe/AWARDS/-AnnualMeetingTravelAwards/Undergraduate TravelandMentoringAward.aspx or send an email to Joanna Masel masel@email.arizona.edu.

Society for Molecular Biology & Evolution smbe@allenpress.com

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

YosemiteNatlPark Symbiosis May4-6

Dear Colleagues,

The Eigth annual Yosemite Symbiosis Workshop will take place on May 4th-6th, 2018 at the Sierra Nevada Research Institute, Yosemite National Park. This has become a great venue for a diversity of symbiosis researchers. We hope to continue to attract a diverse group in 2018!

Keynote speaker 2018: Dr. Tadashi Fukami from Stanford University!

Information about our meeting:

Why: Our continuing goal is to better integrate the broad groups of scientists that focus on symbiosis and microbiome research. Yosemite serves as an ideal site as it is both beautiful and secluded. This will be our 8th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

Who: The meeting is small by design (~50 participants) and we seek to focus on scientists interested in the microbiome, cooperation, mutualism, and symbiosis. In the past we have covered a range of symbiosis topics from ecology and evolution to molecular mechanisms in different model and non-model systems. We would like to make room for a diverse group of people so we will initially accept up to 3 lab members per group (including the PI) on a first come first served basis.

When: The talks and formal meeting will be held May 5-6, 2018, though we make accommodation arrangements available for attendees to arrive on Friday the 4th to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting.

Past attendees and talks can be found here: http://www.sachslab.com/symbiosis-2015.php Abstract and early bird registration are due on March 16th, 2018.

Where: SNRS has a set of cabins in Wawona and all within a short walk of the conference room. Costs: See details in the registration page. We will only be able to accept credit card payments this year.

Link to meeting information: http://www.sachslab.com/symbiosis-2015.php The registration form for the 2018 Symbiosis Workshop is active: https://snri.ucmerced.edu/form/symbiosis-workshop-2018-registration Payments should be made at: https://intelforms.ucmerced.edu/Form/Symbiosis Please direct any questions to the organizers:

Joel Sachs joels@ucr.edu

A. Carolin Frank cfrank3@ucmerced.edu

– *Joel L. Sachs* *Associate Professor & Vice Chair* Evolution Ecology & Organismal Biology University of California, Riverside

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

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

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REMINDER OF A COMING DEADLINE

Three Ph.D. studentships - Biodiversity and evolution of plant-pollinator interactions

We are seeking three highly motivated Ph.D. students to join a project assessing studies of plant-pollinator relationships in tropical and temperate environments. The research is focused on changes of general characteristics of pollination networks with environmental gradients, as well as on case studies of selected pollination systems. All the new team members will process already collected data and material, as well as actively participate on field sampling (at least two larger expeditions during the study/work) of data and their subsequent processing in collaboration with international specialists. The length of the study is 4 years.

The successful applicants will be supervised within the multi-disciplinary team (www.insect-communities.cz) at the Faculty of Science, Charles University, Prague, Czech Republic, with a close collaboration with the Institute of Entomology and Institute of Botany, Czech Academy of Sciences. The fieldworks will be performed in Cameroon and/or Czech Republic. We have more than ten years continuous experience with various field projects in Cameroon. All senior members of our team have also worked in field in the Czech Republic since their studies.

Offered for all positions

- attractive scientific topic in an established international team

- sufficient financial and logistical sources for the projects (currently we hold three large grants for pollination research)

- 240,000 CZK net annual income for the Ph.D. students (combination of scholarship and salary), plus various student/employee bonuses; the income sufficiently covers living expenses in the Czech Republic (the national average net income is ca. 260,000 CZK annually)

Required for all positions

- enthusiasm in nature and ecological science

- ability to work as a team member, but also being independent

- fluency in English, both written and spoken

Desirable (but not necessary) for all positions

- previous experience of collaboration in scientific projects evidenced by a (co)authorship of research papers or conference contributions

All applicants will send a structured CV, contacts for three referees, and a cover letter stating their previous work, qualification (especially all field experience and less usual field/laboratory techniques) and motivation to our group email insectcommunities@gmail.com. Each application for the Ph.D. studies will include information to which position(s) it is related, one application for more positions is acceptable if the specific interests are described in the motivation letter. Any questions should be sent to the same email as well. The review of applications will begin on 20th February 2018 and will continue until the position has been filled. Selected applicants will be interviewed through Skype in the first ten days of March 2018. The Ph.D. positions are available from October 2018.

#1 Ph.D. position: Pollination networks in fragmented Afromontane grasslands

The main aim of this project is to reconstruct pollination networks in fragmented open habitats in Cameroonian mountains (Mount Cameroon and Bamenda Highlands). For these purposes, we use direct collecting and observations of visitors of all currently flowering plant species in communities, as well as video-recording of these interactions. Our aim is to reconstruct plant-pollination networks in grasslands on the whole community level under different seasonal, isolation and community composition conditions, and to disclose factors responsible for shaping of these interactions networks. The results will be directly comparable with similar dataset originated from the Czech Republic by the same sampling protocols allowing us to compare pollination networks in tropical and temperate regions. The student will be jointly supervised by Dr. Robert Tropek and Dr. Â©tÃán Janeèek.

Required for this position

- a MSc degree in biology or related fields (in summer 2018 at the latest)

- ability to lead a field research in challenging conditions of tropical environments

Desirable (but not necessary)

- reasonable knowledge of insects and/or plants

- experience with standard entomological sampling methods

- basic knowledge of French

#2 Ph.D. position: Organization of Afrotropical plant-bird pollination communities

The aim of the project is to study plant-bird interactions along the tropical altitudinal gradient of Mount Cameroon in different seasons, filling the knowledge gap in the Afrotropics. The main target is to gain complex plant-bird interaction matrices together with explanatory matrices related to abundance of flowers, energy supply, plant-bird morphological

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CharlesU Prague SpeciationGenomic

A PhD position in Genomics of speciation at Charles University in Prague

Position available from October 2018

Application deadline: 18ˆth February 2018

We are looking for a highly motivated PhD student to join our group working on genomics of speciation in two hybridizing songbirds, the Common Nightingale and the Thrush Nightingale. These species hybridize in a secondary contact zone and produce viable hybrid progeny. In accordance with Haldane's Rule, hybrid females are sterile, while hybrid males are fertile, allowing gene flow to occur between the species. The two species also show marked differences in sperm morphology, which could contribute to post-mating prezygotic isolation. The main goal of the project aims at identifying genetic basis and molecular mechanisms of both hybrid female sterility and postmating prezygotic isolation. The project will combine QTL mapping experiments and population genomic analyses of transcriptomes and whole genome sequences of both species. The candidates are expected to have experience in analyses of next-generation sequence data and at least some background in population or quantitative genetics. A previous experience in wet-lab is an advantage.

Scholarship:

The scholarship (per month) will be 600 EUR (ca 15,000 CZK) with the possibility of increase each year. Note that living expenses in the Czech Republic are generally lower than in Western European countries.

How to apply: If interested, please, send (1) CV including a list of publications, (2) motivation letter, and (3) contact details for 2-3 references to Radka Reifova (radka.reifova@natur.cuni.cz) by 18th February 2018.

Contact: Further information about the position can be obtained from Radka Reifova (radka.reifova@natur.cuni.cz).

You can also find further information about our group at our web page: http://web.natur.cuni.cz/~radkas/ "RNDr. Radka Reifová, Ph.D." <radka.reifova@natur.cuni.cz>

CSU Monterey Bay Applied Bacterial Genomics

Graduate Masters Position in Applied Bacterial Genomics.

The bioinformatics and genomics-focused Jue lab (https://csumb.edu/juelab) at California State University, Monterey Bay is recruiting a graduate student (M.S. Environmental Science) position in applied microbial genomics. This position is part of a broader project to identify the genetic mechanisms used by bacteria to remediate pesticides from agricultural runoff and understand the metagenomic community dynamics that contribute to optimal remediation activity. Prospective students should be interested in using genomics and bioinformatics to understand the functional genetic basis of complex phenotypes and/or how genetics can inform us on the ecological contexts for successful pesticide remediation. This position in our M.S. program starts Fall 2018. Please contact Dr. Nathaniel Jue (njue@csumb.edu) for more information. A successful applicant will be passionate about functional and evolutionary genomics, interested in microbial genetics, and familiar with sterile technique and basic genetic lab techniques. Experience with programming and statistics is also valued. Students working in the Jue lab get professional training in scientific computing, applied data science and advanced genomic lab techniques. Details about the M.S. program in Environmental Science at CSUMB can be found here: https://csumb.edu/amws. Our program provides excellent training required to enter technical positions in industry (~30% of graduates) and government (~40% of graduates) or academia (~20% of graduates) with a 90% graduation rate. Through CSUMB membership in the NOAA Center for Coastal and Marine Ecosystems, the Coastal and Marine Ecosystems Program (CMP) provides additional opportunities for financial support for graduate studies leading to the Masters of Science degree at CSU Monterey Bay. Center research emphases include Coastal Resilience, Coastal Intelligence and Place-Based Conservation. Prospective students must be applying to the thesis track and must be interested in working in the priority areas of the CMP. Please review the eligibility criteria and application instructions in the CMP graduate page (https://csumb.edu/cme/graduate-students) and contact Dr. Jue if you have questions about it. The Jue Lab celebrates having members from diverse backgrounds and training and encourages underrepresented and underserved groups to apply.

–

Nathaniel K. Jue, Ph.D.

Assistant Professor

School of Natural Sciences

California State University, Monterey Bay

Seaside, CA 93955

"njue@csumb.edu" <njue@csumb.edu>

CWilliamMary EvolutionaryGenomics

Graduate position: Plant Evolutionary Genomics

The Puzey lab (http://puzeylab.weebly.com) at the College of William and Mary (Williamsburg, VA) is recruiting a graduate student (M.S Biology) interested in using genomics to understand the development of complex spatial patterns in plants. Positions for MS program start Fall 2018. Please contact Josh Puzey (jrpuzey@wm.edu) for more information.

The successful applicant will be passionate about evolution, interested in plants, 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, 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.

jrpuzey@gmail.com

DeakinU Australia ParrotDiseaseGenomics

We seek two outstanding, highly motivated PhD candidates to work on disease ecology and genomics in Australian parrots.

This is an an ARC Discovery-funded project, 'Genomic diversity, tolerance and ecology of wildlife disease', with Professors Andy Bennett and Soren Alexandersen

(Deakin and GCEID), Dr Matt Berg (Deakin) and Professor Scott Edwards (Harvard). The students will be based at Deakin University, Geelong (near Melbourne, Australia) in a research group in the Centre for Integrative Ecology (CIE) and the Geelong Centre for Emerging Infectious Diseases (GCEID) with opportunities for travel to Scott Edward's lab at Harvard USA. The research project will commence in January 2018 and students need to start by July 2018, preferably earlier.

Emerging infectious diseases are among the most significant threats to conservation, agriculture and public health worldwide. One such disease is caused by the Beak and Feather Disease Virus (BFDV), a single stranded DNA virus which is spreading globally and is poorly understood in wild populations despite being a listed as a 'key threatening process to biodiversity' by the Australian Federal Government. BFDV infects primarily parrots, which are amongst the most highly threatened bird taxa globally. We will study the virus in the crimson rosella (Platycercus elegans) an emerging model system for studying population divergence and disease ecology, using a number of established field sites in south-eastern Australia. The primary aims of the research are to study the influences of tolerance, genomic diversity, and candidate genes on BFDV dynamics in rosellas, by combining genomic, pathological and ecological approaches. Both PhD's are expected to conduct field work and lab work, but have different emphases.

PhD 1: This will be focussed on molecular analyses, genomics and associated bioinformatics of both the host and the virus but will also involve field work (to assist with sample collection). The main objectives of this project is to test the role of genetic diversity and genotype rarity in infection, infer the roles of selection and candidate genes, and conduct phylogenetic analyses. The project will be based in Deakin's CIE, with additional training provided by GCEID and at Harvard University.

PhD 2: This will focus on field ecology and pathology/immunology, with training provided in the CIE and GCEID. The objectives are to investigate the pathological and fitness effects of BFDV infection in rosellas, and to combine these data with quantification of infection levels to evaluate the contributions of resistance and tolerance mechanisms to infection dynamics in this system.

Recent publications by our other PhD students on P.elegans include:

- Eastwood et al. (2017) Host heterozygosity and genotype rarity affect viral dynamics in an avian subspecies complex. Scientific Reports 7: 13310 - Eastwood et al. (2014) Phylogenetic analysis of beak and feather disease virus across a host ring-species complex. Proceedings of the National Academy of Sciences USA 111 (39): 14153-14158 doi 10.1073/pnas.1403255111 - Mihailova et al. (2014) Odour-based discrimination of subspecies, species and sexes in an avian species complex, the crimson rosella. Animal Behaviour 95: 155-164 - Ribot et al. (2012) Learned vocal variation is associated with abrupt cryptic genetic change in a parrot species complex. Plos One e50484

For further information on the research group, see:

- Deakin's Centre for Integrative Ecology: ciedeakin.com/ - Prof Andy Bennett (project lead; Deakin University): www.deakin.edu.au/profiles/andy-bennett - Prof Soren Alexandersen, Geelong Centre for Emerging Infectious Diseases: gceid.com/ and http://www.deakin.edu.au/about-deakin/people/-soren-alexandersen - Dr Mathew Berg, Deakin University: www.deakin.edu.au/about-deakin/people/mathew-berg - Prof Scott Edwards, Harvard University: edwards.oeb.harvard.edu/

Who should apply? The projects would suit students with strong interests in avian evolution and ecology, genomics, and/or disease ecology. Prerequisites for the positions include: Masters or First Class Honours (or equivalent in a relevant field); excellent written communication skills; high levels of enthusiasm, motivation and ability to work effectively as part of an interdisciplinary team; willingness to work long hours under arduous field conditions; and a driver's licence (for field work). Experience in field work with birds and/or molecular methods such as PCR, sequencing or bioinformatics would be desirable. Selection will be based on academic merit and previous experience.

Why apply? The projects offer exciting opportunities in the burgeoning fields of genomics and disease ecology with extensive training in

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DurhamU EvolutionaryGenomics

BBSRC CASE PhD studentship: The evolution of inbreeding depression in wild flax and implications for crop development.

Supervisory team: Dr Adrian Brennan, Prof Rus Hoelzel (Durham, UK), Dr Catherine Kidner (Royal Botanic Garden Edinburgh, UK) Novelty: Our research in wild flax will use new genotyping by sequencing technologies to obtain an unprecedented genome-wide perspective on inbreeding and its evolution, allowing the identification of relevant genes, and therefore the consideration of molecular mechanisms. These insights could then be applied to genetic improvement of flax to sustainably enhance agricultural production as well as improving our understanding of this fundamental aspect of evolution.

Research training: Research training: The student will gain bioinformatics skills that are in high demand both within academia and in wider industry. The project in general will require attention to detail, careful logical thought, and excellent numeracy, all of which are highly desirable transferable skills across all work sectors.

Background: Avoidance of inbreeding depression is understood to be a major force driving the evolution and maintenance of sexual outcrossing reproductive systems. By outcrossing, diploid organisms ensure the fitness of their offspring by maintaining heterozygosity. Humans have been domesticating species to suit their agricultural needs for the past 10k years. Artificial selection for individual traits often involves inbreeding and fixation of genetic variation. More recently, modern breeding practice has been able to reintroduce genetic variation and hybrid vigour into many domesticated species leading to impressive improvements in performance. Often this involves crosses between distinct varieties but crosses with wild relatives are also vital for introducing novel variation.

New genetic technologies now offer unprecedented opportunities to study the relationship between heterozygosity, reproductive system, and fitness at a genome-wide scale. We will address these questions in a model system, wild flax, which sits at the interface between evolutionary and applied biology. Cultivated flax is a globally important crop for both fibre and oilseed production and inbred varieties have been shown to benefit from hybridization. Surprisingly little is known about reproductive system and fitness in wild flax, a potentially valuable source of genetic variation for crop improvement.

Aims and Methods: We propose to test the extent and nature of inbreeding and its relationship with fitness in wild flax. We will use new genotyping by sequencing technologies to obtain an unprecedented genome-wide perspective on inbreeding and its evolution, allowing the identification of relevant genes and molecular mechanisms. The CASE partner, RBGE, is an internationally important organization responsible for the conservation and study of plant and fungal biodiversity. This project will feed into the core scientific activities of RBGE to generate baseline botanical data, to document and conserve plant biodiversity, and better understand evolutionary processes in plants.

Application details: This PhD will fully fund students with UK resident status or provide university fees only to EU students (see http://www.rcuk.ac.uk/-documents/news/terms-and-conditions-of-research-council-training-grants/). Please contact Dr Adrian Brennan, a.c.brennan@durham.ac.uk for further questions or to apply with a CV and a cover letter by 25th February 2018 deadline. The PhD is available to start as soon as March 2018 but a delay until the end of the current academic year is also possible.

acebrennan@yahoo.co.uk

Europe 15 ITN CONTRA CancerEvolution

15 PHD/RESEARCH POSITIONS ON CANCER GENOMIC EVOLUTION https://itn-contra.org Application deadline: 23:59 CET on the 15 February 2018

Cancer is a major cause of death and suffering. It constitutes a group of diseases characterized by abnormal cell growth, stage-wise progression, heterogeneity, and potential to develop resistance to therapies. All these aspects are consequences of the evolutionary nature of cancer. Fortunately, genomics has recently begun to provide opportunities for unprecedentedly detailed insights into tumour evolution. New techniques are presently emerging for assaying the spatial distribution of tumour heterogeneity, and future yet unforeseen experimental breakthroughs are inevitable.

CONTRA (https://itn-contra.org) is a H2020 Marie-Sklodowska-Curie Innovative Training Network aimed at providing a structured training programme to 15 Early Stage Researchers (ESRs) to study tumor evolution using computational techniques upon novel experimental data including, but not limited to, single-cell genomic data. See the list of projects at the end of this message.

The training structure of CONTRA will include local and network-wide activities and secondments to other labs in the network. Most positions are for 3 years and some for 4 years, contracts starting approximately July 1, 2018, but all of them lead to a PhD degree. Specific conditions may apply to individual positions depending on local regulations. Top-level graduates (master degree or equivalent) in bioinformatics, statistics, mathematics, computer science or evolutionary biology are encouraged to apply. No discrimination will be made on the basis of nationality, gender, race, religion or disability.

H2020 EU funding imposes strict eligibility criteria. At the time of recruitment the researcher must not have resided or carried out his/her main activity (work, studies, etc) in the country of the host institute for more than 12 months in the three years immediately prior to his/her recruitment. The researcher should also be in the first four years of their research careers at the time of recruitment by the host organisation and have not been awarded a doctoral degree. The successful candidate will receive a very generous financial package. The exact conditions varies across the universities, but the gross amounts of EU funding for an ESR is in the range 3710 euro -4210 euro . The net salary will result from deducting all compulsory (employer/employee) social security contributions as well as direct taxes from the gross amounts, according to the law applicable to the agreement concluded with the ESR. Some universities will also supplement the EU funding. For details see the EU Guide for applicants (https://goo.gl/d6LtsE).

Candidates may apply for the positions through the KTH application system (https://goo.gl/yTThgg). The application should include the following documents:

1. Curriculum vitae with at most 3 pages 2. Transcripts from University / University College 3. Contact details for three references 4. Brief description of why the applicant wishes to become a PhD student within this network 5. Ranking of 3 ESR projects based on the applicant's preference

Each project supervisor will revise the candidates' documentation and, on the basis of the completeness and adequacy of the requested material and eligibility, will score candidates based on: (1) academic profile; (2) personal motivation; (3) scientific skills and relevant experience; and (4) English proficiency. Shortlisted candidates will be invited to teleconference interviews with the relevant project supervisor(s).

Application deadline: 23:59 CET on 15 February 2018. Candidates are invited to contact the supervisors for more details. For individual descriptions of the 15 projects, please use the following link: https://itn-contra.org/esr-projects. List of projects, including supervisor and host institution:

- ESR1: Comparing tumour phylogenies from single cell data versus bulk sequencing data. Florian Markowetz, University of Cambridge, Cambridge, UK. - ESR2: The mechanisms of coding and non-coding oncogenic alterations. Nuria Lopez-Bigas, IRB, Barcelona, Spain. - ESR3: Identification of drivers of relapse and metastasis. Nuria Lopez-Bigas, IRB, Barcelona, Spain. - ESR4: Estimating tumour phylogenies from single-cell SNV and CNA data. Niko Beerenwinkel, ETH Zurich, Basel, Switzerland. - ESR5: Evolutionary history of circulating tumour cells and distant metastases. Ewa Szczurek, University of Warsaw, Warsaw, Poland. - ESR6: Identification and impact of clonal and subclonal driver alterations on cancer progression. Francesca Ciccarelli, KCL/Crick Institute, London, UK. - ESR7: Inferring tumour evolution and migration. Niko Beerenwinkel, ETH Zurich, Basel, Switzerland.

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Europe 15 ITN IGNITE CompGenomicsInverts

We are happy to announce that 15 PhD/Early Stage Researcher (ESR) positions now available in the Pan-European MSCA-ITN "Comparative Genomics of Non-Model Invertebrates" (IGNITE) Network of institutions and companies for a maximum duration of 36 months.

All positions will open on 1st July 2018 or as soon as possible thereafter. The deadline for applications is 28th February 2018 (23:59 CET).

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

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

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

For a detailed description of the individual projects please see:

< http://www.itn-ignite.eu/projects/ >

best wishes

Gert

– Prof. Dr. Gert Wörheide Department of Earth and Environmental Sciences, Division of Paleontology & Geobiology & GeoBio-CenterLMU Ludwig-Maximilians-Universität München, and Director, Bavarian State Collections of Palaeontology and Geology Richard-Wagner-Straße 10 80333 München Germany

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New ITN IGNITE to start in 2018: www.itn-ignite.eu Publications: www.publications.woerheide.eu orcid.org/0000-0002-6380-7421

GPG-Fingerprint: *9644 7211 5BE6 9EF5 3C5C 80B9 8B8D 2D6D 8DCC 8499*

Gert Woerheide <woerheide@lmu.de>

Europe 15 PlantID

15 PhD positions across Europe

The EU H2020-ITN-ETN project Plant.ID on molecular identification of plants is recruiting 15 PhD fellows across nine European host institutions.

We are still looking for excellent candidates! Application deadline January 15, 2018. These are fully funded positions with contracts and research funding. For more information and how to apply: www.plantid.uio.no All nationalities can apply as long as you do not have more than 4 years of research experience and have not lived in the country of the host institute for more than 12 months in the last 36 months. Check eligibility criteria in detail below.

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

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

EU eligibility criteria The applicant may be of any nationality but in order to be eligible for the positions the following criteria applies to all applicants: - The applicant shall at the time of recruitment be eligible as an Early Stage Researcher (ESR) by being in the first four years of his/her research career and not have been awarded a doctoral degree. - The applicant must not have resided or carried out his/her main activity in the country of the host institute for more than 12 months in the 3 years immediately prior to the recruitment.

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

Gothenburg - PhD 15 - Logging forensics: mining ebony wood collections as references - Naturalis Biodiversity Center, Degree Awarding University of Leiden

Brecht Verstraete <brecht.verstraete@gmail.com>

GhentU ExptEvolution

Ph.D. position in Experimental Evolution and Evolutionary Genomics

A Ph.D. position is available in the Van de Peer Lab in Bioinformatics and Evolutionary Genomics (BEG), VIB 'V Ghent University, Ghent, Belgium (http://bioinformatics.psb.ugent.be/). The student will work on an FWO funded project in collaboration with Olivier De Clerck (Phycology, Ghent University, Ghent, Belgium). The position is for three years (a one-year extension might be possible) and is available immediately.

Project: Testing big evolutionary hypotheses with small organisms - The effects of whole-genome duplication (WGD) on plant evolution

Polyploids, organisms that underwent a WGD, possess one or more extra copies of their genome, which has the potential to facilitate the evolution of new functionality. Many WGDs are accordingly found in very successful eukaryotic lineages characterized by particular biological innovations and/or diversifications. However, the acquisition of two complete genomes is generally not well tolerated by cells, leading to harmful effects on the overall fitness and fertility of the organism. This results in a paradox between the observed immediate negative effects of WGDs, and their attributed long-term positive effects. Phylogenomic dating of WGDs in plants suggests that many polyploids became established during times of environmental upheaval or extinctions. Present-day polyploids are also often more abundant in harsh environments such as the Arctic, which together would suggest that environmental turmoil and stress may enhance polyploid establishment, because their increased genetic variation could potentially enable rapid adaptive changes. To test this hypothesis, we are conducting evolutionary experiments in unicellular green algae (the model system Chlamydomonas), aiming to gain novel insights into why and how polyploids can obtain an evolutionary advantage over their non-polyploid ancestors.

The project has two components. 1) Experimental evolution of algae to study the effects of stress and changing environmental conditions on the survival and establishment of polyploids. 2) Evolutionary genomics of evolved algae using next-generation sequencing to correlate genomic and transcriptional dynamics with fitness, adaptation, and establishment.

Candidate'Âs Profile:

Candidates should have a Master'Âs degree (or equivalent), a strong background in evolutionary biology, and a keen interest and preferably experience in both empirical research and bioinformatics. The student needs to be dedicated to carrying out long-term multidisciplinary research which involves regular maintenance of algal cultures, some molecular work, as well as evolutionary genomic analyses. Basic knowledge of programming/scripting and statistics is required. Fluent English and good communication skills, oral and in writing, are essential.

Application:

Send your application containing a CV, a motivation letter (max. 1 page) and contact information of two referees, combined in a single PDF, to Dr. Eylem Aydogdu (eyloh@psb.ugent.be). For further information about the position also contact Dr. Eylem Aydogdu directly.

Prof. Dr. Yves Van de Peer

Department of Plant Biotechnology and Bioinformatics, Ghent University VIB - UGent Center for Plant Systems Biology

Technologiepark 927, B-9052 Ghent, Belgium

Phone: +32 (0)9 331 3807 Cell Phone: +32 (0)476 560 091 email: yves.vandepeer@psb.ugent.be

Department Chair - Elect Part-time Professor at the Department of Genetics, Pretoria, South Africa

Yves Van de Peer <yvpee@psb.vib-ugent.be>

Gottingen BacterialEndosymbiontGenomics

The Johann-Friedrich-Blumenbach Institute of Zoology and Anthropology at the Georg-August-Universitat Gottingen is looking to fill the position of a Doctoral/Ph.D. Student for research on Exploring and optimising long-read sequencing techniques for bacterial endosymbiont genomics

The position is funded by the Georg-August-Universitat Gottingen for a period of 3.5 years (42 months), with a salary according to the German salary scale TV-L E13 (50 %), and should be filled by April 1st 2018.

Within this project the sequencing of bacterial endosymbiont genomes (e.g., Wolbachia, Rickettsia) from insect hosts should be optimised based on long-read sequencing techniques (e.g., nanopore sequencing).

For this purpose, different DNA extraction methods, as well as enrichment techniques will be compared. The resulting genomes shall be analysed comparatively using bioinformatic pipelines.

Applicants need to hold a diploma or MSc degree in biology or a related field and to have experience with molecular methodology, particularly with respect to DNA extraction and sequencing. Moreover, experience with computational work in a UNIX/Linux environment is recommendable.

Experience in entomology would be helpful, but not necessary. Working language is German and English. Doctoral students are supposed to take part in supervising students during internships and seminars.

This position is designed to foster young researchers and scientists and give the successful applicant the opportunity to pursue a doctoral degree.

The University of Gottingen is an equal opportunities employer and places particular emphasis on fostering career opportunities for women.

Qualified women are therefore strongly encouraged to apply in fields in which they are underrepresented. The university has committed itself to being a family-friendly institution and supports their employees in balancing work and family life. The mission of the University is to employ a greater number of severely disabled persons. Applications from severely disabled persons with equivalent qualifications will be given preference.

Applications including a full cv, description of previous research interests (e.g., summary of the master thesis) and names and email addresses of at least two possible references should be sent by February 15, 2018 in electronic form or by ordinary mail to Prof.

Dr. Christoph Bleidorn, Johann-Friedrich-Blumenbach-Institut fur Zoologie und Anthropologie, Georg-August-Universitat Gottingen, Untere Karspule 2, 37073 Gottingen, Germany, cbleido@gwdg.de.

The advertisement can be found at http://www.uni-goettingen.de/de/305402.html?cid=13336 Prof. Dr. Christoph Bleidorn Georg-August-University Gottingen Johann-Friedrich-Blumenbach Institute for Zoology & Anthropology Animal Evolution and Biodiversity Untere Karspuele 2 37073 Gottingen Germany

Follow me on twitter! https://twitter.com/C_Blei Christoph Bleidorn <cbleido@gwdg.de>

GuangxiU EvoDevo

Funded graduate positions at Guangxi University, China

Eco.Evo.Devo (EED) Lab Group at Guangxi University (GXU) China (PRC) has several graduate student positions for PhDs and MScs (preferably Ph.D.). Broadly, we study ecology, evolution and development of fishes and amphibians. Based on the student's interests, the Principle Investigator (PI) and the student will craft a PhD research topic; any research focusing on ecology, evolution and development in a biodiversity conservation context is encouraged.

The students accepted will receive a stipend, on-campus housing and medical insurance through a China Government Scholarship (CGS) for the duration of the study period. The deadline for the CGS program is 31st of March 2018. Successful students will also receive, through the EED lab, the airfare for arriving and leaving China upon successful completion of studies. For this recruitment round, the graduate students will need to begin their degree program by September 2018.

Funding for research is available, and the EED lab will generate additional funding as needed. The lab is equipped to do research in molecular evolution & phylogenetics, development and ecological research. Our lab also has a clean room (for RNA, Environmental DNA and Ancient DNA work), modern aquarium and vivarium facilities. The Associated Guangxi Key Laboratory in Forest Ecology and Conservation is well equipped for all modern research work. It is expected that all work pertaining to graduate research work will be published in reputed scientific journals.

The working language of the International Training program is English. However, all graduate students should undergo a Chinese language related course within the first year. The international program will also offer several graduate level courses in Ecology and Evolution (in English), which are, together with a dissertation thesis are required for matriculation for the degree.

GXU is situated in Nanning, the largest city in Guangxi Province (in Southwestern China), bordering Vietnam. Nanning is a vibrant city with a diversity of restaurants, shopping malls and recreational areas. Guangxi province harbors a remarkable biodiversity in its plains, mountains, Karst habitats and associated underground rivers and waterways. The proximity to two biodiversity hotspots is an added advantage for biodiversity related research work.

Interested applicants, please send a CV, unofficial transcripts (official transcripts will be required later), names and email addresses of three references, and a brief statement of research interests (less than 700 words) to eed.gxu.edu@outlook.com by the 30 th of January 2018.

Students from a diversity of backgrounds are encouraged to apply. Review of applications will begin immediately.

Lab Manager

Eco.Evo.Devo group

International Training Program

College of Forestry and Guangxi Key lab in Forest Ecology and Conservation

Guangxi University

Nanning

PRC

Phone: - +85-137-8830-0340

eed.gxu.edu@outlook.com

GuangxiU PlantEvolution

International Graduate Program 2018 with multiple MSc and PhD positions available at the College of Forestry of Guangxi University, Nanning, China

The Plant Ecophysiology and Evolution Group, Conservation Biology Group and Forest Dynamics Research Laboratory at Guangxi University (Nanning, China) are seeking highly motivated and productive International MSc and PhD students to engage in 3-4 year projects, starting in September 2018, in the following research fields:

(1) Plant Ecophysiology -A: Plant Physiological Ecology including water relations -B: Functional Plant Anatomy -C: Photosynthesis and Photoprotection -D: Functional traits and community assembly of subtropical forests

Projects are supervised by Prof. Kun-Fang Cao (kunfang.cao@gxu.edu.cn or caokf@xtbg.ac.cn) and Associate Prof. Shidan Zhu (zhushidan@gxu.edu.cn). More information here: http://www.plant-ecophysiology-evolution.com/person/cao-kunfang/ http://www.plant-ecophysiology-evolution.com/person/shi-dan-zhu/ (2) Biodiversity Genomics -A: Plant Genomics and Evolutionary Diversification -B: Molecular Systematics and Plant Taxonomy -C: Historical Plant Biogeography and Biome Assembly

Projects are supervised by Associate Prof. Joeri S. Strijk (jsstrijk@gxu.edu.cn). More information here: http://www.plant-ecophysiology-evolution.com/person/joeri-sergej-strijk/ (3) Genetics -A: Ecological Genomics. -B: Conservation Genetics.

Projects are supervised by Associate Prof. Alison Wee (alisonwks@gmail.com). More information here: http://www.plant-ecophysiology-evolution.com/person/alison-kim-shan-wee/ (4) Seed Ecophysiology Uromi-A: Seed Ecology and Physiology

Projects are supervised by Associate Prof. Uromi Goodale (uromi.goodale@outlook.com). More information here: http://www.plant-ecophysiology-evolution.com/person/uromi-manage-goodale/ (5) Ecophysiology and Coevolution Gou-Feng Jiang-A: Plant Ecophysiology of Mangroves. -B: Phylogenetics and Coevolution in Gymnosperms.

Projects are supervised by Dr. Jiang Guofeng (gfjiang@gxu.edu.cn). More information here: http:/-

/www.plant-ecophysiology-evolution.com/person/-jiang-guofeng/ (6) Ecology -A: Animal Behavior. -B: Breeding and Nesting Ecology. -C: Ecotoxicology. -D: Social and Economic Influences on Conservation Species Interaction Networks. -E: Urban Ecology.

Projects are supervised by Faculty members of the Conservation Biology Group (Prof. Eben Goodale (eben.goodale@outlook.com), Dr. Aiwu Jiang, Dr. Christos Mammides, Dr. Myung-bok Lee, Dr. Ari Martinez).

More information here: http://animal-ecology-guangxi.com/ (7) Tropical Forest Botany and Ecology -A: Biodiversity Monitoring Forest Plots in Guangxi Province. -B: Distribution and composition of the Philippine Island Flora: phylogenetics, ecological features, plant functional and reproductive traits. Projects are supervised by Prof James V. LaFrankie of the Forest Dynamics Research Laboratory. https://-www.researchgate.net/profile/James_Lafrankie3/ The International Graduate Program at the College of Forestry offers fully funded MSc and PhD Fellowships for 3-4-year projects, with complete waivers for tuition fees and housing fees. Housing is provided in the International Student dormitories of the campus in Nanning. The first year consist of project orientation and study of Chinese language through courses in combination with introductory courses taught by faculty members of the three research groups. The other three years will be filled with fieldwork, professional courses and the research project.

Project applications are now invited for starting dates of projects in September 2018. The application deadline is March 31, 2018. Fellowships come with an ample monthly allowance for the full duration of the project. Applicants with a proven track record of successful publication in peer-reviewed journals will have an advantage.

Opportunities for the development of individual research projects as well as collaborative work, exist within our lab and with external groups. Candidates will be integrated in growing and multidisciplinary teams of Chinese and foreign researchers, providing a creative and stimulating research environment, and will work as part of teams studying the evolution, ecology, distribution, conservation and/or ecophysiology

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IVB MUni Czech LizardHybridZoneGenomics

A PhD position in hybrid-zone genomics of a legless lizard (Anguis)

Deadline for expressions of interest: 16 February 2018

The HerpDiv Research Group (Vaclav Gvozdik's group) at the Institute of Vertebrate Biology, Studenec, Czech Academy of Sciences, is seeking a highly motivated student who ideally holds (or will finish soon) MSc in population genetics, mathematical biology, bioinformatics or a related topic. The successful applicant will be involved in a project focusing on population/landscape genomics of the hybrid zone of a legless lizard (Anguis).

Project: Anguiomics: Genomic insights into the evolutionary history and contact zones of slow-worm lizards (Anguis)

The project will combine multidisciplinary techniques using three types of genomic data (phylo-, cyto-, and population) and GIS-based environmental niche modelling in Anguis lizards. The first two parts, phylogenomic inference and cytogenomic characterization of the species will be separate sub-projects. Within the announced position, the successful applicant will be focusing on genome-wide variation (reduced representation; ddRAD-seq) at a population level across the secondary contact zone of A. fragilis and A. colchica in two geographic regions (central Europe and northern Balkans). This will allow us to empirically assess levels of introgression and estimate the strength of barriers maintaining divergence between the species, and to compare the situation in the two regions. We will further test association between genomic variation and environmental parameters, potentially identifying loci under selection by environmental factors. This will allow us to assess if the two species respond to environmental factors in a similar or different way, and to understand the balance between endogenous and exogenous selection acting in the contact zone.

The successful applicant will be enrolled in the PhD program of the Masaryk University in Brno (MUNI), Faculty of Science, Department of Botany and Zoology. Employment and analytic work will be realized at the Institute of Vertebrate Biology, Studenec, and the study will be supervised by Dr. Vaclav Gvozdik (evolutionary biology of reptiles). The pool of potential co-supervisors includes Dr. Stuart J.E. Baird (speciation research, genomics). The length of the PhD study is 4 academic years starting in September 2018, with a preferred start of employment in July 2018.

Main responsibilities - analytic works: -——— bioinformatics - working with reduced-representation genomic data (ddRADseq or possibly other type of genomic data) -——— working with GIS-based environmental data -——— involvement in field work and wet-lab is welcome but not necessary (depending on interests of the successful candidate)

Applicant's profile: We seek a bright and highly motivated candidate with -——— a master's degree in a relevant field such as population genetics, mathematical biology, bioinformatics or molecular/evolutionary biology (summer 2018 at the latest) -——— experiences in bioinformatics, programming (or at least basic scripting in Linux) and/or GIS-based analyses -——— enthusiasm in both biological and computational questions -——— ability to work in a team but also independent initiative -——— good oral and written communication skills in English -——— documented experience with scientific writing will be advantageous -——— driving licence, if interested in taking part in field work, will be also advantageous

We offer: -——— attractive research topic in an established international team -——— possibility to take part in field work both in the Czech Republic and abroad (Balkans) -——— sufficient financial and logistical sources for the project -——— salary will be paid according to the Czech academic standards - 60% position for PhD candidate + scholarship, i.e. approx. 240,000 CZK annual income (this sufficiently covers living expenses in the Czech Republic) -——— plus various student/employee bonuses (e.g. a possibility of being accommodated in an institutional apartment in Studenec for a reasonable rent)

Applicants should send a structured CV with contacts for two referees and a motivation letter (one page) to Vaclav Gvozdik, vaclav.gvozdik@ivb.cz with email subject “PhD position”. Any questions shall be sent to the same email address. The review of applications will begin on 17 February 2018 and continue until the position is filled. Selected applicants will be interviewed via Skype in the second half of February 2018. The PhD position is starting between July - September 2018 but candidates must register for the study at the MUNI till the end of April 2018.

Dr. Vaclav GVOZDIK, PhD INSTITUTE OF VERTEBRATE BIOLOGY Czech Academy of Sciences Research facility STUDENEC Studenec 122, CZ-675 02

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JMU Liverpool SocialEvolGenomicsConservation

Liverpool_JMU.SocialEvolutionGenomicsConservation

I am looking for a student with an excellent track record (e.g. 1st Class undergraduate degree and/or Masters level qualification) to apply for a fully funded PhD Scholarship at Liverpool John Moores University https://www.ljmu.ac.uk/research/phd-scholarships. Students must be UK/EU nationals to qualify for funding.

The topic of research is flexible and can be tailored to your interests so feel free to suggest your own project or to join an existing project. Current research conducted by my lab includes the evolution of social behaviour, inbreeding/genetic diversity, scent communication, and conservation/population genetics/genomics. Species studied include the banded mongoose (Uganda), meerkat (South Africa), Asiatic wild ass (Israel), molerats (southern Africa) and pilot whales. See my website for further details on current projects https://hazelnichols.weebly.com/ . The final application deadline is 28th Feb 2018 but please contact me much earlier than this to prepare your application.

If interested, please contact me on h.j.nichols@ljmu.ac.uk

H.J.Nichols@ljmu.ac.uk

Krakow ClimateAdaptation

Climate change effects on life history and physiology: intra- and interspecific interaction approach

PhD position under National Science Centre, Poland (http://www.ncn.gov.pl), Opus 13

Study field: ecological interactions, evolution of life history, physiology, species geographic range, climate change

General theme

Climate change effects on species ecological interactions in damselflies. The PhD project will address the following questions: (1) How individuals that hatch earlier affect life history and physiology of individuals that hatch later in the season and vice verse. (2) What consequences this will have on species geographical ranges?

Job description: * Field sampling (Poland, Scandinavia) and larval rearing in laboratory conditions * Measuring life history traits, e.g. larval size, growth rate and development time * Quantification of physiological traits (Leuven University, Belgium) * Writing manuscripts

Institution

Institute of Nature Conservation in Krakow, Polish Academy of Sciences (http://www.iop.krakow.pl)

Requirements: * Master degree in biology, ecology or relevant field * Fluency in English, written and spoken * Strong motivation for research work (field and laboratory) * Involvement in realization of the grant, including irregular working hours (availability) * Additional attributes: documented research experience (e.g. publications, attendance in scientific conferences, involvement in research projects), basics in statistical analyses, ability to work as a team member, but also being independent, enthusiasm for working abroad, driving licence

Offer

PhD scholarship 3 000 PLN monthly for 3 years (36 months). Funds to cover travel and accommodation costs during project meetings, research stays at project partners and scientific conferences.

Interested?

Please email your (1) CV, (2) a letter of motivation including relevant experience, (3) two letters of reference from academic referees, (4) copies of the scientific contributions (articles, conference presentations, etc), (5) a copy of the MSc degree or equivalent to Dr. Szymon Sniegula (szymon.sniegula@gmail.com).

Deadline for application

The documents should be combined into a single PDF file and emailed by 31 January 2018 midnight 23:59 CET with the subject “Opus PhD application”.

The pre-selected candidates can be invited for an interview through Skype during the first half of February 2018.

For more information email Szymon Sniegula, szymon.sniegula@gmail.com

or go to: http://www.iop.krakow.pl/projekty,2,research_projects_(national_financing).html

– Institute of Nature Conservation Polish Academy of Sciences Mickiewicza 33 31-120 Krakow, POLAND phone: +48 602 152996 e-mail: szymon.sniegula@gmail.com my personal website

Szymon Sniegula <szymon.sniegula@gmail.com>

LordHoweIsland ConservationGenetics

Project

The Lord Howe Island Stick Insect, ’Â© thought to be extinct but recently rediscovered, has become emblematic of the dangers faced by island species in the face of anthropogenic change. A planned reintroduction effort aims to rescue this species, one of the rarest insects in the world, from the brink of extinction. This project aims to assess the genetic diversity of the rediscovered population, currently maintained in a captive breeding program, and aid the development of plans for release. The project will combine cutting-edge molecular techniques and innovative approaches to genotyping of unusual material (historical and non-destructively sampled in the field) with analysis of next-generation sequencing data. In addition to the primary objectives, the unique biology of this insect provides opportunities to investigate more general biological questions, ranging from the effect of polyploidy on the animal body, to how massive body size evolves. Crucially, research outcomes of this project will directly contribute to ongoing conservation efforts.

Suitable applicants need to be highly motivated with a strong academic and research background. Demonstrated ability to conduct independent research is required, with experience in the molecular lab, and some experience in programming or data analysis being desirable. Applicants should hold first class honours or equivalent experience. The successful student will need to apply to ANU for enrollment. The successful applicant will receive a stipend scholarship and research funds including computer and travel funding.

Location

We will be based in the Division of Ecology and Evolution at the Research School of Biology at the Australian National University in Canberra, Australia. Lab work and/or training will likely take place at the Okinawa Institute of Science and Technology in Okinawa, Japan.

Both locations feature excellent facilities and intellectual environments. The project will also be supported by Zoos Victoria, who hold a large captive population at Melbourne Zoo, and are closely involved with the recovery effort. Field work to collect additional samples may also be involved.

Expression of interest

Expressions of interest should be submitted directly to Alexander.Mikheyev@anu.edu.au by March 1, 2018. Please include a brief statement on why you are interested in this project, a CV and contact details for references. Following assessment of applications one applicant will then be invited to formally apply to the ANU. The successful applicant will be able to start as soon as possible. You can also find out more information about the graduate program by clicking on the "Higher Degree by Research'Â± tab at http://biology.anu.edu.au/-education/degree-programs Alexander Mikheyev

Group Leader, Research School of Biology The Australian National University

alexander.mikheyev@oist.jp

Marburg Germany PlantAnimalInteractions

Starting in June 2018, we offer a three year PhD position in a project on vertical stratification of plant-animal interactions and their impact on pollination and seed dispersal within a single Neotropical plant species.

The PhD student will be based at the Philipps University Marburg, Germany, and field work will take place close to Iquitos in the Peruvian Amazon.

Field work includes focal observation of birds, mist-netting of bats, collection of nectar and fruit samples across a vertical gradient (which requires tree climbing), and camera observations. Subsequent lab work includes nutrient analyses of fruits, and a population genetic study with microsatellites.

This project is carried out by Dr. Katrin Heer in collaboration with Prof. Dr. Eckhard Heymann (DPZ) and Prof. Dr. Marco Tschapka (University of Ulm), and is funded by the German Research Council (DFG).

More detailed information on the project and the job announcement can be found here: https://-www.uni-marburg.de/fb17/fachgebiete/naturschutz/-naturschutzbiologie/staff/academic-staff/index_html-en

Please do not hesitate to contact us if you have further questions. katrin.heer@uni-marburg.de

– Dr. Katrin Heer Conservation Biology Philipps Universität Marburg Karl-von-Frisch-Strasse 8 35043 Marburg

Phone: +49 (0) 6421 2823374 Fax: +49 (0) 6421 2826588

"katrin.heer@uni-marburg.de" <katrin.heer@uni-marburg.de>

MississippiStateU ButterflyGenomics

We are recruiting two students for NSF funded PhD assistantships studying the genomic changes responsible for wing color pattern variation in Heliconius butterflies. The projects offer opportunities for students to develop projects that integrate population genomics, gene expression assays, references genomes, and genome-editing to better understand how changes in the genome cause phenotypic variation. These PhD assistantships are part of an NSF EPSCoR funded collaboration between Mississippi State University (Brian Counterman) and the University of Puerto Rico (Riccardo Papa) aimed to provide training in genomics through the study of butterfly wing patterns. For more information about this NSF EPSCoR project, please visit https://sites.google.com/-view/genome-to-phenome/home The students will be enrolled in the PhD program in the Department of Biological Sciences, but will have opportunities for extended visits and work closely with a collaborative team of Heliconius researchers including Robert Reeds lab at Cornell University, Arnaud Martins lab at George Washington University, and Owen McMillans lab at the Smithsonian Tropical Research Institute. Students will be expected to work with our live Heliconius colonies at the Smithsonian Tropical Research Institute rearing facilities in Gamboa, Panama. At Mississippi State University, the students will be housed in the Counterman lab (https:/-/www.countermanlab.org/) and have opportunities to work closely with other labs participating in the NSF EPSCoR project: Federico Hoffmann (gene family evolution) and Ryan Range (pattern development).

The Graduate Program in the Department of Biological Sciences at Mississippi State University offers a PhD in Biological Sciences. There is a vibrant and growing graduate program with over 60 students funded through teaching and/or research assistantships. Further details about the PhD program can be found in Graduate Handbook here: http://www.biology.msstate.edu/pdf/-2016-BIO-Graduate-Student-Handbook.pdf MSU is located in Starkville, a quaint college town in northeast Mississippi. The small town of nearly 25,000 permanent residents offers a diverse and progressive community with strong town-and-gown relationships that host several cultural festivals and events throughout the year. The university is surrounded by remnants of Blackbelt prairies, agricultural experimental stations and the Sam B. Hamilton Noxubee National Wildlife Refuge, which offer a diversity of local outdoor activities and research opportunities. MSU is centrally located in the southeastern United States, with Memphis ~2 hrs North and New Orleans ~5 hrs South, and a regional airport ~20 miles from MSU that offers daily flights to Atlanta.

Required qualifications: The applicant must have a BS or equivalent in a biological sciences discipline, experience working with genomic datasets in a Unix environment AND/OR basic molecular biology laboratory methods.

Preferred qualifications: Preference will be given to applicants with that have a record of scholarly publication, completed an MS in a biological sciences discipline, and/or any of the following skills: experience with high-throughput sequence data, Unix environment, genomic analyses, performing CRISPR-cas9 gene editing.

The project team is committed to increasing diversity in STEM, and we especially encourage applications from women, minorities, veterans and other underrepresented groups.

Application: Please send a single PDF containing a CV, unofficial transcripts, and contact information for three references to regulatorylogic@gmail.com with GraduateStudent:ButterflyGenomics in the subject line. Review of applications will begin January 31, 2018 and continue until the position is filled. The start date/semester is flexible. Please contact me at bcounterman@biology.msstate.edu with inquiries.

bc650@igbb.msstate.edu

Muenster AppliedPlantEvolutionaryEcol

PhD Position in applied evolutionary ecology Rapid evolution in wild plants cultivated for ecosystem restoration

The Biodiversity and Ecosystem Research Group in the Institute of Landscape Ecology at the University of Münster (Germany) invites applications for a Doctoral Research Position (salary scale 65% of 13 TVL, for 36 months).

We are seeking to fill a 3-year PhD position, part of research project on rapid evolution in cultivation of wild plants, which has been recently granted to Dr. Anna Lampei Bucharova (currently at the University of Tübingen, from spring 2018 at the University of Münster) and Dr. Walter Durka (UFZ Halle). The project focuses on evolution in cultivation. To provide sufficient amount of seeds for ecosystem restoration, wild plants are cultivated in monocultures on specialized farms. In Germany, this cultivation is region-specific. Seeds of individual provenances are cultivated at many farms around the country, and produced seeds are sold as "Regionalsaatgut" for ecological restoration. However, the conditions in cultivation strongly differ from the wild and it is likely that plants adapt to cultivation ("cultivation syndrome") and consequently, lose their adaptation to wild environment, resulting in negative impact on restoration success. The successful candidate will work with many species and investigate how common and how large are the evolutionary changes during cultivation. At the same time, the system is an excellent opportunity to investigate fundamental evolutionary questions about rapid evolution, evolutionary trade-offs and parallelism in evolution across large number of species and thus, derive general patterns (in contrast to working with one model species).

The core of the project is a set of common garden experiments, complemented by molecular analysis. The PhD student will be supervised by Dr. Anna Lampei Bucharova, in cooperation with Prof. Oliver Bossdorf (University Tübingen). Further details can be obtained from Dr. Anna Lampei Bucharova (anna.lampei-bucharova@uni-tuebingen.de).

The University of Münster is a large vibrant university hosting number of excellent scientific institution and provides stimulating research environment. The Biodiversity and Ecosystem Research Group is led by Prof. Norbert Hölzel and works on various topics, for example grassland ecology, rare species, restoration ecology or land use change and landscape dynamics in Western Siberia and Kazakhstan (https://-www.uni-muenster.de/Oekosystemforschung/en/). The city of Münster is characterized by its many students and presents a dynamic environment with many cultural and social events throughout the year (http://-www.muenster.de/en/). The main transportation mean in the city is bicycle, which gives the city unique atmosphere.

Applicant should have keen interest in applied evolutionary ecology and a Master degree (or equivalent) in the relevant research fields (e.g.

plant ecology, evolution, botany). The applicant must have experience with quantitative statistics (optimally using R) and have proficiency in both written and spoken English, German is not necessary. Experience with large common garden experiments is a plus. As the first common garden experiment must start early spring 2018, the position starts in April 2018.

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

Applications should be written in English and have a form of single Pdf congaing 1) cover letter with a statement of your research interests and motivation (max. 1 page), 2) CV including details of research experiences and 3) contact to at least two referees. Applications are to be sent to Prof. Norbert Hölzel, nhoelzel@uni-muenster.de till 21.1.2018.

Walter Durka <walter.durka@ufz.de>

Munster WildPlantEvolution

Rapid evolution in wild plants cultivated for ecosystem restoration

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– Dr. Anna Lampei Bucharova Plant Evolutionary Ecology University Tübingen Auf der Morgenstelle 5 72076 Tübingen Phone:+49 7071 2974248

Anna Lampei Bucharova <anna.lampei-bucharova@uni-tuebingen.de>

Napoli Italy PlanktonEvolution

Investigating the role of connectivity in plankton ecology and evolution by genomics

The Stazione Zoologica of Napoli, Italy and Genoscope in Evry, France propose a PhD internship to study how the oceanic connectivity affects marine ecosystem diversity using environmental genomics approaches. A master internship on related topics is also possible.

An enduring challenge is to comprehend how marine plankton has developed and maintains its relatively large diversity, characterized by a complex web of interactions, while living in a largely unstructured environment. As the local composition of plankton communities are controlled by ocean circulation and resource delivery, together with organism acclimation and adaptation, understanding the relation between the local distribution of species and the large scale oceanographic patterns becomes crucial. At this regard, since the 1930s, the hypothesis that everything is everywhere but the environment selects has shaped theories of marine biogeography, questioning the possibility of an actual endemicity for plankton species. However, recent progresses in genomics allowed to acquire and to compare data from different types of wild marine organisms at ocean scale. In particular, genomics data from the expedition Tara Oceans provide the possibility to address the question of physical connectivity between organisms by ocean circulation at DNA level.

In this project, with the student we will bring together expertise in theoretical ecology, genomics and oceanography to explore how the physical connectivity between oceanic regions may contrast the stable coexistence of many species, and favor the establishment of new species. We will pay particular attention to the hypothesis that on ecological time scales gyres and main current systems do actually isolate the species into local populations. We will develop and use models to test specific hypotheses on plasticity, adaptation, micro-evolution, speciation and collective processes.

The position will be held in Napoli, Italy with multiple stays at Genoscope near Paris, France. Daniele Iudicone, Reno Sanges and Olivier Jaillon will supervise this work. Numerous interactions with other members of Tara Oceans consortium are to be considered.

Ideal candidate will have a strong background in one or several of following skills: oceanography, marine ecology, numerical ecology, evolutionary genomics, comparative genomics. The student work will be computational. A desirable asset would be knowledge of the linux operative system, a scripting language, sequencing and functional genomics data and biological and bioinformatics databases and tools.

Email to Daniele Iudicone : iudicone@szn.it and/or to Olivier Jaillon ojaillon@genoscope.cns.fr and/or Remo Sanges remo.sanges@gmail.com.

Applications should be posted here : http://-www.szn.it/index.php/it/formazione/doctorate-phd-iii-level/positions-on-offer .

Olivier Jaillon <ojaillon@genoscope.cns.fr>

NorthCarolinaStateU InsectEvolutionDiversity

Graduate position in insect evolution and diversity

The newly established Blaimer lab in the Department of Entomology and Plant Pathology at NC State University is seeking to fill a graduate student position (PhD or MSc, depending on prior experience) beginning in the Fall semester. Our research group focuses on applying cutting-edge molecular technologies to address relevant questions in insect evolutionary biology, systematics and community ecology, mainly by studying ants and other

Hymenoptera. We value collection-based research and actively conduct field surveys for ants and other insects, with a particular focus on canopy diversity.

We are looking for a highly motivated student with a keen interest in evolutionary biology and entomology, and matching research interests to the above. Thesis projects will likely be tied into ongoing research in the lab, but specifics could be developed according to the student's interests. Potential projects, for example, could be centered around the evolution of ant community structure, both locally in North Carolina or within ongoing research in Madagascar, or could investigate color pattern evolution in large carpenter bees in the context of mimicry. Systematic, taxonomic, or other collection-based project components are further encouraged. Preference will be given to students interested in working on Hymenoptera, and particularly on ants.

NC State University's Entomology Department offers a highly-rated research environment and is situated in a vibrant and scientifically stimulating atmosphere in the Research Triangle, with both UNC and Duke University, as well as NESCENT and the North Carolina Museum of Sciences close by. Our NC State Insect Museum is a mid-size insect collection that provides state-of-the-art training opportunities in specimen-based research techniques and curation. Raleigh is a lively town with an inexpensive, yet high standard of living, and its surroundings offer numerous recreational activities.

Interested students should contact me directly at bonnie_blaimer[at]ncsu.edu <bonnie_blaimer@ncsu.edu> with a brief description of research interests and experience and a CV, preferably by January 31. Note that the departmental website is currently being redeveloped and information found online about the NCSU Entomology graduate program may not be up-to-date.

Bonnie B Blaimer

Assistant Professor

Director, NCSU Insect Museum

Department of Entomology & Plant Pathology

North Carolina State University

Raleigh, NC 27695-7613

Bonnie Blaimer <bonnie_blaimer@ncsu.edu>

NorthDakotaStateU EvolutionaryBehavioralEcol

The Dochtermann Lab in the Department of Biological Sciences at North Dakota State University is seeking to fill a PhD assistantship as part of a project examining how evolutionary factors and habitat change shape behavioral syndromes (trait correlations). The student will develop and pursue their own research topics while also working within a broader NSF funded project.

In our lab we focus on evolutionary questions regarding the maintenance of variation within and among populations and the evolutionary implications of how traits are correlated.

The position will start Fall Semester 2018. The student will be housed and working in the Department of Biological Sciences (https://www.ndsu.edu/biology/) with their degree awarded through the NDSU Environmental Sciences and Conservation Program.

Requirements: Bachelors or Masters in ecology, evolution, animal behavior, or related field; experience collecting and analyzing data; ability to work independently and as part of a larger collaborative group.

Preferred: MSc preferred; experience conducting quantitative genetic experiments; field research experience

If interested please contact me at ned.dochtermann@gmail.com and provide a brief synopsis of your research interests.

Ned

– Ned A. Dochtermann Assistant Professor / Department of Biological Sciences / NORTH DAKOTA STATE UNIVERSITY p: 701.231.7353 / f: 701.231.7149 / http://www.ndsu.edu www.neddochtermann.com ned.dochtermann@ndsu.edu

ned.dochtermann@gmail.com

OldDominionU MarineBiodiversity

Graduate Research Assistant (PhD) - Marine Molecular Ecology at Old Dominion University

The Department of Biological Sciences at Old Dominion University, a "Doctoral Research - Extensive" state university, has an opening for a PhD Graduate Research Assistant in marine molecular ecology. The appointment will begin in the summer or fall semester of 2018. This position involves participation in an NSF-funded PIRE (Partnerships for International Research and Education) Project to examine genetic and species-level changes in marine biodiversity over the past century of intense fisheries exploitation and habitat degradation in the Philippines. The successful candidate will be expected to live in the Philippines during summer sessions to conduct research in the field and laboratory in a collaborative, multinational setting. Applicants must have a bachelor???s or master???s degree at the time of employment, and demonstrate interest or experience in molecular ecology, population genomics, marine phylogeography, or a closely related field. Competitive applicants will have some experience conducting molecular ecology research in the field and/or laboratory; AAUS Scientific Diver certification is desired. Underrepresented minorities are particularly encouraged to apply.

Interested applicants should send an email to Kristene Parsons (kparsons@odu.edu) that includes (1) a cover letter describing your interest in the position, prior research, and future career goals, (2) your curriculum vitae, (3) a copy of your college transcript(s), and (4) the names, telephone numbers, and addresses (postal and email) of three references. Review of applications will begin in February, 2018 and will continue until a suitable candidate is found. For more information about the department, other faculty and students, please see the websites of the Department of Biological Sciences (http://www.odu.edu/biosci) and Kent Carpenter (http://www.odu.edu/directory/people/k/-kcarpent). Additional information on the Philippine PIRE Project can be found at https://sites.wp.odu.edu/-PIRE/. AA/EOE/M/F/Disability/VETS/Drug Free.

Kristene T. Parsons NSF PIRE Project Administrator Department of Biological Sciences Old Dominion University Norfolk, VA 23529-0266 USA

kparsons@odu.edu | 757-683-3481

"Parsons, Kristene" <kparsons@odu.edu>

RHUL London EvolutionInsectCognition

PhD position: Metabolic costs of learning and memory in a key pollinator Closing date: 7th Feb 2018

Application details: https://www.findaphd.com/-search/projectDetails.aspx?PJID=94048&LID=4663 Eligibility: UK residency requirements apply, please see here for full details: http://www.bbsrc.ac.uk/-documents/studentship-eligibility-pdf/ Investment in cognitive traits, such as learning and memory, is expected to yield fitness benefits through better decision-making, producing behavior that is fine-tuned to the local environment. Yet the fact that animals vary in their cognitive abilities, both between and within species, suggests that such investment comes at a significant cost. We currently understand little about what these costs are, because it is difficult to manipulate cognitive abilities, and thus any relationship with other traits is by nature correlational. In this project, we will capitalize upon recent developments in insect cognitive neuroscience to overcome this problem, using a uniquely tractable experimental system (the bumblebee Bombus terrestris). We will focus upon (1) metabolic costs of investment in cognition (2) potential evolutionary trade-offs with immune function (3) impacts on life-history variables. In the latter stages of the project, there will be the opportunity for the student to develop further research questions according to their interests, which may include (but are not limited to) the use of transcriptomics to understand the genomic basis for cognitive investment.

The successful applicant will be based at Royal Holloway University of London in the research group of Dr. Elli Leadbeater (http://ellileadbeater.wixsite.com/-insectcognition), and will be co-supervised by Dr. Steve Portugal at Royal Holloway and Dr. Samraat Pawar at our DTP partnership institution, Imperial College. The project will capitalize upon excellent ERC-funded social insect research facilities at Royal Holloway, including indoor and outdoor apiaries, bee rearing rooms and a dedicated cognition laboratory. The student will join a large group of researchers interested in social insect behaviour within our department, which provides an exceptionally stimulating and collaborative environment for the proposed research. Experimental work will involve laboratory-based studies during both the summer and the winter months, with the potential for campus-based fieldwork during the summer months according to the student's interests. Pre-application informal enquiries are strongly encouraged. Please direct these to Elli Leadbeater (Elli.Leadbeater@rhul.ac.uk).

Dr. Elli Leadbeater elli.leadbeater@rhul.ac.uk School of Biological Sciences Royal Holloway, University of London Egham TW20 0EX

+44 (0)1784 443547 +44 (0)7901 918423

"Leadbeater, Elli" <Elli.Leadbeater@rhul.ac.uk>

RoyalVetC London AnimalGenomicsEvolution

FULLY FUNDED PHD STUDENTSHIP IN GENOMICS (ROYAL VETERINARY COLLEGE, LONDON, UK)

Dr. Denis Larkin's group at the Royal Veterinary College, University of London currently has a three year fully funded PhD studentship position in animal genomics available for EU applicants. Applicants from other countries please see conditions below.

Mammalian and avian chromosomes drastically differ in structure and evolutionary stability. While avian genomes tend to be small and structurally similar across the majority of avian species, the mammalian genomes are about three times larger and often differ in chromosome structures even among closely related species. This PhD programme will investigate the evolutionary basis of this difference and its implication on phenotypic diversity in the two animal classes. To achieve this the student will first develop and apply a novel technique for a fast improvement of fragmented mammalian genomes to complete chromosome assemblies to make them suitable for comparison with other genomes. This part of the project will focus on several species of neglected agricultural and biomedical importance. The genome assemblies produced by PhD student will then be combined with other genomes of suitable quality and compared to genomes from two phylogenetic Classes: mammals and birds. The student will focus on distribution of genomic features that are likely be related to evolutionary stability of avian genomes and structural dynamics of mammalian genomes. Among other features these will include genes, transposable elements, conserved non-coding sequences. The student will test the hypothesis that distribution of these features contributes to stability and evolutionary dynamics of animal genomes.

The student will join a vibrant research group with lots of experience and expertise in comparative animal genomics and will have a chance to contribute to several large international genomics projects led by Broad Institute, Sanger Institute and the Ten thousand genomes (G10K) community of scientists. They will obtain complementary training in bioinformatics, wet lab techniques and scientific presentations to develop skills for a successful genomics-oriented career in biology.

Desirable requirements:

Experience in bioinformatics (analyzing large datasets, programming, or data visualization). Experience in genomics.

This is a three year fully funded studentship. It is open to UK/EU applicants only. International students are welcome to apply but must be able to pay the difference between UK/EU and international tuition fees.

The studentship will commence in October 2018.

We welcome informal enquiries - these should be directed to: dlarkin@rvc.ac.uk

To apply please follow this link: https://www.rvc.ac.uk/study/postgraduate/phd/studentships/structural-comparative-studies-of-genomes-from-neglected-livestock-species-and-mammals-of-biomedical-importance Deadline for applications: 13/02/2018

"Larkin, Denis" <dlarkin@rvc.ac.uk>

StAndrews EvolutionaryGenomics

PhD in Modelling Evolutionary Trajectories

Applications are invited for a PhD position to work with Dr. Carolin Kosiol at the Centre of Biological Diversity of the University of St. Andrews, Scotland.

Research in the Kosiol group focusses on the development of computational methods to the investigate the process of adaptation at different time-scales ranging from a few generations in experimental evolution data to phylogenetic analysis of multiple species diverged millions of years ago. In particular, we are interested in DNA sequence evolution by mutation and shifts of allele frequencies. The position is funded by the University for 3.5years. Applications are welcome from students worldwide.

Candidates will be expected to have a strong interest in applying quantitative methods and modelling to Biology. They will have a degree in Bioinformatics, Computational Biology, Mathematics, Physics or a related field. Prior experience with either population genetics or comparative genomics is a benefit. Preferably the candidate will have experience in programming language such as C, C++, Java and a scripting language such as Python or Perl.

Deadline is the 28th January 2018. Details about the application can be found at

https://synergy.st-andrews.ac.uk/research/phd-study/-phd-study-projects/ phd-study-cbd-projects/

Please send informal inquires to Carolin Kosiol ck202@st-andrews.ac.uk

Carolin Kosiol Lecturer in Bioinformatics Centre for Biological Diversity University of St Andrews St Andrews, Fife KY16 9TF, UK https://synergy.st-andrews.ac.uk/-genomemoleculardating/ Carolin Kosiol <ck202@st-andrews.ac.uk>

StockholmU CognitionAndBrainEvolution

PhD position in Ethology

at the Department of Zoology, Stockholm University, Sweden

Deadline for application: January 31, 2018.

A PhD position focused on cognitive evolution is available in Alexander Kotrschal's research group in the Department of Zoology at Stockholm University. The project uses the guppy (Poecilia reticulata) as a model to comparatively and experimentally investigate the factors driving cognitive evolution. As such, the project spans over multiple disciplines including field collections, artificial selection, assays of behaviour and detailed tests of cognitive ability, brain imaging and neural density estimations, and analyses of the genomic architecture that orchestrates changes in brain anatomy and cognitive ability.

The project will use both animals from wild populations with known differences in ecology, and from a selection experiment. These animals will be subjected to relevant assays of behaviour, brain anatomy and genomics. The overall aim of the project is thus to increase our understanding of the evolutionary relationship between brain anatomy, cognitive ability and the genome.

The work will mostly be lab-oriented but includes at least one trip to Trinidad. The project will require hard work but at the same time provide excellent opportunities for personal initiatives and development towards a successful academic career. An important task will be to undertake laborious selection experiments followed by the collection and analysis of complex data in a way that controls for the setup of replicated artificial selection designs. The project is undertaken in Trinidad and in a brand new section of the large tropical freshwater fish labs in the Department of Zoology with established assays of brain anatomy, several different aspects of cognitive abilities, swimming parameters, personality, individual and collective behaviour, etc.

The successful candidate will be part of an international team consisting of an Ethologist (Alexander Kotrschal, Stockholm University), Evolutionary Biologist (David Reznick, University of California & Trinidad), Genome Biologist (Alison E. Wright, University of Sheffield), and Information Technology researcher (Kristiaan Pelckmans, Uppsla University) that investigate the evolution of cognition, brain anatomy and the genome using state-of-the-art methods.

Qualification requirements

The applicant must have completed a research degree (e.g. Master's or equivalent) within Ethology, Zoology, Behavioural Ecology, Evolutionary Biology or a related subject. We are looking in particular for candidates with a strong interest in cognitive evolution, with excellent analytical ability and experience from quantitative analyses of behaviour and other traits of interest. Experience in genomic analyses and working with aquatic animals in the lab is not mandatory but especially meriting.

For more information on the position (Ref: SU FV-4158-17) and to apply follow this link:

http://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=4449&rmlang=UK

Contact

Questions? Please contact Dr Alexander Kotrschal, alexander.kotrschal@zoology.su.se

For more information about research in the Kotrschal lab see: https://www.su.se/english/-profiles/akotr-1.218779 Alexander Kotrschal <alexander.kotrschal@zoologi.su.se>

StockholmU EvolutionaryGenomics

PhD student position at Stockholm University

We are looking for a highly motivated PhD student in Ecology and Evolution, to work on the ERC-funded project SuperGenE in the group of Dr. Tanja Slotte at Stockholm University. The position is for four years, and the deadline for applications is February 23, 2018.

The complete ad is available on the Stockholm University webpage: http://www.su.se/english/about/working-at-su/phd?rmpage=3Djob&rmjob=3D4610&rmlang=UK Project description: In this project, we will investigate evolutionary processes at one of the first discovered supergenes, the distyly S-locus. We will conduct these studies in Linum, where the dynamic nature of distyly presents an outstanding opportunity to study supergene evolution. To do so, we will first generate multiple de novo genome assemblies of Linum species, and then use this genomic framework to comprehensively test hypotheses on the evolution and breakdown of the distyly supergene.

The project will involve a large component of evolutionary genomic analyses. The student will also carry out experimental plant work and some molecular genetic lab work. There may be opportunities for field trips in the Mediterranean region.

Infrastructure and environment: The PhD student will join a group of postdocs and PhD students led by Dr. Tanja Slotte. For recent examples of our work, see e.g. Laenen, Tedder et al. 2018 PNAS, Steige, Laenen et al. 2017 PNAS, or Steige et al. 2015 MBE. The PhD student will be based in the Slotte lab (http://tanjaslottelab.se), a part of the Dept. of Ecology, Environment and Plant Science, Stockholm University.

We are located at the Science for Life Laboratory in Stockholm (http://www.scilifelab.se), which holds considerable expertise in high-throughput sequencing technology and bioinformatics. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both genomicists, evolutionary biologists and ecologists at SciLifeLab and Stockholm University.

Qualification requirements: A completed second-cycle degree (at least 240 credits), including at least 60 credits in the second cycle. Applicants must have at least 15 credits from second-cycle courses in Ecology/Evolution, and 30 credits from a project in Ecology/Evolution.

Documented training and interest in evolutionary genetics or population genetics is required. Experience of bioinformatic analyses of genomic data, or proficiency in programming/scripting is a merit. Experience of basic molecular genetics lab work or experimental plant work is beneficial.

Application: Apply for the positions through Stockholm University's recruitment system: http://-www.su.se/english/about/working-at-su/phd?rmpage=-3Djob&rmjob=3D4610&rmlang=UK Contact: For further information about the position, please contact Dr. Tanja Slotte directly at tanja.slotte@su.se

"tanja.slotte@su.se" <tanja.slotte@su.se>

StockholmU:SexualSelection

PhD position in Evolutionary Ecology at Stockholm University

APPLICATION DEADLINE: MARCH 1, 2018

A fully funded 4-year PhD position on sexual selection and sexual conflict is available in Rhonda Snook's group, recently relocated to the Department of Zoology, Stockholm University. The successful applicant will work on the coevolution of female behaviour and male reproductive physiology, using Drosophila. If you are enthusiastic about evolutionary biology with a good understanding of population genetics and/or are skilled in molecular genetics, you are most welcome to apply. You must hold a master of science (or equivalent) in Biology/Ecology or a related field.

Stockholm University's Department of Zoology is a vibrant international and interactive community. Working language in the lab is English.

For informal queries, contact Rhonda on rhonda.snook@zoologi.su.se

Details to apply, including more about the project, are available here:

https://www.su.se/english/about/working-at-su/-phd?rmlang=UK&rmpage=job&rmjob=4678 Rhonda Snook <rhonda.snook@zoologi.su.se>

TexasCU TreePopulationGenomics

M.S. position: A fully funded graduate research assistantship position (funding provided by teaching assistance) is available in the lab of Dr. Matt Hale in the Biology Department at Texas Christian University starting in August 2018. The project will be based on the population genetics of the American Chestnut. The applicant should have previous lab experience including, but not limited to, DNA and RNA extraction, PCR amplification, and DNA sequencing. Ideally, the candidate will also have experience with computational analysis and bioinformatics, although training in these areas will be provided. Interested applicants should send a CV, a cover letter describing their research interests and reasons for applying, and the names and contact details of THREE potential referees to Dr. Matt Hale (m.c.hale@tcu.edu). Review of applicants will begin on January 22. For more details on the Biology department at TCU please see http://biology.tcu.edu/ m.c.hale@tcu.edu

TrentU AmphibianEcoEvoBio

The Integrative Wildlife Conservation (Murray) lab at Trent University, Peterborough, Ontario, is offering a project (PhD or MSc) to assess responses of amphibians to environmental stressors (e.g., pathogens, contaminants, food limitation, predation risk), exploring the heritability and plasticity of traits within and across life stages. Our recent investigations in this area highlight the opportunity to test fundamental questions in stress ecology, evolutionary biology, and conservation biology via experimental, field, and molecular techniques. The student will have the opportunity to develop specific research questions within the scope of the larger project.

The funding package includes a competitive stipend, foreign tuition waiver (if the student is not a Canadian citizen or permanent resident) as well coverage of all research expenses. Successful PhD candidates will have an MSc in Biology, Ecology, Conservation Biology, or related field, and demonstrated evidence of peer-reviewed publications. All applicants must have strong quantitative, laboratory and/or field skills, and an interest in working collaboratively as part of a larger group. The student will join the Integrative Wildlife Conservation laboratory at Trent University (www.dennismurray.ca) and be part of an interdisciplinary team addressing innovative solutions to environmental change (www.create-enviro.ca).

To apply, please send a cover letter, curriculum vitae, unofficial academic transcript, and contact information for 3 references to: Dennis Murray (dennislmurray@gmail.com) Application deadline is Feb 16th, but review of applications will begin immediately and continue until a suitable candidate is found. Applicants are strongly encouraged to apply early.

Angela Eads <angelaeads@trentu.ca>

UBath 3 Extinction

The Longrich Lab at the University of Bath, UK is currently seeking an outstanding PhD candidate to work on a project investigating Diversity dynamics of invertebrates over mass extinctions: recovery and radiation

Project Description

Mass extinctions both destroy, and create, biodiversity. Fossils show that mass extinctions- rapid, global, and severe events wiping out upwards of 50% of all species on Earth- have repeatedly occurred, and yet diversity inevitably recovers, or even increases, in the aftermath. The K-Pg mass extinction is the most recent of the Big Five events and therefore has the most complete record. It can therefore serve as a model system and a starting point for testing hypotheses, but any attempt to infer universal patterns (or their absence) will require comparing the K-Pg both against other mass extinctions, such as the E-O, Tr-J, and P-Tr events, and also periods of background extinction.

The terrestrial record, in particular the demise of the dinosaurs and the radiation of mammals, has been the focus of intensive study, but the marine fossil record is far more complete owing to the relatively continuous deposition of marine sediments. Marine invertebrates have hard, durable shells that promote preservation and are therefore, excellent model organisms to study macroevolutionary trends over mass extinctions. The marine invertebrate record therefore provides our best opportunity to understanding fundamental patterns of extinction and recovery and to understand the role of mass extinction as a driver of macroevolution. Over 100 years of paleontological literature, and large-scale databases and resources including the Palaeobiology Database, Treatise of Invertebrate, and Compendium of Fossil Marine Genera mean that a wealth of data are available to test evolutionary hypotheses.

The project aims to test many scenarios of invertebrate diversity dynamics over mass extinctions. This will be achieved by taking a quantitative approach to exploring the fossil record. Questions of interest include:

1. How severe are mass extinction events? Does improved sampling of fossils tend to push estimates of extinction up, or down over time? To what extent does poor sampling of survivors exaggerate extinction rates, and to what extent might poor sampling of victims obscure it?

2. What separates survivors and victims? How do size, ecology, geographic range, latitudinal distribution, and rarity determine risk of extinction?

3. How rapid is the recovery of both taxic and functional diversity? To what extent do survivors refill previously occupied niches, or not? Does innovation in the aftermath of extinction, facilitated by extinction of incumbents potentially lead to a long-term increase in total diversity? Are ecosystems fundamentally similar before and after, with different actors filling the same role, or has the script of the play somehow changed?

4. How does mass extinction affect biogeographic patterns? Do mass extinctions tend to decrease or increase endemicity in their aftermath? How are latitudinal gradients affected by extinctions with a strong element of climactic selectivity?

This PhD is fully funded for up to 4 years. Applicants should have a strong research background; publications and a masters degree are highly desirable. A background in palaeontology is not necessary but students should have a strong background in quantitative approaches to science, including statistics and scripting. To help build the group, we seek students who are hardworking, curious, creative, and collaborative. The project is part of a 5-year research project to understand mass extinction and recovery and your project is designed to result in a series of significant research papers and to train the student to pursue a research career in palaeontology. If applicants have any queries please contact Nick Longrich (nrl22@bath.ac.uk). We will also assist students seeking their own funding.

The student will be trained in quantitative ecological and palaeontological methods, also with training in management and collection of invertebrate fossil and environmental data. We will develop your oral and written work and help you turn your science into academic publications. You will also become part of the University of Baths Palaeontology Group which is young but rapidly growing. We currently have three faculty members, Dr. Nicholas Longrich, Professor Matt Wills and Dr. Daniel Field, the palaeontology group is in turn a central part of Baths new Milner Centre for Evolution, a unique research centre focused on fundamental research on major problems in evolutionary biology.

Formal applications should be made via the University of Baths online application form for a PhD in Biology:

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UCambridge BacterialPathogenEvolution

We are advertising a funded 4-year PhD studentship at the University of Cambridge (Department of Veterinary Medicine) for a project on the evolutionary dynamics of bacterial pathogens, combining mathematical models and bioinformatics.

The funding is available to UK citizens or residents as part of the Cambridge-BBSRC Doctoral Training Programme (DTP): https://bbsrcdtp.lifesci.cam.ac.uk/ The programme includes two initial rotation projects as well as formal training in scientific computing and a short internship in a non-academic setting.

Application deadline: 26 January 2018

Title of project: Modelling the evolution of bacterial pathogens in the real world.

Supervisors: Dr Olivier Restif, or226@cam.ac.uk, Dept Veterinary Medicine http://www.research.vet.cam.ac.uk/research-staff-directory/principal-investigators/disease-dynamics/Olivier-Restif Dr Lucy Weinert, Dept of Veterinary Medicine, lw461@cam.ac.uk, https://www.research.vet.cam.ac.uk/research-staff-directory/principal-investigators/disease-dynamics/lucy-weinert Dr John Welch, Dept of Genetics, jjw23@cam.ac.uk, https://www.gen.cam.ac.uk/directory/john-welch Aims. The student will develop mechanistic models for the evolution of AMR in bacterial pathogens, with a specific focus on species relevant to the pig farming industry (including Streptococcus suis, Salmonella enterica and Escherichia coli). The models will be validated using data from farm surveys and experiments recently or currently conducted by the Department. Both supervisors are investigators on existing grants funded by the BBSRC and the MRC that cover sample collection, AMR testing and genome sequencing.

Objectives.

(i) Develop a dynamic framework for the circulation of bacterial species and mobile AMR genes within farms in the absence of disease and treatment.

(ii) Estimate key parameters by fitting models to genomic data from asymptomatic carriage.

(iii) Model selection pressures created by interspecific competition and antibiotic treatment, within and between hosts, using data from clinical cases in pig farms and experimental infections (collected as part of an MRC grant).

(iv) Simulate alternative drug regimens and treatment strategies (guided by veterinary expertise) that may reduce or counter selection for AMR.

Learning opportunities. By bringing together mathematical modelling, bioinformatics and epidemiological data, this project will fill a gap in the field of bacterial evolutionary epidemiology (lagging years behind research on viral pathogens). With joint expertise from Restif and Weinert (Vet Medicine) and Welch (Genetics), the student will learn a variety of programming, statistical and genomic skills at the cutting edge of science. The student will benefit from interactions with other modelling experts within the Disease Dynamics Unit, as well as microbiologists, veterinarians and geneticists.

For further information on the project and how to apply, contact Olivier Restif or226@cam.ac.uk or consult https://www.findaphd.com/search/ProjectDetails.aspx?PJID=90665 Dr. Olivier Restif Alborada Lecturer in Epidemiology Fellow of Robinson College

University of Cambridge Department of Veterinary Medicine Disease Dynamics Unit Madingley Road Cambridge CB3 0ES Great-Britain

Tel: +44 (0)1223 764963 Fax: +44 (0)1223 764667

Homepage < http://www.research.vet.cam.ac.uk/research-staff-directory/principal-investigators/disease-dynamics/Olivier-Restif > http://www.alboradatrust.com/ http://www.robinson.cam.ac.uk/ Olivier Restif <or226@cam.ac.uk>

UExeter UCardiff TroutAdaptation

We invite candidates to apply for a PhD position based at the University of Exeter, UK and the University of Cardiff, UK

Title: Metal tolerance and local adaptation in brown trout in the mining areas of Cornwall and Wales

Supervised by Dr Jamie Stevens (Exeter - j.r.stevens@exeter.ac.uk) and Professor Mike Bruford (Cardiff - brufordmw@cardiff.ac.uk)

This project will uncover the basis of local adaptation and resilience to environmental change in an economically important fish. It will use cutting-edge genomic, bioinformatics and geospatial tools to ask how genomic changes have enabled brown trout populations to adapt to different and changing environmental conditions, including pollution in three different regions: southwest England, mid-Wales and southeast Ireland. Specifically, you will use genome sequencing to examine the roles of colonisation, natural river conditions and metal pollution on patterns of diversity in the brown trout genome. Your PhD will be based at Exeter and Cardiff Universities and will involve collaboration and training with local partners,

This is a novel project because whole genome (re)sequencing has not yet been carried out in brown trout or applied to its conservation and adaptation. This PhD is now possible because a brown trout reference genome will be produced as part of the Sanger Institute's 25 Genomes Project (http://www.sanger.ac.uk/news/view/25-species-revealed-25-genomes-project) in 2018. Riverscape genomics is a very recent concept combining genome-scale and environmental data in a geospatial (GIS) context, where connectivity and gene flow can be accurately assessed using genetic, environmental and river management/engineering data. Evidence for local adaptation in brown trout is widespread, as shown by analysis of wild populations in a variety of different habitats, and the often poor survival of stocked or translocated fish and fish farm escapees. Adaptation to metals (i.e. metal tolerance), river water temperature during the egg phase, photoperiodicity and seasonal timing of smoltification have all been reported. Brown trout populations can survive (and thrive) in rivers in very close proximity to disused-mine sites.

To apply, please follow this link: http://

www.gw4fresh.co.uk/projects/ Click on the project title to download full details about the project and contact details of the supervisory team

Applications open on 15th January and close on 15th February.

Josie Paris Evolution, Behaviour and Environment Group School of Life Sciences University of Sussex Brighton, UK BN1 9RH

Josephine Paris <J.Paris@sussex.ac.uk>

UGreifswald EcolDriversRangeExpansion

PhD position at the University of Greifswald, Zoological Institute and Museum Application deadline: 19.01.2018 Thesis topic: Ecological drivers and genetic consequences of range expansion in lesser horseshoe bats

The Zoological Institute and Museum at the University of Greifswald invites applications for a PhD position within the Research Training Group RESPONSE: https://biologie.uni-greifswald.de/forschung/dfg-graduiertenkollegs/research-training-group-2010/job-offers/.

Starting date: April 1st 2018. Duration: 3 years. Salary: German salary scale (TV-L 13, 65%).

Background: The European vertebrate fauna is highly dynamic due to both historical climatic variation and anthropogenic pressures. The ability of a species to track climatic changes by range shift is expected to be a major determinant of extinction risk (Science 313: 789). For some species, such as the Palearctic bat species *Rhinolophus hipposideros*, regressions and advances are quite well documented and represent unique opportunities to study how and why range limits move. Such dynamic range boundaries can be observed at the Northern edge of the current distribution of *R. hipposideros*, regions in which models of climate change predict a northward progression of this species during the next decades (Global Change Biol. 16: 561). Here we will investigate colonisation and colony formation via dispersal in the focal species, study trade-offs / associations between dispersal and life history traits, and elucidate factors influencing dispersal, paying special attention to social and environmental factors.

Goals of the projects: Interconnected wild colonies at the Northern edge of the species' range will be surveyed in Germany and combined with data already obtained from France (via associated partner E. Petit). Droppings will be collected from all colonies and genotyped using available microsatellite loci (protocol already optimised), allowing for individual identification and pedigree reconstruction. Non-invasive genotyping over consecutive years in the colony networks will be used to estimate demographic parameters (i.e. population size, population growth, vital [births, deaths] and dispersal [emigrations, immigrations] rates). Temperature and humidity will be monitored throughout the year within and outside the colonies, and habitat characteristics around the colonies will be mapped (Corine Land Cover). The project will focus on associations between realised dispersal and reproductive rate as well as on the influence of population density, social and environmental factors on dispersal and colony formation. The obtained results will be used to parametrize a hybrid correlative/mechanistic model to predict range expansion in the species. This study will be carried out in collaboration with local conservation agencies and Dr. E. Petit, INRA (Rennes, France).

Required skills: §The candidate should have (or at least be willing to develop) skills in population dynamics and population genetics, landscape ecology, management/treatment of geo-referenced databases (GIS), §Good writing skills (in English; this is very important), §Good knowledge of German (speaking; required for the fieldwork), §Knowledge of statistics, §Good knowledge of programming in R (important), §Experience with fieldwork (preferentially with bats) will be an advantage but is not mandatory, §Driving license and willingness to use own car for field-work, §Good organizational skills and ability to work in a team (incl. with NGOs),

To apply, please visit our website: https://www.uni-greifswald.de/universitaet/information/stellenausschreibungen/oeffentliche-stellenausschreibungen/wissenschaftliches-personal/graduiertenkolleg-rtg-2010-17wi23/

Applications (application form, CV, degree certificates, motivation letter, two recommendation letters) can be sent to: kerstin.wulf1@uni-greifswald.de, s.puechmaille@gmail.com, gerald.kerth@uni-greifswald.de Forms and more information can be found here: https://biologie.uni- greifswald.de/forschung/dfg-graduiertenkollegs/research- training-group-2010/job-offers/

s.puechmaille@gmail.com

UGreifswald ResponsesChangingEnvironments

*PhD position in **responses to changing environments **in bats*

Application deadline: 19.01.2018.

The Zoological Institute and Museum at the University of Greifswald invites applications for a PhD position within the Research Training Group RESPONSE: *https://biologie.uni-greifswald.de/forschung/dfg-graduiertenkollegs/research-training-group-2010/job-offers/* .

Starting date: April 1st 2018.

Duration: 3 years. Salary: German salary scale (TV-L 13, 65%).

*Project A3: Life history responses of bats to climate change *

*Supervisors: *Prof. Dr. Gerald Kerth & Dr. Caroline Schöner, Applied Zoology and Conservation

*Thesis topic: *Relative importance of genetic and plastic responses to adverse weather conditions in long-lived bats.

*Background: *Recent studies have reported decreasing body size as a response to climate change in various taxa (*Nat. Clim. Change 1: 401*). As body size and fecundity are often positively correlated, shrinking body size may lead to higher extinction risk. Interestingly, in a few species increasing body size in response to climate change has been observed, which may occur if warm weather is required for growth. However, the fitness implications of such poorly documented trends are unclear. Bats are particularly interesting for studying the potential impact of climate change on individual fitness and ultimately on population persistence, as bats are long-lived, of high conservation concern and as they show behaviours that allow them to cope with weather variation, such as social thermoregulation, torpor, and roost switching.

*Goals of the projects: *This project aims at assessing to which fitness-relevant responses to adverse weather conditions are caused by genetic factors or phenotypic plasticity, and whether the relative impact of genetic versus plastic responses depends on local conditions or the respective species. Existing field and genetic data of up to 25 years will be combined with new (experimental) data collected during the project period to quantify the influence of weather conditions on the behaviour, morphology, reproductive success and/or survival of four bat species (*M. bechsteinii*, *M. daubentonii, M. nattereri*, *Plecotus auritus*). Multigenerational family pedigrees will allow us to measure the heritability of body size and other potential fitness relevant traits such as departure timing from the hibernaculum or age at first reproduction, using parent-offspring regression and animal models. We will test whether behavioural, demographic and morphological responses to varying weather conditions differ between syntopic bat species. We will also analyse to which extent local environmental conditions and social factors influence the fitness consequences of the observed responses to weather conditions. The relative importance of larger body size in response to increasing temperature, roosting behaviour and social factors (e.g. position in the social network) on fitness (survival, reproductive success) will be investigated together with local partners within RESPONSE and associated partners from the Max-Planck-Institute for Demographic Research in Rostock.

*Required skills: *

- - Strong background in behavioral and evolutionary ecology - - Knowledge of statistics, data handling and graphics in R - - Expertise with databases such as mySQL - - Basic knowledge in modelling and computer simulations - - Profound knowledge of English (speaking and writing); basic knowledge in German - - Expertise in field methods (preferentially with bats) and to a lesser degree in population genetic techniques - - Organizational skills and ability to work in a team - - Driving license and willingness to use own car for field-work

To apply, please visit our website:

*https://www.uni-greifswald.de/universitaet/-information/stellenausschreibungen/oeffentliche-stellenausschreibungen/wissenschaftliches-personal/-graduiertenkolleg-rtg-2010-17wi23/ * Applications (application form, CV, degree certificates, motivation letter, two recommendation letters) can be sent to: *kerstin.wulf1@uni-greifswald.de*, *gerald.kerth@uni-greifswald.de Forms and more information can be found here: *https://biologie.uni-greifswald.de/forschung/dfg-graduiertenkollegs/research-training-group-2010/job-offers/* s.puechmaille@gmail.com

UInnsbruck EvolutionaryGenomics

PhD position: Evolutionary genomics of a Daphnia waterflea species complex

We are looking for a PhD candidate interested in studying the genomic consequences of human-facilitated gene flow in a Daphnia species complex. The position is part of the INTERREG SEEWANDEL research initiative, which includes seven institutions in Switzerland, Germany, and Austria and seeks to investigate the effects of environmental change on biodiversity and resilience in Lake Constance and other large peri-Alpine lakes.

The position is funded for 48 months and to be filled at the earliest possible date. The successful candidate will be based at the Molecular Ecology Group at the Institute of Ecology of the University of Innsbruck which is highly interdisciplinary and internationally very well connected: https://www.uibk.ac.at/ecology/forschung/-molecular_ecology.html.en Lake-eutrophication during the last century has facilitated secondary contact between ecologically important Daphnia species in peri-Alpine lakes. The extent of secondary contact depends on the degree of trophic change. The successful candidate will use recent population samples and Daphnia resting eggs from sediment cores to quantify and characterize gene flow between species and study the consequences of the secondary contact on species integrity and functional traits. The project comprises sedimentological work (collecting sediment cores), molecular lab work (DNA extractions and library preparation), and extensive bioinformatics analyses as well as some experimental work with Daphnia. The study will focus on three large peri-Alpine lakes with different trophic histories - Lake Constance, Lake Walen, and Lake Zurich - and will include close collaborations with the members of the SEEWANDEL initiative. Part of the experimental work will be conducted at Eawag (Switzerland).

Candidates should be highly motivated and have a strong interest in evolutionary biology, ecology, and population genetics. The planned work will require a high degree of independence and the ability to work in a team. Experience in (i) molecular lab and field work, (ii) analysis of whole-genome re-sequencing data, (iii) and basic programming skills (e.g. R, Python, bash) will be an advantage. The project includes several collaborators and international groups in Switzerland, Germany, and the UK, and therefore good English skills are essential.

Salary The annual gross salary is EURO 28,994 for a 48-months employment. The contract includes health insurance and 5 weeks of holidays per year. Furthermore, the university has numerous attractive offers: https://www.uibk.ac.at/universitaet/-zusatzleistungen/index.html.en ***How to apply*** Please send a single pdf file including a letter of motivation, curriculum vitae, a complete list of publications and contact details of two references to Markus.Moest@uibk.ac.at. Applications must be written in English and submitted until 16 February 2018.

The University of Innsbruck is striving to increase the percentage of female employees and therefore invites qualified women to apply. In the case of equivalent qualifications, women will be given preference. An offer of employment is contingent on a satisfactory pre-employment background check.

The research institution and its environment Detailed information about the Molecular Ecology group can be found here: http://www.uibk.ac.at/ecology/-forschung/molecular_ecology.html.en. The University of Innsbruck has a long-standing and internationally renowned tradition in life sciences and offers a vibrant research atmosphere. It has 27,000 students and 4,000 staff members. Innsbruck is situated in the Alps, very close to Switzerland, Germany, and Italy. Excellent train connections and airports in Innsbruck and close by in Munich and Salzburg ensure good connections and easy travelling. The scenery and possibilities for outdoor recreation are fantastic.

Any questions? For more information on the position, the project, the group, or the University, please do not hesitate to contact Markus Möst or Birgit Schlick-Steiner directly.

MÃST Markus, PhD University of Innsbruck Institute of Ecology Research Group: Molecular Ecology Technikerstrasse 25 (Room 517) A-6020 Innsbruck Tel: +43 (0)512 507-51771 Fax: +43 (0)512 507-51799 E-mail: markus.moest@uibk.ac.at

SCHLICK-STEINER Birgit Dr., Univ.-Prof. University of Innsbruck Institute of Ecology Deputy Head of the Institute Head of the Research Group: Molecular Ecology Technikerstrasse 25 (Room 516) A-6020 Innsbruck T +43 (0)512 507-51750 F +43 (0)512 507-51799 E-mail: Birgit.Schlick-Steiner@uibk.ac.at

"Markus.Moest@uibk.ac.at"
<Markus.Moest@uibk.ac.at>

ULouisiana EvolutionaryBiol

Doctoral Fellowships available for entering Ph.D. students in Environmental and Evolutionary Biology at the University of Louisiana

We will be awarding University of Louisiana and Board of Regents Fellowships to qualified applicants entering the doctoral program in Fall 2018. UL Fellowships are awarded for 3-4 year terms and no teaching is required in the first or last years, while BoR Fellows are funded for 4 years and have no formal teaching duties; fellows may qualify for Teaching Assistantships following the completion of the fellowship term. Stipends are up to $30,000 per year (plus a tuition waiver). Eligibility requirements include US citizenship (or permanent residency) or a prior degree from a US institution. Potential applicants are strongly encouraged to directly contact prospective advisors. Faculty contact information and research interests can be found at our departmental web site (http://biology.louisiana.edu/). More information about the graduate program can be found at http://biology.louisiana.edu/programs/graduate . Scott C. France france@louisiana.edu Graduate Admissions Coordinator Department of Biology University of Louisiana at Lafayette

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Scott C. France france@louisiana.edu Professor & Graduate Admissions Coordinator Mr. Charles R. Godchaux/BORSF Professorship in Coastal Biodiversity Research Development

Department of Biology University of Louisiana at Lafayette P.O. Box 43602 Lafayette, LA 70504

For more information about the graduate program please visit: http://biology.louisiana.edu/programs/graduate Office: (337) 482-6320 Lab: (337) 482-6494 FAX: (337) 482-5834 For information on my research please visit: http://www.ucs.louisiana.edu/~scf4101/ "To learn and from time to time to apply what one has learned - isn't that a pleasure?" - Confucius, 500 B.C.

Scott C France <france@louisiana.edu>

UMainz 2 InsectEvolution

ADVERTISEMENT #1:

PhD position on the 'Impact of the microbiome on Drosophila cold tolerance'

Microbial symbionts represent major sources of evolutionary innovation by providing novel ecological traits to their hosts. While the impact of bacterial mutualists on the interaction of insects with their biotic environment (antagonists, diet, etc.) has received increasing attention over the past decades, the importance of microbial symbionts for the adaptation to abiotic conditions remains poorly understood. Preliminary data indicate that microbes associated with Drosophila can improve the fly's cold tolerance in a diet-dependent manner. We offer a 3-year PhD position (65% TV-L EG13) in the group of Dr. Martin Kaltenpoth at the JGU Mainz to investigate (i) which microbial taxa that are naturally associated with fruit flies enhance cold tolerance, (ii) how they do so on the mechanistic level, and (iii) whether these effects are ecologically relevant.

The project will be embedded into the project consortium on "Seasonal temperature acclimation in Drosophila" (headed by Suzanne Eaton at the Technical University in Dresden), which is funded by the German Science Foundation (DFG). The interdisciplinary consortium includes experts in molecular biology, biochemistry, biophysics, mass spectrometry, epigenetics, evolutionary biology, and ecology, who will closely collaborate to gain a comprehensive understanding of the mechanisms that allow Drosophila to acclimate and adapt to different climatic conditions. The PhD candidate will benefit from the integration into the consortium by regular meetings, workshops, retreats, and the exchange of methodological expertise.

We are looking for a highly motivated student with an MSc degree in evolutionary biology, ecology, or molecular biology (or equivalent), excellent English speaking and writing skills and a deep interest in the evolutionary ecology of insect-microbe interactions. Previous experience with insect rearing, microbiology, molecular biology, and/or bioinformatics techniques are of advantage.

We offer a dynamic, international working group with broad expertise and state-of-the-art equipment in entomology, microbiology, molecular biology, and chemical analytics at the new Biocenter of the Johannes

Gutenberg-University in Mainz. The research group is integrated into the recently established Institute for Organismic and Molecular Evolution (iOME) at the Faculty of Biology. Mainz is a charming, medium-sized, historic city situated at the river Rhine, in close vicinity to the Frankfurt metropolitan area.

Applications should include a cover letter (1-2 pages) describing the motivation, previous research activities and current research interests of the applicant; the CV of the applicant (with BSc/MSc grades, publications if applicable); and two reference letters. Please send all documents as a single PDF file (except for the references, which should be sent directly by the referees) before February 20th, 2018, to Prof. Dr. Martin Kaltenpoth (mkaltenpoth@uni-mainz.de). The PhD position is available at the earliest convenience.

The Johannes Gutenberg University of Mainz is interested in increasing the number of women in science. Applications from women are therefore strongly encouraged. Qualified candidates with disabilities will be preferred.

— Prof. Dr. Martin Kaltenpoth Department for Evolutionary Ecology Institute of Organismic and Molecular Evolution Johannes Gutenberg University Mainz Johann-Joachim-Becher-Weg 13 55128 Mainz, Germany Email: mkaltenpoth@uni-mainz.de

ADVERTISEMENT #2:

PhD position on 'Molecular host-symbiont interactions in grain pest beetles'

Microbial symbionts represent major sources of evolutionary innovation by providing novel ecological traits to their hosts. Several Silvanid and Bostrichid grain pest beetles engage in symbiosis with single or multiple Bacteroidetes bacteria. These bacteria were shown to enhance cuticle synthesis and thereby contribute to desiccation resistance in the saw-toothed grain beetle Oryzaephilus surinamensis. The group around Dr. Tobias Engl at the Evolutionary Ecology department of the Johannes Gutenberg University Mainz offers a 3-year PhD position (65% TV-L EG13) to elucidate symbiont functions and host-symbiont interactions across several Silvanid and Bostrichid beetles by symbiont genome sequencing, experimental manipulation of the symbiosis, transcriptome sequencing, and RNA interference experiments.

We are looking for a highly motivated student with an MSc degree in evolutionary biology, ecology, molecular biology or bioinformatics (or equivalent), excellent English speaking and writing skills and a deep interest in the evolutionary ecology of insect-microbe interactions. Previous experience with insect rearing, microbiology, molecular biology, and/or bioinformatics techniques are of advantage.

We offer a dynamic, international working group with broad expertise

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UMaryland BC 2 EvolutionAging

PhD Student Openings - Genetics of aging - Leips Lab UMBC

Two PhD students are sought for work on the genetic basis of aging. Topics are flexible but students interested in age related declines in immunocompetence and/or physical performance traits are encouraged to apply. Please contact Jeff Leips (leips@umbc.edu) and send your CV and short paragraph on research interests.

If you'd like to learn more about our department please visit our website

https://biology.umbc.edu/ . Jeff Leips Professor Department of Biological Sciences 1000 Hilltop Circle University of Maryland Baltimore County Baltimore, MD 21250 Office Phone: 410-455-2238 Lab Phone: 410-455-3479 Lab Website: http://biology.umbc.edu/directory/faculty/leips/leips- lab/ UBM@UMBC Website: http://www.umbc.edu/ubm/index.html Jeff Leips <leips@umbc.edu>

UMuensterGermany NicheConstructionEvolCapacitance

2 PhD positions: Niche construction and evolutionary capacitance in the red flour beetle

We invite applications for two PhD positions to study niche construction or evolutionary capacitance in the red flour beetle Tribolium castaneum. The positions are available for three years at the Institute for Evolution and Biodiversity at the University of MÃÂ¼nster in

Germany. They are part of the recently funded collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3), as granted by the German Research Foundation (DFG).

The start date is from February 1st 2018 or soon thereafter.

Within the first project, the interested candidate will experimentally study how flour beetles modify the microbial community of their environment, the flour. This form of niche construction is mediated by chemical secretions of the beetles. The project will test for the role of prior immunological experience of individuals, and analyse its long-term evolutionary consequences, using experimental evolution. The chemical ecology as well as the genetic underpinnings of the evolved phenotypes will be studied.

Within the second project, the interested candidate will experimentally study how cryptic genetic variation is stored and released in the red flour beetle, and how this process of evolutionary capacitance may speed up evolutionary adaptation. The project will in particular focus on the role of heat shock protein 90 (Hsp90) and the effect of immunological experience of group members on this process. Long-term evolutionary consequences will be studied with experimental evolution, and the genomic consequences will be analysed.

WWU is a large vibrant university hosting a number of excellent scientific institutions (http://www.uni-muenster.de/en/). The Institute for Evolution and Biodiversity (http://www.uni-muenster.de/Evolution/index.shtml) provides a stimulating research environment with a number of scientific groups researching on diverse topics centred on different aspects of the study of Evolution and the student can benefit from the structured PhD program offered by the MÃÂ¼nster Graduate School of Evolution (http://www.uni-muenster.de/Evolution/mgse/). As a part of the collaborative research centre SFB/TRR 212 (http://www.uni-bielefeld.de/biologie/crc212/index.html), the project (http://www.uni-bielefeld.de/biologie/crc212/C01.html) will involve intensive collaboration with consortium partners at the Universities of MÃÂ¼nster and Bielefeld. The town of MÃÂ¼nster itself is characterised by its many students and presents a dynamic environment with many cultural and social events throughout the year (http://www.muenster.de/en/).

Qualifications: We search highly motivated students of any nationality and those with the equivalent of a Master's degree in evolution, behaviour, ecology or related fields are invited to apply. A background in any of the following subjects will be useful: previous experience with practical insect work, good molecular skills and an additional preference of previous experience with chemical ecology, immunology or bioinformatics and a good understanding of statistics. Applicants should have excellent communication skills and be able to work both independently and as part of a multidisciplinary team. The working language of the institute and the lab is English and good proficiency in spoken and written English is a requirement.

Please send your application in one single PDF file to Prof. Dr. Joachim Kurtz (joachim.kurtz@uni-muenster.de). Included should be 1) a cover letter with a statement of your research interests and motivation (max. 1 page), 2) your CV including details of your research experience (with the abstract of your masters thesis) and 3) contact details of at least two referees.

Applications should be written in English and the deadline is the 14th of January 2018.

The salary will be for 36 months (TV-L E13/65%) with regular weekly working hours of 39 hours and 50 minutes. Applications of women are especially invited. In the case of similar qualification, competence and specific achievements, women will be considered on preferential terms within the framework of the legal possibilities. Preference will be given to disabled applicants in case of equivalent qualification.

Prof. Dr. Joachim Kurtz

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

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UNewOrleans ComputationalModeling

Graduate positions (M.Sc. and Ph.D.) are available in the Atallah Lab (https://sites.google.com/view/atallahlab) in the Biological Sciences Department at the University of New Orleans (UNO). We are currently looking for students interested in simulating the role of transposable elements in evolution and human disease.

In recent years, evidence has accumulated that transposable elements (TEs) play important roles in both evolutionary processes (such as changes in gene regulation) and the progression of diseases such as cancer. We are developing computer simulations of the activity of TEs in both the soma and the germline. Students interested in this project should be familiar with Shell scripting and computer programming. Interested students should send an email to jatallah@uno.edu. Please include a brief description of your background (or a CV or resume), and mention why you're excited about this project.

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

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

UNewOrleans DrosophilaGenomics

Graduate positions (M.Sc. and Ph.D.) are available in the Atallah Lab (https://sites.google.com/view/-atallahlab) in the Biological Sciences Department at the University of New Orleans (UNO). We are currently looking for students interested in working on the evolution of the early embryonic transcriptome in Drosophila species. Embryonic transcriptomes from diverse species can be readily compared due to similarities in embryonic stages. We are analyzing transcriptomes from different stages of early embryogenesis in flies. Students interested in this project should be prepared for molecular lab work, bioinformatic analysis and field collection of samples.

Interested students should send an email to jatallah@uno.edu. Please include a brief description of your background (or a CV or resume), and mention why you're excited about this project.

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

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

UNorthDakota AncientGenomes

U. North Dakota. Computational analysis of ancient and environmental genomes. The Laboratory of Human and Forensic Genetics at the University of North Dakota (www.und.edu) is inviting applications from potential graduate students who purs ue the MS or PhD degree.

A student will be engaged to a project on computational analysis of ancient and environmental genomes from the American Midwest, Eurasia, and Africa. It is a collaborative effort with institutions in the U.S. and the world. This cross-disciplinary project represents an opportunity to get intensive hands-on training in the methods of ancient DNA analyses including next-generation sequencing, computational biology and statistical modelling.

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

If you are interested you need to apply to the University of North Dakota Biology Graduate Program using the regular procedure that can be found in the UND Graduate School website: http://graduateschool.und.edu/-future-students/apply.cfm The additional information can be also found in the Biology Department website:

http://arts-sciences.und.edu/biology/graduate/-programs.cfm The position starts in August 2018. To receive full consideration, applications and required materials should be received by the Biology Graduate Program by Feb ruary 15, 2018.

Potential graduate students are strongly encouraged to make contact with Dr. Igor Ovchinnikov. Contact information:

Dr. Igor Ovchinnikov Associate Professor Lab. of Human and Forensic Genetics Department of Biology Forensic Science Program University of North Dakota Email: igor.ovtchinnikov@email.und.edu

"Ovtchinnikov, Igor" <igor.ovtchinnikov@email.und.edu>

UppsalaU GenomicsPlasticity

We are looking for a highly motivated PhD student to join Dr. Arild HusbyÂs lab group at Uppsala University (http://www.ieg.uu.se/evolutionary-biology/husby-lab/) to study genetic basis of plasticity in wing development in waterstriders in collaboration with Prof. Abderahman Khila at IGFL, Lyon (http://igfl.ens-lyon.fr/equipes/a.-khila-developmental-genomics-and-evolution).

Phenotypic plasticity is one of the main mechanisms by which plants and animals adapt to changing environmental conditions and thus of major evolutionary interest. This project will combine fieldwork, lab experiments and genomic work (crosses, RNA seq, RNAi) to study how temperature and photoperiod influence plasticity in wing development in different species of waterstriders. Waterstriders are a well known group of insects displaying wing polymorphism both between species as well as within species in response to the environment (e.g. Järvinen & Vepsäläinen1976. Hereditas, 84, 61-68) and are also model species in evolutionary biological studies (Rowe et al. 1994. TREE, 9, 289-293). Several species of waterstriders will be collected in early summer 2018 and nymphs raised in the lab under different photoperiod and temperature regimes followed by RNA seq analyses to identify differentially expressed genes between apterous (wingless) and macropterous/brachypterous morphs. Functional work will be done using established RNAi protocols developed for waterstriders (Khila et al. 2012 Science 336, 585-589).

The overall goal is to identify the genetic variants responsible for wing development and their interaction with temperature and photoperiod but there are several lines to examine depending on the candidate interests and qualifications.

We are looking for candidates with a strong interest in evolutionary developmental biology and evolutionary genetics, with excellent analytical ability and experience in the analyses of life history traits. Experience in working with aquatic animals in the lab is meriting.

The venue for the position, the Evolutionary Biology Centre, is situated in central Uppsala (http://-www.ieg.uu.se). The working atmosphere is highly international with a regular recruitment of PhD students and post-docs from abroad. The Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 300 scientists and graduate students, and with research programs in, for example, ecology, genetics, genomics and developmental biology. Our graduate school offers a creative and stimulating environment and offers a rich variety of seminars, journal clubs, courses and possibilities to interact with other scholars and students. Local platforms for next-generation sequencing (http://www.scilifelab.uu.se) and high-performance computational analyses are very useful. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant college town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm. The graduate program covers four years of full-time, fully paid study. The position can be combined with teaching (maximum 20%), which prolongs the employment with the corresponding time.

Informal inquiries are welcomed and can be directed to Arild Husby (arild.husby[AT]ebc.uu.se).

Applications will only be accepted when submitted through the Uppsala University web portal no later than 28th February using this web address: https://www.uu.se/en/about-uu/join-us/-details/?positionId=190120 Arild Husby Department of Evolutionary Biology Norbyvägen 18D, Uppsala University, SE-75236 Uppsala, Sweden

labpage: http://www.ieg.uu.se/evolutionary-biology/-research/husby-lab Office phone: 018-471 4120 E-mail: arild.husby@ebc.uu.se Room:1041, 1st floor EBC

Arild Husby <arild.husby@ebc.uu.se>

UQueensland FishVisionEvolution

The Marshall Lab at the Queensland Brain Institute, The University of Queensland, Brisbane, Australia, is currently seeking an outstanding PhD candidate to work on a project investigating the colour vision of coral reef fish. The aim of this PhD is to enhance our understanding of visual neuroscience and the genetic control of vision. Specifically, the project will determine the genetic and environmental control of damselfish visual sensitivities, using the anemonefish, Amphiprion percula, as a model system. Novel techniques will be used to address these aims such as new CRISPR/Cas9 gene-editing technique and Next Generation Sequencing.

The student will be supervised by Professor Justin Marshall, Dr Fabio Cortesi and Dr Karen Cheney, and will also collaborate with international researchers in the USA and the UK. This PhD project will provide excellent scope for integrative research, unique skill acquisition, as well as for personal development.

To know more about the Marshall Lab Group, please go to: https://qbi.uq.edu.au/marshallgroup . THE PERSON Expressions of Interest are invited from outstanding and enthusiastic, international and Australian, science graduates ideally with a background in neuroscience or biological sciences, and should be strongly motivated to pursue cross-disciplinary research in sensory ecology and genetic research. Candidates will have a First Class Honours degree or equivalent and should be eligible for UQ scholarship consideration. Applicants should have strong interests and preferably experience in bioinformatics, molecular biology, neurobiology, sensory biology, fish behaviour, evolution of visual signals, and/or animal communication mechanisms.

Applicants must fulfil the PhD admission criteria for the University of Queensland, including meeting English language requirements, and demonstrating excellent capacity and potential for research. Demonstration of research ability through publication output in peer reviewed international journals is desirable.

ENQUIRIES Detailed Information in relation to the project can be found here: http://jobs.uq.edu.au/caw/en/job/501649/phd-research-project-in-understanding-reef-fish-vision-through-geneediting-crisprcas9 To submit an Expression of Interest (EOI) for consideration, ensure you use the UQ Jobs online recruitment system by following the Apply button. All applicants must supply the following documents: cover letter; complete official tertiary academic transcripts (with grades/GPA scores, and official grading scale details) and award certificates (testamurs); and a detailed academic resume/CV.

Please note the different EOI closing dates below for domestic and international candidates Expression of Interest Closing Dates: International candidates: 19 January 2018 ’V for consideration in relation to the next available UQ international scholarship round with commencement in Research Quarter 3 (July) 2018.

Domestic candidates: 13 April 2018 ’V for consideration in relation to the next UQ domestic scholarship round with commencement in Research Quarter 3 (July) 2018.

Fabio Cortesi <fabio.cortesi@uqconnect.edu.au>

USouthFlorida 2 Evolution

Graduate Position in Conservation and Evolutionary Genomics

University of South Florida

The Cassin Sackett Lab at the University of South Florida is looking for a highly motivated graduate student to study population genomics and the evolution of tolerance to avian malaria in Hawaiian honeycreepers. The student will use comparative genomics to investigate the evolution of tolerance to *Plasmodium relictum* in several closely related species of Hawaiian honeycreepers. This work is part of a large collaborative research effort funded by NSF’s Ecology and Evolution of Infectious Diseases program, and work will be done in coordination with Rob Fleischer at the Smithsonian Institution and Jeff Foster at Northern Arizona University. A PhD student is preferred, but Master’s student applications will also be considered.

The position is supported by a research assistantship for two years, with additional time supported by teaching assistantships. The position will be based in USF’s Department of Integrative Biology (http://biology.usf.edu/ib/). Interested applicants should contact SackettL@usf.edu for inquiries. The desired start date is summer/fall 2018.

Qualifications:

Applicants should have a bachelor’s degree in biology, computer science, or a related field. We are looking for a student who is motivated, hard-working, and passionate about topics in evolutionary biology. The student should have or be willing to develop excellent organizational and communication skills, bioinformatics skills, and experience in population genetics and molecular evolution. Students should also possess the desire/willingness to engage in outreach. The Cassin Sackett lab is committed to increasing diversity in STEM, and we especially encourage applications from women, minorities, veterans and other underrepresented groups.

How to apply:

Interested candidates should notify me at SackettL@usf.edu of their intent to apply; applications are due by February 15 following the guidelines at http://biology.usf.edu/ib/grad/admission/ . Earlier applications are encouraged.

– Loren Cassin Sackett, Ph.D. Research Affiliate, Smithsonian Institution Assistant Professor, Integrative Biology University of South Florida Tampa, FL 33620-8100 www.cassinsackett.com ——

Graduate Positions in Conservation and Evolutionary Genomics

The Cassin Sackett Lab at the University of South Florida is looking for highly motivated graduate students to join the lab. The lab uses ancient DNA, field methods, next-generation sequencing and bioinformatic approaches to answer fundamental questions in evolutionary biology, especially those with conservation applications. Some major questions being asked in the lab are:

§How do humans influence the evolution of wildlife? We study the ways in which climate change, habitat alteration, and introduced diseases impact the distribution of genetic variation, rates of gene flow, and the probability of adaptation.

§What is the genomic basis of rapid adaptation to novel pathogens? We examine the demographic and environmental constraints to adaptation and whether genomic architecture of rapid adaptation differs from that of more gradual adaptation (e.g., to climate).

Please visit the lab website for more details on current projects: www.cassinsackett.com Students will be involved in a project that uses genomic approaches to analyze genetic diversity in fleas, prairie dogs and related species, and to investigate the potential for resistance to plague in prairie dogs. Specific duties may include: 1) sampling historical museum specimens, 2) field sampling of prairie dogs and fleas in the western U.S., 3) optimizing genomic assays (e.g., SNP capture, highly multiplexed amplicon sequencing), 4) performing wet lab work to genotype individual prairie dogs (both modern and historical) and/or fleas, 5) conducting bioinformatic analyses of population genomics and adaptation, 6) writing and submitting manuscripts related to the project.

The position is funded for its duration by a teaching fellowship, with the possibility of 1-2 years on a research assistantship, pending funding. The position will be based at the University of South Florida in the Department of Integrative Biology, but requires funded travel to several museums (e.g., at Berkeley, Harvard, and University of New Mexico). The position will be based in USF's Department of Integrative Biology (http://biology.usf.edu/ib/). Interested applicants should contact SackettL@usf.edu for inquiries. The desired start date is summer/fall 2018.

Qualifications:

Applicants should have a bachelor's degree in biology, computer science, or a related field. We are looking for a student who is motivated,

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USussex PlantGenomeEvolution

PhD Studentship Subject area: Plant genome evolution and epigenetics University of Sussex

Project title: Evolutionary and epigenetic interactions between transposable elements and their plant hosts

A Ph.D. studentship (42 months) is available from September 2018 under the supervision of Dr. Alexandros Bousios, in the Evolution, Behaviour and Environment Group, School of Life Sciences.

Deadline: 4th February 2018

The Bousios lab is looking for a PhD student to study the impact of transposable elements (TEs) in the function and evolution of plant genomes. TEs represent the most abundant component of eukaryotic genomes, and especially in plants they can occupy up to 80-90% of their genomic content. TE activity can be deleterious for the host, because it can cause chromosomes to break or because new copies can insert within genes and disrupt their function. As a result, hosts have developed epigenetic defence mechanisms to suppress TE activity, although given the abundance of TEs, these mechanisms are not always successful.

By focusing on maize but also other fully-sequenced plant genomes, and mostly using bioinformatics approaches, the candidate will attempt to shed light on the very first steps of TE silencing, i.e. how epigenetic defences recognize the mRNA of active TEs. It is hypothesized that specific regions on the TE may play a crucial role in the recognition process, and, hence, are the foci of an ongoing evolutionary battle between TEs and hosts. In addition, the candidate will study the extent to which TEs positively influence host gene function, by lending some of their sequences to the host regulatory system. This process, known as TE exaptation or co-option, is poorly understood in plants.

For an overview of our research, please visit http://-

www.sussex.ac.uk/lifesci/bousioslab/ Please submit a formal application using our online application system at http://www.sussex.ac.uk/study/phd/apply, including a CV, degree transcripts and certificates, statement of interest and names of two academic referees. On the application system use Programme of Study 'V PhD Biology.

Please make sure you include the project title and Supervisor'Âs name with your statement of interest on the application form.

This School funded position, which covers fees and a stipend at standard RCUK rates, is open to Home / EU applicants. Ideal candidates will have a strong background in bioinformatics and computational biology with additional experience in epigenetics, genome evolution or genomics areas, and the analysis of large datasets. Eligible applicants will have recently received an MSc and/or a First or high 2:1 BSc in a relevant subject. Candidates for whom English is not their first language will require an IELTS score of 6.5 overall, with not less than 6.0 in any section.

Contact Anna Izykowska for application enquiries (a.izykowska@sussex.ac.uk) Contact Alexandros Bousios (ab35@sussex.ac.uk) for enquiries about the project.

– Alexandros Bousios, PhD Royal Society University Research Fellow

University of Sussex | UK

alexandros.bousios@gmail.com | email http://infspire.org/ | www alexandros bousios | Skype

Alexandros Bousios <alexandros.bousios@gmail.com>

UValencia EvolutionSexualConflict

Dear Colleagues,

We are advertising a fully-funded PhD position on the evolution of sexual conflict in Drosophila melanogaster, based at the Cavanilles Institute of Biodiversity and Evolutionary Biology (University of Valencia, Spain).

Please see attached for further details.

Best wishes,

Pau

Dr. Pau Carazo RamÂÂn y Cajal Fellow Instituto Cavanilles of Biodiversity and Evolutionary Biology University of Valencia Tel: +34 963544051 http://paucarazo.com PhD Student- Evolution of male-male competition and sexual conflict

What do we offer? We offer a 4-year PhD fellowship starting on September 2018 to January 2019.

To do what? We are looking for a PhD student interested in studying the evolutionary factors modulating the intensity of male-male competition and sexual conflict, and its consequences in terms of population viability. Strong sexual selection can improve population viability and evolvability through a number of processes, such as genetic capture. However, strong sexual selection will also often give rise to sexual conflict and female harm, which does not only tend to deviate females from their evolutionary optima, but can drastically affect population viability, leading to a "reproductive tragedy of the commons". We are still far from understanding what factors modulate the evolution of male-male competition, female harm levels, and sexual conflict at large, and how this all feeds back into population viability.

Our on-going research aims to contribute to fill these gaps in knowledge by investigating factors potentially modulating the evolution of sexual conflict. For example, we are currently investigating the role of kin selection in leading to reproductive cooperation (or "reproductive altruism"), how temperature affects male- male competition levels and the potential for sexual conflict, or the evolutionary interplay between ageing and sexual selection (e.g. can ageing magnify sexual conflict?).

The research project mainly involves behavioural experiments and lab work with Drosophila melanogaster, some experimental evolution, and some fieldwork in Europe, the USA and potentially in Australia.

Where? The student will be supervised by Dr. Pau Carazo, and based at the Behaviour and Evolution group of the Ethology Lab, at the Cavanilles institute of Biodiversity and Evolutionary Biology (University of Valencia, Spain). For information about our group visit our website (http://paucarazo.com).

Who? We are looking for a motivated, enthusiastic, hard-working candidate with some background (and a strong interest) in sexual selection, and evolutionary biology and animal behaviour at large.

Contact For further information and expressions of interest, please contact Pau Carazo (University of Valencia; pau.carazo@uv.es). The deadline for applications is the 31st March.

Pau Carazo <pau.carazo@uv.es>

Vienna PopulationGenetics DueJan14

The Vienna Graduate School of Population Genetics is looking for PhD students:

Over the past years, Vienna has developed into one of the leading centres of population genetics. The Vienna Graduate School of Population Genetics has been founded to provide a training opportunity for PhD students to build on this excellent on site expertise.

We invite applications from highly motivated and outstanding students with a background in one of the following disciplines: bioinformatics, statistics, evolutionary genetics, functional genetics, theoretical and experimental population genetics. Students from related disciplines, such as physics or mathematics are also welcome to apply.

Topics include:

§Comparative population genomics in Drosophila species.

§Contribution of transposable elements to adaption during experimental evolution.

§Developing new statistical tools for the identification of adaptive QTLs.

§Evolution of gene expression.

§Evolution of phenotypic plasticity.

§Evolution of sex chromosomes in Drosophila species.

§Evolution of sperm competition in Drosophila.

§Functional characterization of adaptive QTLs.

§Maximum likelihood inference of population genetic parameters using genome-wide data from nearly neutral sites.

§Sex-specific arms race between transposable elements and small RNAs.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by January 14, 2018 will be considered. Two letters of recommendation need to be sent directly by the referees. Accepted PhD students will receive a monthly salary based on currently EUR 2071 before tax according to the regulations of the Austrian Science Fund (FWF).

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator

CALL FOR PHD STUDENTS OPEN! www.popgen-vienna.at https://twitter.com/PopGenViennaPhD c/o Institut für Populationsgenetik Veterinärmedizinische Universität Wien (Vetmeduni Vienna) Veterinärplatz 1, 1210 Wien

T +43 1 25077 4338 F +43 1 25077 4390

http://www.vetmeduni.ac.at/en/population-genetics/ https://twitter.com/PopGenVienna julia.hosp@gmail.com

Wageningen InsectEvoDevo

Wageningen.InsectEmbryogenesis

We invite applications from highly motivated candidates with relevant research experience and a passion for studying insect development. Most molecular information about insect embryogenesis has come from studies of model-organisms like Drosophila melanogaster. However, understanding the extent of gene expression variation during embryogenesis from diverse insect lineages could elucidate broad developmental constraints and novelty during insect evolution. Towards this end, the PhD student will combine in vivo documentation of embryogenesis of several phylogenetically diverse insect species and transcriptional analysis from next-generation sequencing to identify temporal gene expression dynamics in a comparative manner. The PhD project will be imbedded within The Graduate School Experimental Plant Sciences (EPS) under the supervision of Dr. Sabrina Simon in the Biosystematics Group, Wageningen University&Research. The inter-university Graduate School 'Experimental Plant Sciences' (EPS) is a collaborative research and teaching institution of Wageningen University (WU), Radboud University (RU), Vrije Universiteit Amsterdam (VU), Leiden University (LU), University of Amsterdam (UvA), Utrecht University (UU) and University of Groningen (RUG). The mission of EPS is to organize the training of PhD students and postdocs to become self-reliant researchers.

Requirements The successful candidate will have an MSc degree in Biology. Students with an interest in insect embryogenesis and development, transcriptomics, gene expression analyses, evolutionary biology, and bioinformatics are encouraged to apply. We are looking for a highly motivated insect biologist who can work in a collaborative and multidisciplinary team. The candidate should know or be willing to learn protocols for setting up insect cultures, next-gen sequencing methods and analyses, and computer programming languages. The candidate will be proficient in the English language. Within the Biosystematics group, PhD students have the opportunity to assist in teaching of undergraduates and / or two courses Biodiversity of the Netherlands and Webs of Terrestrial Diversity.

Applications should include: - a cover letter including a statement about your motivation to apply and your requirements for the position - curriculum vitae - copies of your University degree

Working conditions We offer a full-time position (38 hours), initially for 1 year after which a go/no go decision will be taken on extension with another three years. Gross salary per month euro 2222 in the first year rising to euro 2840 per month in the fourth year, for a full-time appointment. The candidate will be based at the Biosystematics group. Further information and application details: https://www.wur.nl/en/Jobs/Vacancies/Show/PhD-position-Transcriptomics-of-Insect-embryogenesis.htm Deadline: February 15, 2018

Dr. Sabrina Simon | Assistant Professor Biosystematics | Wageningen University & Research phone: +31317-483175

Wageningen Campus | Radix Building 107 | Room W2.Ca.103 Droevendaalsesteeg 1 | 6708 PB Wageningen The Netherlands

"Simon, Sabrina" <sabrina.simon@wur.nl>

WesternU 3 VirusEvolutionBioinformatics

The Virus Evolution and Bioinformatics lab of Dr. Art Poon at Western University (Canada) is seeking applications to fill 3 PhD graduate student positions. All positions are fully funded for up to 5 years by two newly awarded grants.

Research areas

Evolution of HIV-1 within hosts.

Despite the availability of highly effective drug treatments, HIV-1 establishes a life-long chronic infection for which we have yet to develop a cure. When HIV-1 infects a cell, it integrates itself into the host genome and, in some cases, enters a dormant state where it becomes invisible to the immune system. This creates a long-lived reservoir of "latently" infected cells that is the main barrier to a cure. We are developing new phylogenetic methods to reconstruct how this rapidly-evolving virus spreads through the body and to identify potential targets to eradicate the virus reservoir.

Detecting transmission outbreaks.

For infectious diseases, a genetic cluster is a subset of infections that have barely accumulated any genetic differences since their recent descent from a common ancestor. Clustering has become a popular method for rapidly screening clinical databases for potential transmission outbreaks. Based on recent work, we now know that clustering methods can be badly confounded by when the infections were sampled from the population. We are developing and validating a new approach inspired by speciation models to detect lineage-specific shifts in branching rates, and working with global partners to develop open-source monitoring systems to support public health efforts in real time while protecting individual privacy.

Training environment

The Poon lab is an entirely "dry" research computing and open-source software development group (http://github.com/PoonLab). The lab is housed in a newly renovated space in the Department of Pathology, and equipped with custom-built Linux workstations, a small high-performance computing cluster and an espresso machine. My lab mostly runs on Python, R and LaTeX – my objective is to enable all my trainees develop a working knowledge of all three languages.

Western University is one of Canada's top research-intensive universities, and home to the Western HIV Investigators Group (WHIG), a highly collaborative team of 8 principal investigators with diverse and complementary research programs, including evolution and pathogenesis (Dr. Eric Arts), natural resistance and host microbiomes (Dr. Jessica Prodger), and bioinformatics and phylogenetics (Dr. Poon). The adjacent London Regional Genomics Centre provides state-of-the-art next- generation sequencing services on Illumina MiSeq and NextSeq systems.

Known as "Forest City", the city of London, Ontario, features river valleys, abundant parks, tree-lined streets, bicycle paths, frequent city festivals, an international airport and a reasonable cost of living.

Qualifications

* An undergraduate (bachelor's) and/or master's (MSc) degree in biology, microbiology, bioinformatics, mathematics, statistics, computer science, or a related field.

* An avid, demonstrable interest in evolutionary biology and infectious disease research.

* Previous training or experience in *any* programming or scripting language from course work, workshops, or online/self-directed learning. Applicants without prior programming experience may be considered if they have a strong background in quantitative methods (e.g., statistics, linear algebra, probability, discrete math).

* Proficiency in communicating and writing in the English language.

* An ability to work effectively in a collaborative environment.

All applicants must also meet the admission requirements of the university (http://grad.uwo.ca/-prospective_students/applying/index.html) as well as the specific department (I hold appointments at the Departments of Pathology, Microbiology, and Applied Mathematics).

If you're interested and meet these qualifications, please contact me with a cover letter, CV, and contact information for at least two references at <apoon42@uwo.ca>.

Best, - Art.

— Art FY Poon MSc PhD

Assistant Professor Department of Pathology & Laboratory Medicine Western University

CIHR New Investigator MSFHR Career Investigator

github.com/ArtPoon

"apoon42@uwo.ca" <apoon42@uwo.ca>

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BarnardC ParttimeTech PlantEvolution

Part-time position supporting in-class teaching and curriculum development for a new college course examining plant evolution and biogeography, herbaria, and digital natural history.

Link to job description and portal to apply: https://-careers.barnard.edu/postings/3180 Candidates should already be located in New York City or its suburbs Needed January 2018 Graduate students or recent graduates Potential to develop or deliver publications or presentation

hcallaha@barnard.edu

Bayer California EvolutionaryBiostatistics

Biostatistics Scientist I West Sacramento, CA Apply online at: https://www.career.bayer.us/en/job/-Biostatistics-Scientist-I–SF14596.html YOUR TASKS AND RESPONSIBILITIES

The primary responsibilities of this role, Biostatistics Scientist I, are to:

- Proactively identify, develop, and incorporate experimental design and biostatistical tools to facilitate bioassay optimization in the lab and in the greenhouse; - Support bench scientist teams in the analysis of large data sets integrating different data types into statistical frameworks; - Train research staff in experimental design, basic statistical concepts, and the use of relevant statistical tools; - Keep abreast of new statistical techniques, including technological developments in machine learning; - Liaise with external experts and opinion leaders on these topics; - Develop, test, and document novel statistical analysis tools; - Be able to work with Data Engineers to translate statistical analyses and experimental designs into standardized pipelines; - Be able to communicate effectively through listening, documentation, and presentation, especially using compelling visualization tools to share analysis and interpretation of data.

WHO YOU ARE

Your success will be driven by your demonstration of our LIFE values. More specifically related to this position, Bayer seeks an incumbent who possesses the following:

Required Qualifications:

- Ph.D. in Statistics, Ecology, Evolutionary Genetics, Plant Genetics/Biology, Quantitative Genetics/Biology or related field or Master's degree and two (2) years of experience; - Expertise in the statistical analysis software R.

Preferred Qualifications:

- Knowledge of other programming languages (UNIX, Python, SQL); - Knowledge of crop science, bacterial genetics and/or plant genetics;

*Position may offer domestic relocation assistance.

Freundliche Grüße / Best regards,

Matt Armstrong Recruiter

Bayer U.S. LLC 100 Bayer Road Pittsburgh, PA 15205 United States Tel: 412-778-6688 E-mail: matthew.armstrong@bayer.com Web: www.career.bayer.us

Matthew Armstrong <matthew.armstrong@bayer.com>

BetaBugs UK DirectorOfEvolution

At Beta Bugs we're accelerating the evolution of insects to make them the crops of the future and drive forwards a sustainable bioeconomy that produces feed, food, fuel and more. Our current focus is the Black Soldier Fly, the larvae of which are being used as an aquaculture and animal feedstock.

We're now hiring a Director of Evolution to take the team to the next level. You'll be directly responsible for driving forwards our technology efforts, and working closely with our Head of Colonies to maintain and develop our lines. It's also a one-off opportunity to directly shape the way this company and a rapidly emerging industry develop.

You'll have a background in the biological sciences, with an emphasis on evolutionary biology and/or functional genetics at Masters, PhD level or beyond, particularly in arthropods. Hands-on experience of trait generation, selection and the necessary techniques to do both (along the lines of molecular biology, bioinformatics and sequencing) is also desirable. You're preferably a generalist with a deep specialization in this area, focused and self-starting.

Experience with high throughput breeding programmes or breeding for industry requirements is also a plus.

If you're keen, drop Thomas a line with more about you on thomas@betabugs.uk. Salary and equity are negotiable for the right candidate.

– Thomas Farrugia | Beta Bugs

Mobile: +44 7784336183 Skype: thomasjfarrugia

skeletonmanemail@gmail.com

BinghamtonU EvolGenetics

The Freshman Research Immersion (FRI) program at Binghamton University will hire a Research Assistant Professor, to begin August 13, 2018. This full-time position is for a three-year duration and candidates must have graduate degree before starting. This is a 10 month non-tenure track faculty position, with additional extra service commitment for two-summer weeks. This position is *for Ecological Genetics *(open to Ph.D.'s with appropriate ecological genetics background).

FRI Ecological Genetics is a new program in which a Research Assistant Professor guides freshmen and sophomores in innovative research that advances the field of ecological genetics. The Research Assistant Professor shapes the research theme. For example, past FRI cohorts have employed sophisticated techniques under the guidance of the Research Assistant Professor conducting research in that stream's area. Essentially, this position will entail teaching large numbers of college students (~30 per cohort) how to conduct authentic research and, in doing so, will help students develop the professional skills desired by graduate schools and employers. Within that process and working with a faculty advisory team, the Research Assistant Professor maintains and/or expands his/her research program. The Research Assistant Professor reports to the FRI Director, and also works closely with the faculty sponsoring-team of this research stream. Overall, FRI provides an excellent training program for new PhDs and, thus, is an exceptional transition that positions the Research Assistant Professors for a wider array of future STEM positions (from full range of higher education institutions to STEM education research).

Information about the FRI program and the faculty team for this research stream: http://binghamton.edu/-freshman-research-immersion/streams/current-research-streams/index.html *Responsibilities:*

Oversee daily research activities of the research stream

Work with a faculty team to design and implement course materials for the research stream (e.g., lab manual, lab protocols, YouTube for procedures, and so forth)

Coordinate with faculty team to plan and deliver mini-lectures for the research stream courses

Oversee the operation of the research stream laboratory (e.g., with undergraduate peer mentors

Help FRI students with their projects

Serve as a mentor to the FRI students

Facilitate formative and summative assessments of the research stream and FRI students

Participate in a weekly FRI training and preparatory session

Assist with administrative work of the FRI program (e.g., tracking student progress and completion in the FRI)

Co-teach FRI Research Methods Seminar (course delivered in flipped mode) with other FRI staff

Additional summer responsibilities may be contracted for extra payment (e.g., conducting NSF-REU-type program, working on grant research)

Requirements:

Strong candidates must have:

Graduate degree in a discipline that matches the research stream goals

Minimum of two years of experience as a teaching assistant in higher education

Ability to train undergraduate researchers and evaluate their work

Ability to train, evaluate and supervise graduate teaching assistants and undergraduate peer mentor assistants

Ability to manage a research laboratory

Effective communication skills

Proficiency with Microsoft Office suite and web access software

Ability to manage multiple projects and timelines simultaneously with a high degree of accuracy and efficiency

Ability to work both autonomously and collaboratively

Strong professional, organizational and interpersonal skills

Ability to speak, write and communicate in an articulate and successful manner

Ability to problem solve, prioritize, and manage multiple tasks

Ability to analyze and organize information and materials for a variety of research projects

Please submit as separate documents:

1. Cover letter (1 page maximum) telling us why you are interested in the position, why you feel you are qualified, and your contact information 2. Curriculum vita 3. Contact information for three references, then letters of recommendation will be requested upon application submission via http://binghamton.interviewexchange.com 4. Your philosophy of teaching undergraduates how to conduct research (250-500 words)

Review of applications begins February 1st 2018 and continues until the position is filled. Electronic applications are required; please submit your application materials to: *Interview Exchange via Binghamton University*.

https://binghamton.interviewexchange.com/jobofferdetails.jsp?JOBID=93105 You may add additional files/documents after uploading your curriculum

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CanadianMuseumNature Quebec AlgalSystematics

COMPETITION

Research Scientist - Phycologist

MRS-01

Permanent Position

$73,676 - $88,920 per year

Work location : Gatineau (Aylmer sector) in Quebec

https://nature.ca/en/about-us/careers-volunteering/careers/research-sci entist-phycologist

The Canadian Museum of Nature (CMN) is seeking a dynamic, innovative and creative phycologist to conceive, design and conduct a program of independent and collaborative, field and collection-based systematic research on algae; to publish results of scientific research; to contribute to and provide advice on the development and use of the National Herbarium of Canada algae collection; and to work with other museum staff on the development and production of exhibits, outreach and educational programs. The successful candidate will join the CMN's Botany Section, which includes a team of eight research and collection staff. He/she will have access to excellent research infrastructure, including a molecular systematics laboratory, high-powered microscopy facilities, and the largest and most comprehensive algae collection in Canada.

NOTE: A formal procedure for promotion based on achievements is in place to develop the career path of CMN's research scientists. An excellent benefits package comes with the position.

OPEN TO: Employees of the Canadian Museum of Nature and the general public who meet the following qualifications.

EDUCATION: Ph.D. in biological sciences, with a specialization in the taxonomy and systematics of algae.

LANGUAGE REQUIREMENTS:

English and French are essential.

Bilingual imperative: BBB/BBB

EXPERIENCE:

The candidate must have demonstrated expertise in morphological and molecular taxonomy and phylogenetics of algae, with a proven publication record and an active research program, including fieldwork. Experience with the algae of Canada and/or the Arctic would be an asset, as would experience working in a museum context. The candidate should have experience in obtaining external support for research projects. The candidate must be comfortable with a collaborative and multi-disciplinary approach to projects.

NOTE:

The application should include:

- a cover letter describing past and present research experience as well as a proposed long-term research plan, the ways in which this research would contribute to and utilize the CMN algae collection, and the fieldwork this research may include;

- a curriculum vitae;

- Three letters of recommendation may be requested from candidates at a later date.

SEND YOUR COMPLETE APPLICATION BY EMAIL TO: competition@mus-nature.ca

Please state competition: NO.2090-CMN-17-OC-041

Statement of qualifications available by contacting the email address above.

For additional information regarding the position and/or the museum, please contact: Dr. Lynn Gillespie, 613-364-4075. lgillespie@mus-nature.ca

For information on the Museum and its programs, see our web site at: www.nature.ca Please note that only candidates who are selected for the next stage of the selection process will be contacted.

The Canadian Museum of Nature is committed to developing inclusive, barrier-free selection processes and work environments. If contacted regarding this competition, please inform the Senior Advisor, Human Resources should you require accommodation to attend an interview or participate in the selection process.

The Museum supports employment equity.

CLOSING DATE: January 31, 2018 at 5 p.m.

CONCOURS

Chercheur scientifique - Phycologue

MRS-01

Poste permanent

73 676 $ Ã 88 920 $ par annee

Lieu de travail : Gatineau (secteur Aylmer) au Quebec

https://nature.ca/fr/sujet-musee/emplois-benevolat/-emplois/chercheur-sc ientifique-phycologue

Le Musee canadien de la nature (MCN) est Ã la recherche d'un phycologue dynamique, innovant et creatif pour concevoir, realiser et mener un programme independant et cooperatif de recherche systematique sur le terrain et Ã partir des collections d'algues; pour publier des resultats de recherche scientifique; pour appuyer et guider le developpement et l'utilisation de la collection d'algues de l'Herbier national du Canada; et pour travailler avec les autres membres du personnel du Musee au developpement et Ã la production d'expositions et de programmes de sensibilisation et d'education. Le candidat retenu se joindra Ã la Section de botanique du MCN, qui comprend une equipe de huit employes affectes Ã la recherche et aux collections. La personne aura acces Ã d'excellentes infrastructures de recherche, y compris un laboratoire de systematique moleculaire, de puissants microscopes et la plus grande et la plus complete collection d'algues au Canada.

REMARQUE : Une procedure de promotion formelle en fonction des

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CollegeCharleston EvolutionaryMarineBiology

Research area open including evolutionary component to research.

Marine Biologist The Department of Biology at the College of Charleston invites applications for a tenure-track position in Marine Biology at the Assistant Professor level to begin August 2018. Candidates must have a Ph.D. in biology, marine biology, marine science or a related field and a strong commitment to teaching and maintaining an active research program involving undergraduate and graduate students. We seek a marine organismal biologist who will complement strengths of existing faculty. The area of research is open but taxonomic groups of particular interest include marine tetrapods and marine phycology/botany. Primary teaching responsibilities could include courses in the marine biology core, graduate and/or undergraduate specialty courses in an area of expertise, and introductory biology and/or human A&P. 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, the Grice Marine Laboratory close to the downtown campus, 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 a cover letter, curriculum vitae, statements of teaching and research interests, up to three relevant publications, unofficial graduate transcript(s) (with official copies required upon hire), and names and contact information for three colleagues capable of providing a recommendation to http://jobs.cofc.edu/-postings/6793. Questions regarding this position can be directed to Gorka Sancho, search committee chair, at sanchog@cofc.edu. This is a nine-month appointment; salary is competitive and commensurate with experience and qualifications. Review of applications will begin February 4 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.

Assistant Professor of Marine Biology jobs.cofc.edu

“Murren, Courtney J” <MurrenC@cofc.edu>

ColoradoState RootGenetics

Project Manager - Root Genetics for Drought and Carbon Adaptation

The McKay Lab at Colorado State University invites applications for a project manager. This research is part of a larger effort to understand the genetics of adaptation to drought in crops and species in nature. The project goal is to develop new methods for field based root and soil phenotyping, including the development of field devices, spectroscopy, image analysis, genotype-phenotype analysis and process-based soil modeling. The project is funded by the ARPA-E ROOTS program.

https://arpa-e.energy.gov/?q=3Dslick-sheet-project/-root-genetics-drought-and-carbon-adaptation This position involves coordinating project meetings and leading project reporting an evaluation of progress for each of the teams and tasks. The project will generate novel methods as well as data on the genetic basis of root architecture and how it responds to drought. Thus there is ample opportunity for the successful candidate to take part in and lead the writing and publication of science manuscripts.

Minimum requirements: Masters in biology, bioinformatics, genomics, computer science or highly related field; Experience in project management; Experience with project reporting; Demonstrated oral and written communication skills

Complete applications due by 31 Jan 2018 for full consideration.

Full job description and application procedures at https://jobs.colostate.edu/postings/52675 CSU is an EO/EA/AA employer and conducts background checks on all final candidates.

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

FiskU Tennessee ComputationalBiol

Tenure Track Assistant Professor in Computational Biology.

Fisk University (www.fisk.edu) invites applications for a tenure track position at the rank of assistant professor in the broad area of computational biology, with demonstrated potential for excellence in student-centered undergraduate teaching and for developing a research program capable of attracting external funding and publishing peer-reviewed papers with undergraduate co-authors. This faculty member also will serve as a mentor in the nationally recognized Fisk-Vanderbilt Master’s to PhD Bridge Program. A Ph.D. degree and training that embraces both biological and computational sciences is required, and postdoctoral training is optimal. Application materials should include the applicant’s Curriculum Vitae, Research Plan, and Teaching Philosophy as well as three letters of recommendation. All materials should be sent electronically to Dr. Lee Limbird, PhD, Search Committee Chair [llimbird@fisk.edu] Applications are being considered immediately; the position is available immediately. Fisk University is an Equal Opportunity Employer.

Lee

Lee E Limbird, PhD

Professor and Dean

Lee Limbird <llimbird@fisk.edu>

GeorgiaTech LabTech EvolutionOfMulticellularity

Full-Time Laboratory Technician Position, Evolution of Multicellularity, Georgia Institute of Technology, Atlanta, GA.

The Ratcliff lab at Georgia Tech is looking to hire a full-time laboratory technician to work on the evolution of multicellularity in 'snowflake' yeast. This person will primarily assist a postdoc on experiments examining: 1) the evolution of extremely large size (thousands of cells, easily visible to the naked eye) in snowflake yeast, 2) the role of oxygen in the evolution of multicellular complexity, and 3) how geometric constraints can interact with pre-existing cell biology to give rise to simple multicellular development.

We are looking for someone who is collaborative, well-organized, and has experience with microbial cell biology. Your duties will involve genetic transformation (in both Saccharomyces cerevisiae and Schizosaccharomyces pombe), high-throughput fluorescence microscopy, confocal microscopy, flow cytometry, and sterile cell culture. Experience with these techniques is a plus, but is not required. The ideal candidate will also have experience with scientific programming, preferably in python, R, or MatLab.

We are very open to hiring a 'post-bac', or student who has recently completed a B.S. (or equivalent), and is considering graduate school in a year or two. We are interested in someone who can commit to working for at least one year.

Starting salary is $15 per hour, there are no benefits associated with this position.

To apply, please send a cover letter describing your motivation for the position and relevant research experience, along with contact information for three letters of reference to: William Ratcliff (ratcliff@gatech.edu). The position is open until it is filled.

gonensin bozdağ <ozan.bozdag@gmail.com>

Hawaii InsectEvolution

Title:

Assistant Reseacher (Urban Pest Management)

Position Number:

0083184

Hiring Unit:

C of Trop Agr and Human Resources, Plant and Environmental Protection Sciences

Location:

Manoa Campus

Date Posted:

January 19, 2018

Closing Date:

Continuous - application review begins March 01, 2018

Monthly Type:

11 Month

Tenure Track:

Tenure

Full Time/Part Time:

Full Time

Temporary/Permanent:

Permanent

Other Conditions: * To begin August 2018 or soon thereafter. For best consideration, all application materials should be submitted by February 28, 2018.

Duties and Responsibilities 1. Develop a strong, innovative, nationally recognized externally-funded program addressing research, extension and instruction on the environmental and economic impacts of urban, structural and/or public health insect pests in Hawai'i. 2. Perform research in an applied, ecological and/or evolutionary context aimed at improving urban and/or public health insect pest exclusion and management in these systems, with the goal of promoting safe, sustainable, and ecologically responsible methods. 3. Teach 1-2 courses each year that could include, but are not limited to, General Entomology, Medical Entomology, Urban Pest Management, Social Insect Ecology and Evolution, and/or other courses and seminars as needed. 4. Participate in the Entomology graduate program by teaching, supervising and mentoring graduate students. 5. The faculty member will provide service to the department, college, university, profession and community as his/her expertise allows. 6. Provide service to the department, college, university, profession and community as his/her expertise allows.

Minimum Qualifications 1. Ph.D. in entomology, biology or a related field, from a college or university of recognized standing. 2. Ability to generate independent research reports, publications and grant proposals. 3. Ability to interact effectively with students and/or assistants when appropriate. 4. Initiative, interest in scientific work, and adaptability.

Desirable Qualifications 1. Experience with a range of social and/or urban pest issues. 2. Proven publication record. 3. Teaching experience at the university level. 4. Evidence of successful grantsmanship. 5. Expertise in urban pest biology, ecology and management as demonstrated by thesis or dissertation topic, publications and/or presentations in these areas.

To Apply:

Submit the following to the address listed below: 1) Cover letter indicating how you satisfy the minimum and desirable qualifications, 2) curriculum vitae, 3) statement of research and teaching interests, 4) names and contact information for at least three professional references and 5) official transcripts (copies accepted, however official transcripts will be required upon hire).

Address: 1. Dr. Koon Hui Wang 2. College of Tropical Agriculture and Human Resources 3. Department of Plant and Environmental Protection Sciences 4. 3050 Maile Way, Room 310 5. Honolulu, HI 96822

Inquiries: 1. Dr. Koon Hui Wang; 808-956-7076; koonhui@hawaii.edu

The University of HawaiÊ≫i is an equal opportunity/affirmative action institution and is committed to a policy of nondiscrimination on the basis of race, sex, gender identity and expression, age, religion, color, national origin, ancestry, citizenship, disability, genetic information, marital status, breastfeeding, income assignment for child support, arrest and court record (except as permissible under State law), sexual orientation, domestic or sexual violence victim status, national guard absence, or status as a covered veteran.

Employment is contingent on satisfying employment eligibility verification requirements of the Immigration Reform and Control Act of 1986; reference checks of previous employers; and for certain positions, criminal history record checks.

In accordance with the Jeanne Clery Disclosure of Campus Security Policy and Campus Crime Statistics Act, annual campus crime statistics for the University of Hawaii may be viewed at: http://ope.ed.gov/security/, or a paper copy may be obtained upon request from the respective UH Campus Security or Administrative Services Office.

Daniel Rubinoff <rubinoff@hawaii.edu>

HealthCanada Bioinformatician

Very unique opportunity at Health Canada in the Food Directorate in Ottawa, Ontario.

Have the ability to work with and provide bioinformatics support to amazing research scientists in microbiology, nutritional sciences and toxicology.

Create, use, design and develop bioinformatics programs while working with a very large in-house computer cluster as well as in-house generated next gen sequencing data (MiSeq, NextSeq and MinION).

Creatives and free thinkers welcome.

This is not a stereotypical government job!

2 Positions available.

All details found on the following pages. *You must apply using the "Apply Online" link on the bottom of the following pages*:

English: https://emploisfp-psjobs.cfp-psc.gc.ca/psrs-srfp/applicant/ page1800?poster14687

French: https://emploisfp-psjobs.cfp-psc.gc.ca/psrs-srfp/applicant/-page1800?poster14687&toggleLanguage=fr

Nicholas Petronella <nicholas.petronella@gmail.com>

InstitutJacquesMonod Paris FunctionalGenomics

Dear Colleague,

The Institut Jacques Monod, affiliated with the CNRS and the Université Paris Diderot, is recruiting two group leaders, at the junior or senior level.

We would be grateful if you could circulate the enclosed advertisement in your institute and point it out to researchers who might be interested in setting up their laboratory at the institute. Best regards, Roger Karess and Michel Werner

Call for New Group Leaders

The Institut Jacques Monod (IJM), a leading center of fundamental biological research in Paris, is seeking to appoint several new group leaders. The IJM is comprised of about 30 research groups working in the fields of genetics and genomics, biophysics, cell biology, development and evolution.

Candidates should work in one of the areas of fundamental biology covered by the Institute. Researchers interested in computational biology and/or functional genomics are particularly encouraged to apply. The successful applicants will be selected based on their scientific excellence and their potential to complement and synergize with existing research in the Institute. We will consider group leader applications at both the junior and senior levels.

Research at the IJM is supported by excellent core facilities providing state-of-the-art light and electron microscopy, mass spectrometry, animal facilities, and access to high throughput genomics equipment. The IJM is located in Paris on the campus of the Université Paris-Diderot and is affiliated with the Centre National de la Recherche Scientifique (CNRS). For more detailed information, visit our website (http://www.ijm.fr).

Successful applicants should have upon their arrival at IJM a permanent position with the CNRS, INSERM, the French university system, or a non-permanent position funded by granting agencies such as the French ATIP-AVENIR program or the ERC, which will allow them to apply for a permanent position.

Applicants should provide: a cover letter explaining their interest in joining the IJM; contact details for 3 referees; and a document formatted using this application form comprising a C.V., a summary of scientific achievements, and proposed research program.

Applications should be sent by e-mail to the Institute Director Dr. Michel Werner (direction(at)ijm.fr) as a single pdf file, and should be received not later than 15 March 2018.

Institut Jacques Monod UMR 7592 CNRS-Université Paris Diderot Bât.Buffon - 15 rue Hélène Brion 75205 PARIS CEDEX 13 - France. â 01.57.27.81.42

http://www.ijm.fr BONDIDIER Martine <Martine.BONDIDIER@ijm.fr> BONDIDIER Martine <Martine.BONDIDIER@ijm.fr>

LundU PlantEvolutionaryEcol

Senior University Lecturer in Plant Ecology

The Department of Biology wishes to strengthen research and teaching at the interface between plant community ecology and evolutionary biology, with a focus on terrestrial plants. We are advertising a fully tenured position which will include both teaching and research. The Biology Department in Lund is a large and internationally visible department, has excellent facilities and is a good working place!

There is currently a strong interest in extending studies of evolutionary processes beyond single organisms, or interactions between a small number of organisms, to a more realistic community-based context. Rapid developments within genomics provide increasingly accessible means of characterizing molecular variation with plant communities - and these developments are driving a closer integration of ecological and evolutionary studies. We want to appoint a person with strong competence within the field of terrestrial plant community ecology and a focus on the ecological and evolutionary processes that drive community assembly and biodiversity. Experience in field-based teaching in floristics and vegetation analysis will be regarded as a strong merit.

Application details: https://lu.mynetworkglobal.com/-en/what:job/jobID:177838/type:job/where: 4/apply:1

For more general information, send an email to stefan.andersson@biol.lu.se

Stefan Andersson <stefan.andersson@biol.lu.se>

MfN Berlin Bioinformatics

Researcher (f/m) in the field of bioinformatics

The Museum für Naturkunde - Leibniz Institute for Evolution and Biodiversity Science (MfN) is an excellent and integrated research museum within the German Leibniz Association. Its activities cover and tightly link the fields of collection-based research, development of collections and public engagement with science.

We are seeking a talented and motivated bioinformatician to develop the new core facility for the analysis of genomic data at the Museum für Naturkunde Berlin - Leibniz Institute for Evolution and Biodiversity Science.

The position is full-time and initially for 2 years (tenure-track, salary E13 TV-L Berlin). Tenure will be provided after successful evaluation within the first 2 years.

The jobholder is expected to establish his/her own research agenda in the field of evolutionary genomics and to provide bioinformatics support within the Museum to enable multidisciplinary research projects as for example in the context of the "Center for Integrative Biodiversitydiscovery" at the MfN. Both tasks involve engagement in grant applications as well as training and supervision of students and post-docs.

The Museum für Naturkunde Berlin provides an excellent research environment. It houses state- of-the-art laboratories for molecular genetics and computation. Numerous independent research groups are working in a wide range of research fields including population genetics, phylogenetics, developmental and evolutionary genetics, and taxonomy. Our world-class zoological collections provide unique access to specimens collected over the last 200+ years.

The Berlin- Brandenburg region is characterized by a highly international academic and cultural community. The cities Berlin and Potsdam as well as their water-rich surroundings offer excellent possibilities for recreation. Living costs are still moderate.

We will consider candidates with a PhD in biology or bioinformatics and a proven record of post- doctoral experience in bioinformatic analyses of genomic data sets. Ideally, candidates have a wide experience in basic genomic data processing and analysis including genome/transcriptome assembly, annotation, bait design and metabarcoding. Experience with concepts of population genetics and respective bioinformatics analyses would be an advantage. The ability to work independently and to integrate into a team are required.

More information can be found here https://www.naturkundemuseum.berlin/de/-stellenausschreibungen/wissenschaftliche-mitarbeit-wm-researcher-fm or obtained by contacting Dr. Frieder Mayer (frieder.mayer@mfn-berlin.de).

In the interest of equal opportunity, applications by qualified female applicants will be particularly welcome. Handicapped applicants with equal qualifications will be given priority.

Applications with the usual materials (statement of research interests and experience, curriculum vitae, list of publications, and academic certificates) should be sent until 31.01.2018 reference to job advertisement No. 72/2017 to:

Museum für Naturkunde Personalreferat Invalidenstraße 43 D-10115 Berlin Germany

or to recruiting@mfn-berlin.de. As submitted materials will not be returned, only submit copies with your application.

"Mayer, Frieder" <Frieder.Mayer@mfn-berlin.de>

MississippiU EvolutionaryBiology

Biology Faculty

Mississippi University for Women invites applications for a tenure-track Evolutionary Biology faculty position beginning August 2018.

The successful candidate will have the primary responsibility for teaching a junior-level Evolutionary Biology course in an undergraduate-only program. Applicants must be willing to teach other biology courses in their area of expertise and introductory-level biology courses.

Preference will be given to candidates who can actively pursue extra-mural funding, and initiate and supervise research programs involving our undergraduate students. Rank will be dependent on qualifications and experience. Applicants must have completed or received the Ph.D. degree by August 1, 2018. Individuals with post-doctoral experience and/or teaching experience will be given preference. Applications will be subject to immediate consideration, continuing until the position is filled.

MUW emphasizes excellence in teaching and undergraduate research, and provides a student-centered teaching environment.

Additional information about MUW is available at http://www.muw.edu . For more information about the position, contact Dr. Bonnie Oppenheimer (662-329-7239 or bloppenheimer@muw.edu). Submit letter of interest, C.V., copies of transcripts, three letters of reference, statement of your approach to teaching, and statement of your research plans to: Office of Human Resources, 1100 College Street, MUW-1609, Columbus, MS 39701 or hrinfo@hr.muw.edu or 662-241-7616 (fax). AA/EOE.

Ross Whitwam rewhitwam@muw.edu Professor of Biology Dept. of Sciences and Mathematics Mississippi

University for Women Columbus, MS 39701

Ross Whitwam <rewhitwam@muw.edu>

NationalU Mexico SystematicEntomology

Position opening Instituto de BiologÃa, Universidad Nacional Autonoma de Mexico Systematic Entomologist The Instituto de BiologÃa, Universidad Nacional Autonoma de Mexico (IBUNAM), whose main mission is the study of national biodiversity and houses the national biological collections, invites applications for a tenure track, full-time position of Associate Investigator, level "C", in Systematic Entomology at the main National University campus, Mexico City. Requirements for candidates:

1. A Ph.D. degree or equivalent, preferably in entomology, zoology, or a related discipline.

2. Experience in systematic research of insects, demonstrated by original, high quality publications, commensurate to age and academic trajectory.

3. Be familiar with the entomofauna of Mexico and/or the Neotropics, as well as with the curation of scientific collections, techniques of field collecting, morphology, molecular systematics, and/or evolutionary biology.

4. A commitment to participate in activities complementary to research, such as teaching at educational programs of UNAM, and the direction of theses at the undergraduate and graduate level, activities of science outreach, and institutional participation.

5. Willingness to integrate immediately into the academic activities of the IBUNAM, practice leadership in his or her area of investigation, and demonstrate aptitude to form or integrate into a research group.

6. Proficiency in Spanish. Applicants should submit a letter addressed to the Director of IBUNAM (Dr. VÃctor Manuel G. Sanchez Cordero Davila) with a detailed statement of purpose; a full curriculum vitae with contact information (supporting documentation is not necessary at this stage); PDFs of publications that the applicant considers the most important of his/her professional trajectory (a maximum of five); a brief proposal of his/her activities for the first year at the Institute (5 pages maximum); and a letter of recommendation.

Applications with the required documentation will be received from January 08, 2018 until March 30, 2018, 7 PM Mexico City time.

Shortlisted candidates will be contacted for a personal interview.

Applications should be sent to the email acontreras@ib.unam.mx with copy to sacademica@ib.unam.mx and vinculacion@ib.unam.mx. Inquiries regarding this announcement should be addressed to the Academic Secretary of IBUNAM, e-mail: acontreras@ib.unam.mx, phone (+52) 55-5622-9067, -9068 (www.ib.unam.mx).

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Alejandro ZaldÃvar Riveron Investigador titular B Tiempo Completo Curador en jefe de la Coleccion Nacional de Insectos Departamento de ZoologÃa Instituto de BiologÃa Universidad Nacional Autonoma de Mexico 3er. Circuito Exterior Cd. Universitaria Apartado Postal 70-153 C.P. 04510 Mexico, D.F.

Mexico Phone: 00 52 (55) 56 22 91 58 Fax: 00 52 (55) 55 50 01 64

Alejandro Zaldívar Riverón <azaldivar@ib.unam.mx>

PennsylvaniaStateU Bioinformatics ShortTerm

Assistant Research Professor or Researcher in Bioinformatics

The laboratory of George (PJ) Perry in the Departments of Anthropology and Biology at The Pennsylvania State University is seeking applications for a bioinformatics specialist who has experience working with massively parallel sequencing data and with population genomic analyses. The successful candidate would participate in multiple ongoing human and non-model organism population and comparative evolutionary genomic studies. For more information about our lab: www.anthgenomicslab.com. The appointment would be as an Assistant Research Professor for candidates with a Ph.D. and as a Researcher for those without a Ph.D., with salary commensurate with appointment and experience. The position will start between February and March 2018 with an appointment of up to one year. While the appointment could then potentially be renewed depending on availability of funds, this position would be most ideally suited for a candidate seeking a shorter-term opportunity. To apply for this position, submit 1) a two-page cover letter describing your bioinformatics experience, 2) your CV, 3) and the names and contact information of three professional references. Apply at: https://psu.jobs/job/76591 . CAMPUS SECURITY CRIME STATISTICS: For more about safety at Penn State, and to review the Annual Security Report which contains information about crime statistics and other safety and security matters, please go to http://www.police.psu.edu/clery/, which will also provide you with detail on how to request a hard copy of the Annual Security Report.

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

grgperry@gmail.com

QueensU EvolutionaryEcol

Tenure-track position in Evolutionary Ecology

The Department of Biology at Queen's University invites applications for a Tenure-track faculty position at the rank of Assistant Professor with specialization in Evolutionary Ecology, with a preferred starting date of July 1, 2018.

We seek a broadly-trained evolutionary biologist with research interests in both fundamental and applied questions related to the evolutionary consequences and management of rapidly changing environments. This position could include aspects of plant or animal biology related to climate change, pollution, resistance to pesticides/herbicides/antibiotics, biological invasion, vector-borne diseases, habitat degradation and fragmentation, and restoration ecology. Priority will be given to candidates who envision studying contemporary evolution utilizing the diverse land-holdings and facilities at the Queen's University Biological Station (QUBS). QUBS includes more than 3400 ha of diverse aquatic and terrestrial habitat, located 60 km north of Kingston (https://qubs.ca/). Situated on the Frontenac Arch, QUBS lands provide access to diverse terrestrial and aquatic habitats with a range of human disturbance. The station offers laboratory and teaching spaces as well as accommodation. Queen's is a research-intensive university, with an integrated Biology Department that encompasses observational, experimental and theoretical approaches to gain a fundamental understanding of biological systems and processes. Strong collaborative linkages exist with other departments and faculties at Queen's, and with other national and international institutions.

Candidates must have a PhD or equivalent degree completed at the start date of the appointment. The main criteria for selection are academic and teaching excellence. The successful candidate will provide evidence of high-quality scholarly output that demonstrates potential for independent research leading to peer assessed publications and the securing of external research funding, as well as strong potential for outstanding teaching contributions at both the undergraduate and graduate levels, and an ongoing commitment to academic and pedagogical excellence in support of the department's programs. Candidates must provide evidence of an ability to work collaboratively in an interdisciplinary and student-centred environment. The successful candidate will be required to make substantive contributions through service to the department, the Faculty, the University, and/or the broader community. Salary will be commensurate with qualifications and experience. This position is subject to final budgetary approval by the University.

The University invites applications from all qualified individuals. Queen's is committed to employment equity and diversity in the workplace and welcomes applications from women, visible minorities, Aboriginal peoples, persons with disabilities, and LGBTQ persons. All qualified candidates are encouraged to apply; however, in accordance with Canadian immigration requirements, Canadian citizens and permanent residents of Canada will be given priority.

To comply with federal laws, the University is obliged to gather statistical information as to how many applicants for each job vacancy are Canadian citizens / permanent residents of Canada. Applicants need not identify their country of origin or citizenship; however, all applications must include one of the following statements: "I am a Canadian citizen / permanent resident of Canada"; OR, "I am not a Canadian citizen / permanent resident of Canada". Applications that do not include this information will be deemed incomplete.

A complete application consists of:

- a cover letter (including one of the two statements regarding Canadian citizenship / permanent resident status specified in the previous paragraph);

- a current Curriculum Vitae (including a list of publications);

- a statement of research interests, and how the QUBS would be used to fulfil your interests and research goals;

- a statement of teaching interests and experience (including teaching outlines and evaluations if available);

- a diversity statement describing your past and planned commitment to promoting diversity, inclusion, and equity in your research programs and outreach activities;

- Three letters of reference to be sent directly to Brian Cumming, Professor and Head, Department of Biology, c/o Anne Dumont (ad142@queensu.ca)

The deadline for applications is February 18, 2018. Applicants are encouraged to send all documents in their application packages electronically as PDFs to Anne Dumont at ad142@queensu.ca, although hard copy applications may be submitted to:

Brian Cumming
Professor and Head
The Department of Biology
Room 3102, BioSciences Complex
116 Barrie St.
Queen's University
Kingston, Ontario
CANADA K7L 3J9

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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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RBG Kew PlantSystematics

Senior Research Leader - Plant Systematics and Evolution Comparative Plant & Fungal Biology Department, Royal Botanic Gardens, Kew Closing date: 18/02/2018 https://careers.kew.org/vacancy/senior-research-leader-plant-systematics-and-evolution-339669.html Kew is the world's leading botanic gardens, at the forefront of plant and fungal science, a UNESCO World Heritage Site and a major visitor attraction. We are seeking an excellent scientist to lead plant systematic research in Kew's Comparative Plant and Fungal Biology department, one of six departments in the Science Directorate. Building on Kew's outstanding collections and scientific strengths, you will lead the Integrated Monography group, a team of world-class plant systematic experts, and establish your own research programme focused on a specific plant group of significance to ecosystems and human well-being. Your research will be global and collaborative in outlook, combining research on taxonomy and fundamental diversity with critical studies in phylogenetic, evolutionary and environmental biology, leading to diverse research outputs of the highest standard consistent with Kew's ambitious strategic objectives.

To be successful in this role, you'll be an outstanding and inspiring scientist with a relevant PhD and extensive post-qualification experience in plant systematics and evolution research. You will have an established reputation in the international science community and substantial experience of integrating taxonomy and fundamental diversity research with phylogenetic, evolutionary and environmental biology. You'll also have significant specialist knowledge in an appropriate plant group that will underpin your research programme at Kew, and a track record in excellent science publications and grantsmanship, together with skills in managing budgets and project leadership. We're looking for someone who is a proven leader and mentor of researchers, and has a strong track record in the supervision of students. Experience of teaching and outreach is highly desirable. We want you to have a clear strategic outlook and be quick to engage with the broader strategic landscape of Kew Science and the institution as a whole.

The salary will be 47,353 - 57,285 per annum, depending on skills and experience.

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

If you are interested in this position, please follow this link: https://careers.kew.org/vacancy/senior-research-leader-plant-systematics-and-evolution-339669.html We are committed to equality of opportunity and welcome applications from all sections of the community. We guarantee to interview all disabled applicants who meet the essential criteria for the post.

Closing Date: 18/02/2018

William Baker <W.Baker@kew.org>

SciLifeLab Stockholm Bioinformatics

We have several openings for permanent bioinformatics staff at SciLifeLab Stockholm, Sweden.

SciLifeLab (www.scilifelab.se) is a Swedish national center for molecular biosciences with focus on health and environmental research. The National Bioinformatics Infrastructure at SciLifeLab (www.nbis.se) is a large national infrastructure in rapid development, now looking for several experts to join the Bioinformatics Long-term Support team (a.k.a. WABI). The Bioinformatics Long-term Support team provides advanced bioinformatics analyses to some of the most scientifically exciting projects across Sweden, and with more than 20 full-time senior bioinformaticians, the team is one of the strongest units in Sweden for analysis of large-scale genomics and related "omics" data. The experts will carry out advanced analyses within nationally prioritized projects, develop tools and workflows for such analyses and educate other scientists in bioinformatics.

The new staff members will be employed at Stockholm university, with placement at SciLifeLab Stockholm.

More information: http://www.su.se/english/about/working-at-SU/jobs?rmpage=job&rmjob=4680&rmlang=UK We are looking forward to your application, at the latest February 13, 2018!

Pär Engström, par.engstrom@scilifelab.se Björn Nystedt, bjorn.nystedt@scilifelab.se Joint Heads of SciLifeLab Bioinformatics Long-term Support

Bjorn Nystedt, PhD Joint head of facility Bioinformatics Long-term Support (WABI) National Bioinformatics Infrastructure Sweden at SciLifeLab www.nbis.se, www.scilifelab.se/platforms/bioinformatics

BMC E10:3206, entrance C11 Husargatan 3, SE-752 37 Uppsala

Phone: 018 - 471 4413 E-mail: bjorn.nystedt@scilifelab.se

Björn Nystedt <bjorn.nystedt@scilifelab.se>

SGN Frankfurt BiodiversityDataScientist

Job offer ref. #11-18001

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. SGN conducts natural history research with almost 800 employees and research institutions in six federal states. Within SGN, the Senckenberg Biodiversity and Climate Research Centre (BiK-F) explores the interactions between biodiversity, climate, and society. In the context of the DFG project "German Federation for Biological Data" (GFBio) Senckenberg invites applications for a

Biodiversity Data Scientist (full time)

The German Federation for Biological Data (GFBio) brings together Germany's key players in the field of biological data and information management to harmonize the national biological data landscape. GFBio's multidisciplinary consortium is represented by experts from a variety of institutions ranging from natural history collections, libraries, bioinformatics to environmental data archives.

The Senckenberg Gesellschaft für Naturforschung is one of seven data centers within GFBio offering services for storing, managing and analysing research and specimen data.

Your tasks: • develop/implement tools for managing data according to the scope of GFBio • contribute to the conceptual development of a data visualisation and analysis tool • present the project at national and international conferences • communicate with the other consortium partners • write manuscripts and publish results in international journals in cooperation with the members of the consortium

Your profile: • M.Sc./Diploma/PhD degree in Biology, Bioinformatics, Ecology, Biogeography or an informatics-related subject. • a general overview of biodiversity research • substantial experience with databases (e.g. PostgreSQL, MySQL, Solr, Elastic Search) • substantial experience with at least one programming language like Java, PHP • proficiency in data formats XML and JSON • experience in the information management system Metacat would be an asset as well as knowledge in processing GIS data and in data visualization. • excellent written and oral communication skills in German and English • a strong interest in extending your knowledge in all fields of biodiversity informatics

What is awaiting you? • An interesting task in a dynamic team of researchers in an internationally renowned research institution • The opportunity to gain experience in the above-mentioned research field • The occasion to build a network with scientists in interdisciplinary fields in Germany

Salary and benefits are according to a full time public service position in Germany (TV-H E 13). The contract shall start as soon as possible and will initially be limited until November 30st, 2018. A prolongation is envisioned but depends on funding. The Senckenberg Gesellschaft für Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung. Please send your application, mentioning the reference of this job offer (ref. #11-18001) before February 1st, 2018 preferred by e-mail (attachment in a single pdf document) and including a letter outlining your suitability and motivation, detailed CV, all transcripts and grades, contact details of two potential references, a summary of your Master's or Diploma thesis and, if available, publications to:

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main E-Mail: recruiting@senckenberg.de

For scientific enquiries please get in contact with PD Dr. Thomas Hoernschemeyer, thomas.hoernschemeyer@senckenberg.de or Prof. Dr. Thomas Hickler thomas.hickler@senckenberg.de

Mit freundlichen Grüßen /Best Regards

Jessica Helm Personalsachbearbeiterin

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

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

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

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Gruppe Personal & Soziales - 1319 Elsen, Carina

Mitarbeiter/in Personalbeschaffung (Recruiting) - 1313 di Biase, Maria - 1313 Helm, Jessica - 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1467 Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Uwe Fritz, Prof. Dr. Ingrid Kröncke Präsidentin: Dr. h. c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

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StCloudStateU ConservationZoologist

Tenure-Track Assistant/Associate Professor of Biology (Conservation Zoologist)

Description: The Department of Biological Sciences at St. Cloud State University invites applications for a tenure-track position in Conservation Zoology at the rank of assistant or associate professor. We seek a broadly-trained biologist, with an emphasis on zoological organisms, who addresses questions regarding how to conserve biodiversity at local, regional, and/or global scales. Of interest are individuals with expertise among the following fields that address current issues in conservation biology: population genetics, species interactions, predictive modeling, population demography and regulation, biogeography, and maintenance and function of biodiversity. The successful candidate will be expected to develop and maintain an active research program and teach undergraduate and graduate-level courses in the areas of conservation, management, evolution, ecology, and biodiversity. We especially encourage applications from candidates in underrepresented groups in the biological sciences.

The ideal candidate will share St. Cloud State's commitment to our mission and values, especially our commitment to educating our racially and socio-economically diverse student population. Applicants will be expected to establish and maintain a professional goal to become outstanding teachers through the use of research based, best practices pedagogy. They should be willing to participate in teaching using alternative delivery methods such as online and hybrid. They will regularly engage in ongoing professional development and innovation opportunities focused on pedagogical growth offered within the College and at SCSU.

Responsibilities: Teaching Bachelors and Masters-level courses that may include courses such as Conservation and Management of Animals, Wildlife Populations, Introductory Biology, General Zoology, and a Zoology-related course dependent upon expertise (e.g., Entomology, Herpetology, Ornithology). The faculty member will be expected to participate in a multi-disciplinary research environment that contributes to professional development and involves undergraduate and graduate students at the Masters level. Advising and committee participation are expected.

In order to be considered for tenure, the successful candidate will demonstrate the ability to: 1) teach and/or perform assignment effectively; 2) conduct scholarly achievement or research; 3) continue preparation and study in discipline; 4) contribute to student growth and development; and 5) provide service to the university and community. (IFO Article 22, Section B) *Employment for this position is covered by the collective bargaining agreement for the Inter Faculty Organization which can be found at: http://www.hr.mnscu.edu/contract_plans/-documents/IFO_09_11_Contract.pdf Qualifications and Experience: Required Ph.D. in Biology or related discipline by the hire date Evidence of a research program involving animals Evidence of teaching experience Evidence of demonstrated ability to teach and work with persons from culturally diverse backgrounds.

Preferred Demonstrated experience teaching courses listed including laboratories Post-doctoral experience Evidence of working with animals, biodiversity, and conservation Evidence of grants and peer-reviewed publications A research program that includes a technological or quantitative component Experience mentoring students including underrepresented groups in STEM fields

Application Procedures: To apply for this position, please continue the process via this website or directly at: http://agency.governmentjobs.com/stcloudstate/-default.cfm Application Review begins 1/31/2018; position is open until filled. Only complete applications will be considered. A complete application will include the following: Cover Letter Resume/Curriculum Vitae Contact information for three (3) current, professional references Copies of Transcript(s) (undergraduate/graduate/PhD); if advanced to finalist, official transcripts will be required.

Contact Information: William Cook, Search Committee Chair Professor of Biological Sciences Phone: (320) 308-2019 E-mail: biology@stcloudstate.edu

"Davis, Matthew P." <mpdavis@stcloudstate.edu>

TexasAMU PlantSystematics

Assistant Professor of Plant Systematics/Phylogenetics, Texas A&M University

The Department of Ecosystem Science and Management at Texas A&M University invites application for a full-time tenure-track faculty position at the rank of Assistant Professor in Plant Systematics/Phylogenetics. Applicants whose research integrates field and collection-based studies with state-of-the-art molecular approaches to address fundamental questions in systematics, evolution, or biogeography of vascular plants are encouraged to apply. Specific research areas of emphasis may include, but are not limited to: phylogenetics and genomics applied to organismal evolution; community phylogenetics, including research that complements existing ESSM Departmental strength in savanna ecosystems; systematics applied to conservation and management of plant communities and ecosystems.

Essential Duties: The position is approximately 50% research, 35% teaching and 15% service and herbarium administration. The new faculty member will establish a competitively funded research program in Plant Systematics/Phylogenetics. Teaching responsibilities may include undergraduate classes in Agrostology and Rangeland Plant Taxonomy, along with a graduate course in the candidate's area of expertise. The successful candidate is also expected to hold the position of Director of the S.M. Tracy Herbarium, which currently houses approximately 345,000 specimens including one of the largest collections of grasses in the region, and has ample representation from most vascular plant families. Applicants interested in continuing efforts to diversify and modernize the collection resources are encouraged to apply.

Required: - PhD in Plant Systematics or close equivalent by the time of hire with a researchemphasis as described above. - Evidence of potential to secure extramural funding and a demonstrated ability topublish research results in refereed journals. - The appointee will also show evidence of ability or potential to effectively teach and mentor undergraduate and graduate students.

Desired: - Demonstrated interest and ability to teach Agrostology and Rangeland Plant Taxonomy. - Postdoctoral or similar experience. - A successful record of extramural funding for research. - Experience working with herbarium collections. - Experience and interest in collaborations addressing contemporary research questionsin savannas. - Familiarity with the land grant mission.

A competitive remuneration package with excellent benefits will be offered commensurate with the appointee's capabilities, qualifications, and experience.

Resources: Texas A&M University (TAMU) is a public, land-grant institution with access to excellent resources including Genomics and High Performance Computing facilities, core laboratories, field stations, as well as opportunities to interact and collaborate with a broad range of TAMU System researchers throughout the state of Texas. The Department of Ecosystem Science and Management (ESSM) is an interdisciplinary faculty committed to creating and synthesizing new knowledge on how ecosystems and their components persist, function, assemble, process nutrients and water, evolve, and respond to environmental change. ESSM relies on science- based problem solving to guide departmental education, research, and extension programs. http://essm.tamu.edu/ Application Process: For full consideration, applications should be submitted by February 15, 2018. The position will remain open until finalists have been selected. Applicants should submit a cover letter addressing each of the required/desired qualifications (up to 3 pages), a curriculum vitae, unofficial transcripts, names and contact information for three references, and statements on Teaching and Research relative to the position (up to 2 pages each). Individuals should apply at: https://tamus.wd1.myworkdayjobs.com/-AgriLife_Research_External/job/College-Station-TAMU/Assistant-Professor_R-000843-1 For inquiries please contact Dr. Carol Loopstra, c-loopstra@tamu.edu . The Texas A&M System is an Equal Opportunity/Affirmative Action/Veterans/ Disability Employer committed to diversity. The college is especially interested in qualified candidates who can contribute, through their research, teaching, and/or service, to the diversity and excellence of the academic community. Women, minorities, individuals with disabilities, and veterans are encouraged to appl

ccasola@tamu.edu

UAlgarve Portugal 500 MarineEvolBiol

500 research positions in Portugal

The Foundation for Science and Technology of Portugal (FCT) opened 500 new scientific positions at all levels (Junior researcher, Assistant Researcher, Principal Researcher, Coordinating Researcher). The call is open between January 19 and February 15.

We invite strong candidates to apply to the FCT 'Stimulus to Individual Scientific Employment 2017' having CCMAR- Centre of Marine Sciences at the University of Algarve, Faro, Portugal (ccmar.ualg.pt) as the host institution (where selected candidates will be working).

CCMAR is a top marine research institute in Portugal, including an enthusiastic group of scientists working in evolutionary biology.

Those interested to apply should send, as soon as possible considering the short deadline, an e-mail to ccmar@ualg.pt (subject: Scientific Employment 2017) addressed to the director and include: 1) Motivation letter including planned research goals and up to two contact for references; 2) Curriculum vitae; 3) level of the application. CCMAR will reply shortly and may carry out online interviews.

You can also contact one of the researchers directly to discuss a project, collaborations, etc. find us at: https://www.ccmar.ualg.pt Detailed information about the call can be found here - in Portuguese (but CCMAR will help with translation and the application). http://www.fct.pt/apoios/contratacaodoutorados/-empregocientifico/ci_dez2017.phtml.en The guidelines (In English) can be downloaded here: https://www.fct.pt/apoios/contratacaodoutorados/-empregocientifico/docs/Guiao_de_Avaliacao.pdf Ester Serrao <eserrao@ualg.pt>

UCollegeLondon PlantOrFungalEvolution

Last Advertisement: Closing Date 12 January.

Dear Colleagues,

We would be very grateful if you could bring the following position at University College London to the attention of suitable candidates.

Quain Professor or Associate Professor of Plant or Fungal Evolutionary Biology University College London http://bit.ly/UCL-Quain Closing Date: 12 January 2018

We seek to appoint a scientist as Quain Professor or Associate Professor of Plant or Fungal Evolutionary Biology. The successful candidate will have an international reputation in the field of Plant or Fungal Evolutionary Biology and will provide leadership in expanding the study and teaching in this area across UCL.

The Research Department of Genetics, Evolution and Environment (GEE) is one of four Research Departments in the Division of Biosciences at UCL, one of the world's leading centres for basic biological sciences and part of the UCL Faculty of Life Sciences. The post will be held in the Centre for Life's Origins and Evolution (http://bit.ly/UCL-CLOE), a cross-departmental institute within GEE. The candidate's research will fit into one of the three themes of CLOE: origins of life and of major innovations; pattern of evolution at all time scales, across the tree of life; and the processes underpinning the emergence of biological complexity/diversity. Areas of interest include, but are not restricted to: comparative genomics; diversification of major groups; evolution of plant/fungal interactions; the genetic basis of key transitions; plastid origins; evodevo. We welcome applicants working on any taxa from unicells to angiosperms. The research may be computational, experimental or both.

Many thanks

Max Telford

To apply follow: http://bit.ly/UCL-Quain-apply Max Telford Professor of Zoology Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 (Internal: 32554) Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/academic-staff/telford/telford.html Open access journal EvoDevo: http://www.evodevojournal.com/ "Telford, Max" <m.telford@ucl.ac.uk>

UCollegeLondon StatisticalGenetics RiceChickpea

Genetics Institute, University College London

Research Associate in Statistical Genetics and Bioinformatics - Ref: 1704024

We are recruiting a talented statistical geneticist/bioinformatician with excellent communication skills to determine the genetic basis of complex phenotypes in rice and chickpea, with the aim of improving these important crops. The methodologies developed by the project will apply to many other crops and animals.

The post is funded by the UK Global Challenges Research Fund and the BBSRC. The post-holder will join the group of Richard Mott in the Genetics Institute (UGI) at University College London (UCL), and will work in close collaboration with the International Rice Research Institute (IRRI), Philippines, and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India, and the National Institute for Agricultural Botany (NIAB), Cambridge. The project will involve visits to both IRRI and ICRISAT.

The project focuses on (i) the imputation of genome sequence from crop populations sequenced at low coverage, adapting methods developed previously in the group (e.g. Davies et al Nature Genetics 2015) (ii) the use of low-coverage population sequence to identify structural variants implicated in phenotypes (Imprialou et al Genetics 2017) (iii) The development and implementation of quantitative genetics and genomic prediction methods in crop development, particularly in relation to multiparental advanced intercrosses (MAGIC populations. (iv) Close collaboration, support and knowledge exchange with partner laboratories.

Applicants must have a PhD in Statistical Genetics, Bioinformatics or a related field, and a good understanding of genetic association mapping, and experience of manipulating and analysing Next-Gen sequence data. It is essential candidates demonstrate programming fluency in R, Perl/Python, or C/C++. The successful candidate must have experience of conducting research in statistical genetics or bioinformatics, and in managing long-distance collaborations effectively.

The post is available from now until 30 June 2021 with possibility of extension.

Salary Grade7 34,635 - 41,864 per annum (inclusive of London allowance) Closing Date: 2 February 2018 Further details and application form available from https://tinyurl.com/y7sqh3rr If you would like to discuss the post please contact Professor Richard Mott, r.mott@ucl.ac.uk

r.mott@ucl.ac.uk

UGlasgow MolecularLabTech

Job open for a molecular ecology lab technician at the University of Glasgow:

We invite applications for a full time molecular laboratory technician in the Institute of Biodiversity, Animal Health, and Comparative Medicine (main campus) at the University of Glasgow, Scotland, UK. We have a shared lab facility for research groups on evolutionary and ecological genetics of animals, plants, and pathogens - and we are in need of a new, skilled pair of hands to bring onto the team!

We are seeking an enthusiastic and reliable technician capable of multitasking efforts across research groups and research tasks. Abilities to conduct project planning and troubleshooting, work independently to excellent standards, willingness to learn new techniques, keen attention to detail and organisation, and aptitude for teaching hands-on skills to students, staff and visiting researchers are all required.

The role will involve sample handling and molecular lab techniques for the workflows of DNA and RNA analyses. This includes skills such as (but not limited to) high quality extraction, PCR, qPCR, quantitations and quality control, cloning, and next-gen sequencing library preparation. Skills with protein analysis work would also be desirable. The technician will work closely with multiple PIs and members of their research groups, and will manage the labs for equipment and day-to-day tasks.

Full job description is available at the University website under job reference 019806. https://www.gla.ac.uk/-it/iframe/jobs/ Applications must be made to the university website no later than 21 Jan. 2018. Informal inquiries welcome to Kathryn.Elmer@glasgow.ac.uk

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

“Kathryn.Elmer@glasgow.ac.uk” <Kathryn.Elmer@glasgow.ac.uk>

UGreifswald AnimalEvolution

Professor (W2) of Animal Ecology

The University of Greifswald’s Faculty of Mathematics and Natural Sciences is seeking to fill the position of a

Professor (W2) of Animal Ecology

at the Zoological Institute and Museum, to be appointed as soon as possible.

We are seeking an internationally recognized expert with a strong research record in the areas of animal ecology and evolutionary biology. The applicant (f/m) has experience with innovative approaches for studying mechanisms in animals to cope with changing environmental conditions (phenotypic plasticity, genetic adaptation). Participation in local joint research projects such as the DFG Research Training Group 2010 “Biological RESPONSEs to Novel and Changing Environments” (https://biologie.uni-greifswald.de/-forschung/dfg-graduiertenkollegs/research-training-group-2010/) and the University’s key field of research “Environmental Change: Responses and Adaptation (ECRA)” (https://www.uni-greifswald.de/-forschung/forschungsprofil/forschungsschwerpunkte/-environmental-change-responses-and-adaptation/) is expected.

The successful applicant is expected to participate in teaching (8h per week in each semester) in the bachelor courses ’Biology’ and ’Landscape Ecology and Nature Conservation’ and the master courses ’Biodiversity and Ecology’ as well as ’Landscape Ecology and Nature Conservation’. We expect the candidates to be able to teach in English as well as in German. The candidate should be willing to work in academic committees. International experience is desirable.

Applicants must fulfill the requirements for a university professor according to Â§58 of the Landeshochschulgesetz (State Higher Education Law) Mecklenburg-Vorpommern: a university degree at PhD level, independent teaching and research experience as proven by a junior professorship, habilitation or other equivalent position.

In accordance with Â§61 LHG M-V, the professor appointed will be assigned the status of a civil servant (Beamtenverhältnis) with unlimited tenure; alternatively, if the applicant is not permanently available: limited tenure as a civil servant or public service employee.

The University would like to increase the proportion of women in areas in which they are underrepresented and thus applications from women are particularly welcome and will be treated with priority if they have the same qualifications and as long as there are no clear reasons which make a fellow applicant more suitable.

Please include only copies of documents in your application, as these will not be returned. Unfortunately, application costs cannot be reimbursed by the State of Mecklenburg-Vorpommern.

For more information, contact Prof. Dr. Werner Weitschies, Dean of the Faculty of Mathematics and Natural Sciences.

Applications with all usual documents (Curriculum Vitae (CV) detailing the academic career, list of scholarly publications and courses taught, academic certificates, proof of teaching experience, details of externally raised funds) must be sent by the 16.02.2018 to:

Ernst-Moritz-Arndt-Universität Greifswald Dekan der Mathematisch-Naturwissenschaftlichen Fakultät Friedrich-Ludwig-Jahn-Straße 17a 17487 Greifswald Tel.: +49 3834 420 4000

E-Mail: dekanmnf@uni-greifswald.de

https://www.uni-greifswald.de/en/university/information/jobs/current-vacancies/professuren/professor-w2-of-animal-ecology/ Michael Beaulieu <MiKLvet@hotmail.fr>

UIllinois EvolutionaryImmunobiology

Note: Immunobiology researchers using an evolutionary or comparative genomics approach are very welcome to apply for this position.

FACULTY POSITION ANNOUNCEMENT

Assistant Professor - Immunobiology

University of Illinois at Urbana-Champaign

Position: Assistant Professor, Full Time Tenure-Track Faculty Position in Immunobiology in the Department of Animal Sciences.

Qualifications: Ph.D. degree in immunobiology or a related field, a commitment to teaching, and an ability to establish an externally funded, internationally-recognized program of research in immunobiology. Candidates with postdoctoral research experience, a strong record of publications and evidence of likely success in competing for extramural funding will be preferred.

Responsibilities: The Department of Animal Sciences has a long and prominent history of discovery and excellence in basic immunology, immunogenetics, and immunophysiology. The successful candidate will develop and maintain a nationally and internationally recognized research program supported by extramural funding. The successful candidate will also contribute to interdisciplinary campus initiatives involving the immunology discipline and contribute to the public service missions of the University. Responsibilities will also include mentoring graduate students and postdoctoral fellows, and advising and interacting with undergraduate students. The successful candidate will participate in teaching appropriate courses in immunology and/or related fields. Candidates with research interests in understanding immunophysiology in domesticated animals, model organisms and/or humans are encouraged to apply. Potential research topics may include, but are not limited to: epigenetic modifications and reprogramming of immune cells; immunometabolic signaling networks that link immune responses and metabolism; host-pathogen interactions; neuroimmune interactions via the meningeal lymphatic system; and neuroimmune interactions and behavior, including stress.

Proposed Start Date: Negotiable after the closing date.

Salary: Commensurate with qualifications and experience

Location: The University of Illinois at Urbana-Champaign (http://www.illinois.edu) is located approximately 120 miles south of Chicago in a metropolitan area of approximately 232,000 people.

Resources: The campus is home to internationally recognized facilities and interdisciplinary programs including the Carl R. Woese Institute for Genomic Biology (http://www.igb.illinois.edu), Beckman Institute (http://www.beckman.illinois.edu), W.M. Keck Center for Comparative and Functional Genomics (http://www.biotech.uiuc.edu/centers/Keck), Carle Illinois College of Medicine (http://www.medicine.illinois.edu), Cancer Center at Illinois (http://www.cancer.illinois.edu), and National Center for Supercomputing Applications (http://www.ncsa.illinois.edu). The Department of Animal Sciences (http://www.ansc.illinois.edu) currently has 35 faculty, 500 undergraduate students, and approximately 100 graduate students.

The College of Agricultural, Consumer and Environmental Sciences (ACES) (http://www.aces.illinois.edu) is widely recognized for excellence in undergraduate and graduate education, research, outreach, and international programs. In addition to its mission as a land-grant university, the campus offers exceptional programs in the arts, humanities, sciences, engineering, and computer science.

Application and Closing Date: For initial consideration, the following materials should be uploaded by February 15, 2018. However, the search will continue until a suitable candidate is found. Please create your candidate profile at http://jobs.illinois.edu and upload, as a single pdf file, a curriculum vitae, a statement of research interests (including future plans), a statement of teaching philosophy, the names and contact information of three references.

Questions can be directed to Dr. Rex Gaskins, Chair of the Search Committee (mailto:hgaskins@illinois.edu), (217) 333-4189 or to Dr. Rodney Johnson, Head of the Department, (mailto:rwjohn@illinois.edu), (217) 244-1681.

The University of Illinois conducts criminal background checks on all job candidates upon acceptance of a contingent offer.

The University of Illinois is an Equal Opportunity, Affirmative Action employer. Minorities, women, veterans and individuals with disabilities are encouraged to apply. For more information, visit http://go.illinois.edu/EEO. To learn more about

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ULausanne EvolutionaryEcology

The Faculty of Biology and Medicine of the University of Lausanne, Switzerland, invites applications for the position of

Assistant Professor (tenure-track) in Ecology

at the Department of Ecology and Evolution.

The successful candidate will have an outstanding record of research, a demonstrated ability to attract external research funding, an interest and enthusiasm for teaching ecology, and a desire to establish a strong research group in ecology. All branches of ecology will be considered, but we are particularly interested in candidates with research and teaching interests in experimental population and/or experimental ecology. Pre-existing knowledge of French is not required, but the candidate will be expected to be able to teach in French within two years.

The Department of Ecology and Evolution has a long track record of excellence in research. It is located on a beautiful and vibrant campus on the shore of Lake Geneva, sharing the site with the Federal Technical University, EPFL.

A start-up package, a state-of-the-art research infrastructure, as well as a yearly research allowance for positions and consumables will be available within an environment favouring collaborations.

Applications should include a motivation letter, a curriculum vitae with a complete list of publications in which the five most significant are identified, a brief statement of research program, a statement of teaching philosophy, and the names of three referees. The full applications should be submitted through the UNIL recruitment system: http://bit.ly/2DmXnnM Deadline for application: March 31st 2018 (23:59 GMT+1)

Further information may be obtained from Prof. Christian Hardtke (Christian.Hardtke@unil.ch), chairman of the search committee.

Seeking to promote an equitable representation of women and men among its staff, the University encourages applications from women.

“tadeusz.kawecki@unil.ch” <tadeusz.kawecki@unil.ch>

ULeuven CichlidSpeciation

Research Scientist in Evolutionary Genomics: Cichlid-Speciation

The Royal Belgian Institute of Natural Sciences

Evolutionary and Behavioural Genomics of Cichlid Speciation

Context :

Since Darwins' “The Origin of Species” there has been a continued interest to gain insight in the speciation process. Initially, theories on speciation were mostly narrative and focussed on the geographic modes of speciation, while more recent work investigated the importance of sexual selection or whether speciation rates can be triggered by environmental changes. All these questions have been addressed in the cichlid fishes from the Great African lakes that are often cited as the ultimate animal models to investigate adaptive radiation and speciation.

To date, recently developed techniques that allow exploring genomic evolutionary issues in cichlids have for the most part been used to link genes with the observed phenotypic changes that are so characteristic in the African cichlid species flocks. In contrast, we propose to make use of the opportunities offered by the availability of these novel techniques to investigate the genetic basis of the speciation process itself. Therefore, our two main objectives are to characterize the genomic differentiation that drives the speciation process, and to verify whether/and to what extent the same genomic changes are involved in to maintain the ???????integrity' of the gene pools of the resulting sister species.

GENBAS: a BRAIN.be project: 'Genetic Basis of Speciation' http://genbas.be/ Tasks :

- Assistance of the GENBAS team [RBINS (Brussels), RMCA (Tervuren), University of Leuven and University of Liege) in NGS data analyses (genotyping-by-sequencing and RNAseq data)

- Applying phylogenomic, phylogeographic and population genomic data analysis to resolve species boundaries and connectivity questions

- Identification of divergent genomic regions within and between populations/species

- Linking adaptive genomic regions with gene expression data, potentially linked to speciation/mate choice/sexual selection genes

Profile :

- Diploma: Master in Bioinformatics, Biology or Bioengineering with a strong interest in evolutionary genomics (phylogenomics or population genomics)

- Technical skills: Experience with NGS data analysis (raw data, VCF genotypes), excellent knowledge of R, familiar with scripting in Python/Perl ....

- General skills: eager to learn, team player, good knowledge of English

We offer :

- A fixed-term contract of 12 months with the possibility of extension (but application to National Research Fund mandatory)

- Salary according the standard scale for an assistant (SW1);

- Free public transport;

- A dynamic and interesting working environment

- Starting date: March 2018

How to apply?

E-mail your motivation letter, 2 references and CV before 15/02/2018

to : Erik Verheyen via: erik.verheyen@naturalsciences.be

Gregory Maes, Ph.D.

University of Leuven (KU Leuven)

Laboratory for Cytogenetics and Genome Research

Centre for Human Genetics | Genomics Core

O&N I Herestraat 49 - box 602

UZ Leuven

B-3000 Leuven

Belgium

Phone: +32 (0)16 37 25 22

E-mail: gregory.maes@kuleuven.be

Logo_GC

Gregory Maes <gregory.maes@kuleuven.be>

ULille EvolutionaryGenomics

Dear colleagues,

We are happy to announce that the university of Lille (France) is opening an Assistant Professor position on Evolutionary Genomics and Systems Biology to join our group in the lab Evolution, Ecology and Paleontology (UMR CNRS 8198, http://eep.univ-lille.fr/en/news/-emplois/assistant-professor-evolutionary-genomics-and-systems-biology) in Lille (France). This is a permanent position and our main criterion is scientific excellence.

We welcome all applications focusing on basic research with relevance to the fields of evolutionary genomics and systems biology, broadly interpreted as the study of the evolutionary process taking into account the complexity of interactions between genetic elements within a genome. Research in the group is focusing on theoretical and empirical biology with a strong focus on evolutionary genomics of reproductive systems in plants, but a range of other research topics in a variety of model organisms are welcome. Cutting-edge platforms for molecular biology, computational resources and greenhouse space are made freely available to members of the group.

The successful candidate will develop research using empirical and/or theoretical approaches. She/he will be teaching population genetics, evolutionary ecology and general biology at the undergraduate (Population and Organismal Biology) and graduate levels (Master Biodiversity, Ecology and Evolution, major on Management and Evolution of Biodiversity). Some undergraduate courses will need to be taught in French but research can be conducted in English.

Lille is a vibrant cultural city with a central location in Europe (1h to Paris, 35 min to Brussels and 2h to London by fast train).

Informal inquiries should be sent to Vincent.Castric@univ-lille1.fr or Xavier.Vekemans@univ-lille1.fr. The deadline for formal application is march 29th, 2018.

– Dr. Vincent CASTRIC Directeur de recherche CNRS http://vincentcastric.weebly.com Unite Evo-Eco-Paleo (EEP) - UMR 8198 CNRS / Universite de Lille - Sciences et Technologies Batiment SN2, bureau 207 59655 Villeneuve d'Ascq - FRANCE Tel: +33 3 2033 6303 Fax: +33 3 2043 6979

Vincent CASTRIC <Vincent.Castric@univ-lille1.fr>

ULiverpool 4 FellowsLectureships

I'd like to draw your attention to four open positions at the University of Liverpool, UK. Please note that the research area is flexible, and that these positions are roughly the equivalent of an Assistant Professorship in the U.S.

Informal inquires can be directed to to Ilik Saccheri at I.J.Saccheri@liverpool.ac.uk or Greg Hurst at G.Hurst@liverpool.ac.uk.

https://recruit.liverpool.ac.uk/pls/corehrrecruit/erq_jobspec_details_form.jobspec?p_id=008631 4 x Tenure Track Fellowships/Lecturerships Grade 8 Integrative Biology 008631 39,992 - 50,618 pa 12-Feb-2018 23:30

Applications are invited from candidates with expertise that maps onto existing strengths in our four cross-cutting research themes:

Adaptation to environmental change Dynamics and management of host-microbe interactions >From genomes to biological systems Molecular basis of therapeutic targeting

We are looking to appoint either at Tenure Track Fellow or Lectureship level. You should have a PhD in a relevant discipline, experience as a successful researcher, evidence of high quality publications in your area of expertise and demonstrate research independence. We are particularly interested in applications from candidates who will be able to make use of opportunities afforded by the UK government's Global Challenges Research Fund and the Industrial Strategy Challenge Fund, working in the following areas:

Eco-evolutionary dynamics Plant science Vertebrate behaviour and evolutionary ecology Microbe-host interactions Functional and comparative genomics Cell signaling Metabolomics Computational modelling of complex biosystems

Andrea Betancourt | Senior Lecturer Department of Evolution, Ecology, and Behaviour (DEEB) | Institute for Integrative Biology (IIB) University of Liverpool Biosciences Building Rm 238 / Crown St. / L69 7ZB Liverpool / United Kingdom http://www.flyevolution.net | +44 (0) 151 795 4516 | aabt@liverpool.ac.uk

"Betancourt, Andrea" <A.Betancourt@liverpool.ac.uk>

UNevada LasVegas EvolutionaryNeurobiology

We are looking for a neurophysiologist, broadly defined to include evolutionary, ecological and behavioral aspects of neurobiology. For more information, please contact me or the search committee chair.

Allen Gibbs

allen.gibbs@unlv.edu

University of Nevada Las Vegas: Neurophysiology Assistant Professor

School of Life Sciences, College of Sciences [18546] Category: - Faculty - Medicine - Other Medicine - Faculty - Science - Other Science

Application Due: Open Until Filled

Type: Full Time

Announcement Number: 18546

The University of Nevada, Las Vegas invites applications for the position of Neurophysiology Assistant Professor, School of Life Sciences, College of Sciences [18546]

PROFILE of the UNIVERSITY Founded in 1957, UNLV is a doctoral-degree-granting institution of approximately 29,000 students and 3,000 faculty and staff that is classified by the Carnegie Foundation for the Advancement of Teaching as a research university with high research activity. UNLV offers a broad range of respected academic programs and is on a path to join the top tier of national public research universities.

The university is committed to enhancing efforts to attract and retain top students and faculty, educating the region's diversifying population and workforce, driving economic activity through increased research and community partnerships, and creating an academic health center for Southern Nevada that includes the launch of a new UNLV School of Medicine. UNLV is located on a 332-acre main campus and two satellite campuses in Southern Nevada.

COMMITMENT to DIVERSITY The successful candidate will demonstrate support for diversity, equity and inclusiveness as well as participate in maintaining a respectful, positive work environment.

ROLE of the POSITION The successful candidate is expected to carry out an active and independent research program supported by extramural funding. The successful candidate will teach at the graduate and undergraduate levels and participate in service activities commensurate with the role of an Assistant Professor. Although other research areas may be considered, the ideal candidate will develop an experimental research program in neurophysiology. Preference will be given to those that strengthen or complement current research activities in the School.

Additional information about the School may be obtained from our website, https://www.unlv.edu/-lifesciences . QUALIFICATIONS This position requires a Ph.D. from a regionally accredited college or university and postdoctoral experience preferred.

SALARY RANGE Salary competitive with those at similarly situated institutions.

Position is contingent upon funding.

APPLICATION DETAILS Submit a letter of interest, a detailed resume listing qualifications and experience, and the names, addresses, and telephone numbers of at least three professional references who may be contacted. Applicants should fully describe their qualifications and experience, with specific reference to each of the minimum and preferred qualifications because this is the information on which the initial review of materials will be based.

Although this position will remain open until filled, review of candidates' materials will begin November 27, 2017 and best consideration will be gained for materials submitted prior to that date. Materials should be addressed to Frank van Breukelen Search Committee Chair, and are to be submitted via on-line application at https://hrsearch.unlv.edu/. For assistance with UNLV's on-line applicant portal, contact UNLV Employment Services at (702) 895-3504 or applicant.inquiry@unlv.edu.

Application Information Contact: UNLV Human Resources University of Nevada Las Vegas Phone: 702-895-3504 Online App. Form: https://hrsearch.unlv.edu UNLV is an Equal Opportunity / Affirmative Action educator and employer committed to achieving excellence through diversity. All qualified applicants will receive consideration for employment without regard to, among other things, race, color, religion, sex, age, creed, national origin, veteran status, physical or mental disability, sexual orientation, genetic information, gender identity, gender expression, or any other factor protected by anti-discrimination laws. The University of Nevada, Las Vegas employs only United States citizens and non-citizens lawfully authorized to work in the United States. Women, under-represented groups, individuals with disabilities, and veterans are encouraged to apply.

Allen Gibbs <allen.gibbs@unlv.edu>

UofGuelph ComputationalBiolBioinformatics

Dear colleagues,

We are currently searching for a tenure-track Assistant Professor in the areas of Computational Biology/Bioinformatics/Genomics to join the Department of Integrative Biology at the University of Guelph (https:/-/www.uoguelph.ca/ib/).

Further details about the position and application process can be found here: http://www.uoguelph.ca/-facultyjobs/postings/ad17-80.shtml Applications will be considered beginning on Feb. 19, 2018.

The University of Guelph is a research-intensive institution, with major strengths in the Biological, Environmental and Agricultural Sciences, and ranks among the top agri-food universities in the world. The position is part of a cluster hire to support a University-wide research program to increase exponentially our ability to leverage big data for the benefit of food production and biodiversity at three scales of research and innovation: global, landscape, and microscale (https://arrellfoodinstitute.ca/food-from-thought/).

Thank you for your consideration,

John Fryxell (Chair of the search committee) Sarah Adamowicz Nick Bernier Moira Ferguson Andreas Heyland Hafiz Maherali

Sarah Adamowicz <sadamowi@uoguelph.ca>

UOslo 2 EvolutionaryBiology

RESEARCHER IN EVOLUTIONARY BIOLOGY AND APPLIED MATHEMATICS - TWO POSITIONS

The University of Oslo is Norway's oldest and highest rated institution of research and education with 28 000 students and 7000 employees. Its broad range of academic disciplines and internationally esteemed research communities make UiO an important contributor to society.

Centre for Ecological and Evolutionary Synthesis (CEES) is a research centre and a section at the Department of Biosciences, University of Oslo. CEES combines a broad spectrum of disciplines (population biology, genomics, statistics, mathematical modelling) to foster the concept of ecology as a driving force of evolution via selective processes, with a corresponding influence of evolutionary changes on ecology. CEES has over 180 members (Professors (20), postdocs/researchers (60), PhDs (35), Master's students (40) and technical and administrative staff) and many guest researchers. The members represent 30 nationalities and constitute a vibrant and creative research environment. CEES coordinate several international networks. The budget = 170 million NOK (about 55 externally funded research projects). CEES successfully completed its 10 year status of Centre of Excellence (CoE) in 2017 and is chaired by Professor Nils Chr. Stenseth.

Two researcher positions, one in Evolutionary biology and one in Applied mathematics are available at the Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biosciences, Faculty of Mathematics and Natural Sciences.

The positions is for a period of two years, with the possibilities of extension. The appointed candidates will be working on the project "Drivers of evolutionary change: understanding stasis and non-stasis through integration of micro- and macroevolution", which is funded by the Research Council of Norway (RCN) (there will be no compulsory teaching). The PI of the project is Nils Chr. Stenseth (University of Oslo: www.cees.uio.no/stenseth); co-PIs are Jan Martin Nordbotten (University of Bergen: http://www.uib.no/personer/Jan.Martin.Nordbotten), Indrë Ãliobaitë (University of Helsinki: http://www.zliobaite.com/) and Mikael Fortelius (University of Helsinki: http://www.helsinki.fi/geo/staff/fortelius/). Both positions will have CEES as their home base, but the appointed candidates will be expected to spend time in Bergen and Helsinki.

RESEARCH PROJECT

The primary objective of the funded project is to understand to what extent macroevolutionary patterns and changes can be understood as resulting from microevolutionary and ecological processes. By so doing the project aims at bringing together micro- and macroevolutionary theories. A main objective of the project is to develop common ground between mathematical formulations and biological definitions by developing data proxies and linking them to models. A description of the project can be obtained on request.

POSITION 1 (EVOLUTIONARY BIOLOGY): To fill one of the opened positions we are seeking a person with solid background in evolutionary biology. Candidates with experience in statistical modelling, computational analysis and/or integration of data-driven analysis with mathematical models of ecological and/or evolutionary processes will be prioritized.

POSITION 2 (APPLIED MATHEMATICS): To fill the other opened position we are seeking a person with solid background in applied mathematics. Candidates with experience from multi-scale methods, analysis of partial differential equations, and/or scientific computing will be prioritized. Previous experience from mathematical biology is not necessary, but will be advantageous.

The two appointed candidates will be working as a team together with other members of the project. For this purpose we seek highly motivated and enthusiastic persons interested in working in interdisciplinary teams.

REQUIREMENTS

The Faculty of Mathematics and Natural Sciences has a strategic ambition of being a leading research faculty. The successful candidates for the announced positions will be chosen in accordance with this ambition and will be expected to be in the upper segment of his/her class with respect to academic credentials.

The successful candidates must have a PhD degree or the award pending in appropriate fields. The ideal candidates will have a proven record of publishing high-quality research.

Fluent oral and written communication skills in English.

We offer:

- Salary NOK 490 900 - 569 000 per annum depending on qualifications in position as Researcher (position code 1109) - A professionally stimulating working environment - Attractive welfare benefits and a generous pension agreement, in addition to Oslo's family-friendly environment with its rich

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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

UOttawa QuantitativeBiology

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

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

The successful candidate will join an innovative and collaborative department of over 40 researchers working in all fields of biology including biodiversity, computational biology, cell and molecular biology, developmental biology, ecotoxicology, evolutionary biology, and physiology. The Department maintains close connections and collaborations with researchers in the Ottawa region including federal government science departments, the Ottawa Hospital Research Institute, the Canadian Museum of Nature, and Carleton University. The Faculty of Science supports several core facilities including a Molecular Biology and Genomics Laboratory to provide access to advanced molecular biology/genomics equipment. Access to high-performance computing and data storage is available through Compute Canada. — Application deadline: Review of applications will begin March 15, 2018 and will continue until the position is filled.

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

hrundle@uottawa.ca

USaskatchewan HeadTech GroundSquirrelEvolution

Job Description and Duties: We are looking for a head field technician to assist with, and coordinate, fieldwork on the ecology of two wild populations of Columbian ground squirrels. The head technician will supervise 4 student interns and coordinate with a PhD student and PI involved with the project for the period of Apr 10 to Aug 31, 2018. Fieldwork will will involve monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals, data entry and data verification. The two populations are separated by an approximately 1.5 hr. drive and will each be monitored by two separate teams of interns. As such, it is expected that the head technician will display strong organizational abilities, responsibility and oversight.

This is an excellent opportunity for someone with previous field experience, looking to advance their career in wildlife biology or move towards graduate school. All fieldwork is carried out in the spectacular Rocky Mountains of southwestern Alberta, Canada, home to some of the most majestic wildlife in North America. The head technician will have the opportunity to view many of these iconic species as well as interact with other researchers in the area working on a diversity of species and research projects.

Skills required: The successful candidate will have previous fieldwork experience in a similar work environment. Good organizational, multi-tasking and supervisory abilities are essential. Possession of these skills, as evidenced through previous experience supervising field crews, is desirable. Specific field skills required are: ability to trap, handle and observe wild mammals. The successful applicant will also have experience in data entry, checking and management of databases. A displayed interest in ecology, wildlife, field biology, and animal behaviour is also required. An undergraduate degree in one of these, or a related, field is required. The applicant must be able to work well with members of their own team, as well as other users of the area (i.e., other researchers, tourists).

Salary will be $1800-2100/month, based on level of experience. Food and accommodation are provided. The successful candidate will be required to provide for their own travel to Saskatoon, Saskatchewan. Travel between the field station and Saskatoon is provided.

If you wish to apply for this position, please send a CV with a cover letter and contact details of three references (with e-mail address), by email to Jeff Lane (contact info below) before January 31, 2018. Please indicate in your application that you are applying for the head technician position (we are also posting for student interns). All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Only those selected for interview will be contacted.

Contact:

Dr. Jeff Lane

Department of Biology

University of Saskatchewan

usaskcgsproject@gmail.com

www.lanelab.ca "Lane, Jeffrey" <jeffrey.lane@usask.ca>

UWinnipeg EvoDevo

Tenure-Track Assistant Professor, University of Winnipeg

The Department of Biology at The University of Winnipeg invites outstanding candidates to apply for a tenure track appointment at the rank of Assistant Professor. The ideal candidate will possess a Ph.D. in Biology or a related field with a strong research focus in the areas of Developmental Biology, Genetics, and/or Cell Biology. Postdoctoral experience is preferred. The Department of Biology is looking for a highly motivated and energetic candidate who will develop a strong, independent research program, deliver world-class training for research students, and provide outstanding teaching in the classroom.

The selection committee will begin reviewing applications on January 29, 2018 and will continue until the position is filled; full consideration is assured for applications received by January 28, 2018. Applicants must submit a cover letter, curriculum vitae, outline of proposed research program (maximum two pages), a statement of teaching philosophy including evidence of teaching effectiveness (maximum two pages), and three representative publications (all documents in PDF). Candidates should also arrange to have three letters of reference e-mailed directly to:

Dr. Judith Huebner, Chair

Department of Biology

The University of Winnipeg

biology@uwinnipeg.ca

The University of Winnipeg is an urban, post-secondary institution on Treaty One land in the heart of the Métis Nation. The University appreciates, fosters and promotes values of human dignity, equality, non-discrimination and diversity. The University of Winnipeg is committed to employment equity, welcomes diversity in the workplace, and encourages applications from all qualified individuals including women, members of racialized communities, Indigenous persons, persons with disabilities, and persons of any sexual orientation or gender identity. In accordance with Canadian immigration requirements, first preference must be given to Canadian citizens and permanent residents of Canada. However, all qualified individuals are invited to apply.

For more details, see https://www.uwinnipeg.ca/hr/-docs/fac-posvac/January/Tenure%20Track%20Assistant%20Prof%20Biology.pdf

Susan Lingle Associate Professor, Department of Biology University of Winnipeg Winnipeg, MB R3B 2E9 (204) 258-2964

Susan Lingle <lingle.uw@gmail.com>

WhitmanCollege LabTech PlantEvolution

The Cooley lab at Whitman College seeks *a full-time laboratory technician to carry out research on the molecular basis of repeated evolution in plants.* Exact start and end dates are flexible, but a candidate able to start in summer or fall of 2018 is preferred and *funding is available for two years.*

The successful candidate will work with to design and implement transgenic tests of candidate genes for the regulation of floral pigmentation in the Chilean monkeyflower (Mimulus).

Requirements include: - a Bachelor's degree in Biology or a related discipline - research experience in a molecular lab, preferably including cloning and transgene construction - attention to detail and ability to work independently

I run an undergraduate research lab at Whitman College, a selective liberal arts college located in the small but vibrant community of Walla Walla, in eastern Washington state. Walla Walla receives numerous awards for quality of life thanks to its music, art, and wine scenes: http://www.wallawalla.org/. This is a full-time position with benefits.

To apply, please visit https://whitmanhr.simplehire.com , click on "Staff Position" and then "Laboratory Technician", and upload:

- a cover letter describing your background and reason for being interested in the position - your CV or résumé, including names and contact information for three references Review of applications will begin immediately and continue through January.

Questions may be directed to: Dr. Arielle Cooley cooleya@whitman.edu

paulwhetstone0473@gmail.com

Winnipeg Bioinformatics

Indeterminate SR-03 Bioinformatician position opening in the new Genomics Unit of the Canadian Food Inspection Agency's National Centre for Foreign Animal Disease (NCFAD) based in Winnipeg Manitoba. NCFAD is a unique lab with containment level 3 and 4 laboratory and animal cubicles that performs primarily diagnostic, surveillance and research related to animal and zoonotic viruses. We currently perform Ion Torrent and Illumina sequencing in our level 3 sequencing lab. Secret clearance is needed prior to working at NCFAD. For more information, please contact Dr. Oliver Lung for more information.

Oliver Lung, Ph.D.

Research Scientist/Head, Genomics Unit

Canadian Food Inspection Agency

National Centre for Foreign Animal Disease

1015 Arlington Street, Winnipeg, MB R3E 3M4

Canada

Phone: 1-204-789-2014

E-mail: Oliver.Lung@inspection.gc.ca

"Lung, Oliver (CFIA/ACIA)" <Oliver.Lung@inspection.gc.ca>

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3Dprinting magneticStand

Dear EvolDir community,

I would love to find out if any of you use magnetic stands for eppendorfs and pcr tubes? I know one needs to use them for e.g. RNA library prep, but the stands are ridiculously expensive . . . Did anyone try to print it with a 3D printer? If so, details on price, any potential 3D models etc. would be much appreciated. Also, how strong should the magnets be?

Looking forward to hearing from you all! All the best in 2018! :) All answers will naturally be shown later on, to help peer with similar issues.

Sincerely, Nik (lupsen@natur.cuni.cz)

–

"I don't care that they stole my idea . . I care that they don't have any of their own"â€Nikola Tesla

PhD Zoology candidate Room 225 Division of Animal Evolutionary Biology Department of Zoology Faculty of Science Charles University in Prague

ViniÄná 7, 128 44 Praha

Czech Republic

Nik Lupse <nik.lupse@yahoo.com>

3Dprinting magneticStand answers

Hi, a while ago I asked the EvolDir community to help me with an issue I had regarding 3D printing. Though magnetic stands are essential for library preps, the prices online are ridiculous. Fortunately, I was not alone in my struggle, and I received a variety of very useful answers. Please see enclosed. I hope they will help peer with similar issues. Thanks a million, and take care! Sincerely, Nik

—

Dear Nik,

I do not use magnetic racks regularly, but anyway here are my hints:

3D printing of magnetic stands:

https://www.thingiverse.com/ thing:79424

https://www.thingiverse.com/ thing:66281 https://www.thingiverse.com/ thing:90644

Here is a Russian company that produces relatively cheap magnetic racks:

https://translate.google.com/translate?sl=ru&tl=en&js=y&prev=_t&hl=ru&ie=UTF-8&u=http%3A%2F%2Fmagnoshop.ru%2Findex%2Fmagnitnye_shtativy%2F0-20& edit-text Although the site is in Russian (I've provided the link to Google translation), you can communicate with them in English.

Best regards,

Alexei.

–

Alexei Kostygov, PhD

Scientific Researcher

University of Ostrava

Chittussiho 10, 71000 Ostrava

Czech Republic

Tel: +420-597092340 (office)

+420-731422168 (cell)

Yeah, they are all pretty expensive. Haven't looked recently, but this was the cheapest on I found a couple years ago: http://www.bio-rad.com/en-us/sku/1614916-16-tube-surebeads-magnetic-rac k. Works fine.

Nate

-

Nathaniel K. Jue, Ph.D.

Assistant Professor

School of Natural Sciences

California State University, Monterey Bay

Seaside, CA 93955

Hi Nik,

I needed a 96 well magnetic plate and refused to pay $300 for one.

I made one using a plastic 96 well plate for 0.2 mL PCR tubes like this one (https://www.usascientific.com/Compact-PCR-tube-rack.aspx). I then used a drill press to drill holes at the center of each cluster of four wells (four holes in every-other row in the plate). I inserted cylindrical magnets into the holes like these (http://appliedmagnets.com/n48-neodymium-magnets-1-8-in-x-1-2-in-cylind er-p-723.html).

The resulting plate worked great and cost about $10 to make. You could extend this idea to any style of plastic rack.

Good luck!

Matt

Matthew B. Hamilton, PhD

Associate Professor

Georgetown University

Department of Biology, Regents Hall 506

37th and O Streets NW

Washington, DC 20057

202-687-5924 office 202-687-5662 fax

202-784-7105, 202-784-7181 lab

http://hamiltonlabpage.weebly.com http://reuenvscigeorgetown.weebly.com Dear Nik, I have ordered and constructed 3D-printed magnetic stands and I have been using them for 3 years now. The designs I got were from here: https://www.thingiverse.com/acadey/designs, both for 96-well plates and for eppendorfs. I had them printed and assembled with the magnets at Make Creative Spaces (Thessaloniki, Greece) and you can actually see them here: https://www.make.gr/en/portfolio-items/laboratory-equipment-biolab/ Regarding the magnets, we followed the instructions of the designer (acadey). We did this in 2014 and at the time, we paid for both stands with the magnets cost plus assembly plus shipping, so everything, around 400 euros. And I agree, commercial stands are ridiculously expensive for a piece of plastic. I hope this information helps! Dafni

Here's a link to a short article I wrote about the magnetic plates I printed (48 and 96 wells): http://www.jordanrbrock.com/blog/96-well-magnetic-separator-homemade It includes a link to the files needed to print it, but also check out thingverse.com for other magnetic plate and stand designs. Let me know if you have any questions, and good luck! Best, Jordan

Hi Nik, We bought neodymium magnets on the web and taped them onto other bits and pieces of lab kit and they worked pretty well. Takes a bit of time to get the angles right but does the job!

Best, Mark

You can buy small, very powerful "rare earth" magnets very cheaply online. To save even more money, ask all of your friends for their broken headphones (or collect them from the trash on the side of the road) and smash them open, there's a small powerful magnet inside each one. Drill holes in whatever scrap wood or plastic you have handy, glue

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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

Austria SummerFellowships

Summer Fellowships for Young Scientists at the International Institute for Applied Systems Analysis, Austria

Funding is available for PhD students interested in three months of collaborative research during June to August 2018 on

Evolutionary and Ecological Modeling

at the International Institute for Applied Systems Analysis (IIASA) in Laxenburg, Austria.

Young scientists from all countries are eligible for stipends provided by IIASA's Evolution and Ecology Program (EEP) that contribute to travel and accommodation costs. Students from most of IIASA's member countries - Australia, Austria, Brazil, China, Egypt, Finland, Germany, Indonesia, Iran, Israel, Japan, Korea, Malaysia, Mexico, the Netherlands, Norway, Russia, South Africa, Sweden, Ukraine, the United Kingdom, USA, and Vietnam - are eligible for fellowships that provide full coverage of travel, accommodation, and living expenses.

Model-based summer research projects are invited in the following indicative areas:

Evolution of cooperation Governance of common goods Systemic risk and network dynamics Eco-evolutionary dynamics Evolutionary community ecology Food-web evolution Vegetation dynamics Adaptive speciation Disease ecology and evolution Evolutionary conservation biology Fisheries management Fisheries-induced evolution Adaptive dynamics theory and models Spatial models in ecology and evolution

Applicants are encouraged to propose research that corresponds to their scientific interests and to EEP's agenda. Accepted applicants will begin work before the summer, by planning their research in collaboration with their IIASA supervisors. Previous experiences with implementing and studying evolutionary or ecological models are important assets for working in EEP. To improve chances of being selected, potential applicants are highly welcome to send informal inquiries regarding their specific research interests and plans to EEP's program director Ulf Dieckmann (dieckmann@iiasa.ac.at).

Online applications will be accepted until Thursday, January 11, 2018 (24:00 CET).

Since 1977, IIASA's annual Young Scientists Summer Program (YSSP), has attracted 1900+ students from 86 countries. The YSSP 2018 will take place from June 1 to August 31. IIASA is located in the former summer palace of Austria's imperial family, ca. 15 km south of Vienna. IIASA's summer program offers exceptional opportunities for acquiring experience in an international and interdisciplinary research environment. Research training is based on regular personal interaction with advising scientists, and typically leads to a publication in an international journal, as well as to a chapter in a candidate's PhD thesis.

Some useful links:

+ Information about IIASA's Evolution and Ecology Program http://www.iiasa.ac.at/eep + Details about the summer program, and online application http://www.iiasa.ac.at/web/home/education/yssp/Apply/ConditionsEligibility/Conditions-and-Eligibility.en.html + Examples of successful YSSP projects http://www.iiasa.ac.at/web/home/research/researchPrograms/EvolutionandEcology/AbouttheProgram/YSSP-in-EEP.en.html + General information about IIASA http://www.iiasa.ac.at/web/home/about/whatisiiasa/what_is_iiasa.html Ulf Dieckmann Program Director Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email dieckmann@iiasa.ac.at Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web www.iiasa.ac.at/Research/EEP Online reprints www.iiasa.ac.at/ ~ dieckman Google Scholar scholar.google.com/citations?user=rAcGGSgAAAAJ

DIECKMANN Ulf <dieckmann@iiasa.ac.at>

Dobzhansky Award Deadline Extended

The Theodosius Dobzhansky Prize is awarded annually by the Society for the Study of Evolution to recognize the accomplishments and future promise of an outstanding young evolutionary biologist.

The deadline for this award has been extended to March 1, 2018.

We consider candidates working on all areas of evolutionary biology, broadly defined. We are specifically looking for candidates that take creative approaches to answering pressing questions in evolutionary biology. We will consider people working on any taxonomic group (i.e., plants, animals, fungi, microbes, etc.) and who take empirical and/or theoretical approaches. We value diversity, and are seeking a broad and diverse applicant pool from all axes and components of diversity in the evolutionary biology community.

Each candidacy must be supported by the following materials detailing the candidate's career to date: (1) a curriculum vitae, (2) a summary of research accomplishments of up to 3 pages, (3) a statement of up to 4 pages of research plans for the next 5 years (note length limitation), (4) pdf copies of three recent publications, (5) names and addresses of the three referees (including the nominating scientist where applicable) who have sent supporting letters. N.B.: The three letters of reference are sent separately, but no application will be considered without these letters.

The application/nomination materials must be sent as PDF e-mail attachments, preferably united in a single file. All materials should be sent to the SSE Secretary (John Stinchcombe) at secretary@evolutionsociety.org.

Award - The Dobzhansky Prize is accompanied by a check for U.S. 000, and will be awarded at the annual meeting of the Society for the Study of Evolution, 2018, in Montpellier. The recipient is expected to be present to receive the award and to give an oral presentation about his/her research. To facilitate attendance, the SSE provides funds to cover the costs of conference registration, accommodation during the conference, and expenses for travel to and from the conference. The recipient will be notified of the award by late March 2018 or early April.

fuller@life.illinois.edu

DukeU UndergradInternBiomechanics Summer2018

Duke University: AEOP summer undergraduate internship - Biomechanics of Ultrafast Movements

The Patek Lab in the Biology Department at Duke University is recruiting one undergraduate student researcher through the US Army Educational Outreach Program (AEOP) during the summer of 2018. The student will participate in projects examining fast, impulsive movements of organisms in the natural environment. Possible focal systems for the project are trap-jaw ants and ballistic plants and fungi. Responsibilities of the student researchers may include collecting study organisms from local habitats, obtaining high-speed videos of organisms, analyzing high-speed videos using computer software, performing statistical analyses and scientific writing. The details of responsibilities and tasks will be determined based on mutual interests of the students and the mentors. There are also possibilities for the students to develop individual projects under our mentorship. Students in the URAP program receive an educational stipend equivalent to $15 per hour, and are allowed to work up to 300 hours total.

We are looking for motivated, reliable students who are excited about having first-hand research experience at the intersection of biology and physics. Previous experience performing the above-mentioned tasks are not required. We especially value students who are curious and hard-working. For more information about the Patek Lab, please visit our website: http://www.thepateklab.org. For more information about the URAP program see the AEOP website: http://www.usaeop.com/programs/apprenticeships/urap/ Application DEADLINE: Feb 28, 2018.

All applicants must submit transcripts, a resume, two letters of recommendation, and must have maintained a cumulative GPA of at least 3.2. Applicants must also include a brief essay that explains their interest in working with the Patek lab at Duke and how it relates to their future goals. Generic statements will not be considered.

TO APPLY: Please visit the URAP website: http://www.cvent.com/events/2018-undergraduate-research-apprenticeship-program-urap-/event-summary-efa00dc406b0454b908d11443a42ef70.aspx Select "Apply" at the bottom of the page - Fill out the forms - At "Please select your 1st preference of URAP location," please select "B453 Duke University"

Please direct questions to Postdoctoral Researcher Sarah Longo (sarah.longo@duke.edu)

"Sarah Longo, Ph.D." <sarah.longo@duke.edu>

ESEB AttendanceAidGrant

*** Equal Opportunities Congress Attendance Aid Grants ***

The European Society for Evolutionary Biology is pleased to announce the call for applications for the ESEB Equal Opportunities Congress Attendance Aid Grants 2018.

The grant aims to ensure equal opportunities at the Joint Evolution conference in Montpellier, France in 2018, e.g. by facilitating the attendance of women with caring responsibilities, who would not otherwise be able to attend. The grant provides stipends of financial aid for scientists to help with the additional costs borne privately due to responsibilities for dependents when attending the ESEB congress. The stipend will contribute to covering expenses for care of dependents, but also for travel.

DEADLINE: FRIDAY, 16 FEBRUARY 2018

ELIGIBILITY

- Applicants must be ESEB members (for becoming a member of ESEB please visit http://eseb.org/society/-membership/). - Applications can be submitted by scientists at any stages of their professional career (e.g., undergraduate, Masters and PhD students, postdocs, and lecturers). - Applicants must explain explicitly how their attendance will increase equal opportunities at the society - Applicants must present either an oral communication or a poster at the respective meeting to be eligible for the award. This will be verified before the reimbursement, but no proof that a poster or talk is accepted is necessary at the application stage. - Applicants must detail how they intend to use the grant. Eligible costs include, but are not limited to: childcare on site, childcare at home, extra care at home for dependents, extra travel costs for babysitter (grandparents) etc. - The stipend will be paid out as a flat rate of 250, - EUR (in certain cases up to 500, - EUR) after the congress when confirmation of attendance is provided.

HOW TO APPLY

The application should be no more than 2 pages long and include:

- Name of the applicant - An explanation of how attendance at the meeting improves equal opportunities at ESEB - An explanation of how attendance at the meeting will further the attendant's professional goals - Budget - CV

Please submit the application as a single PDF-file by email to Ute Moniatte <office@eseb.org, subject: EO conference grant at the ESEB Office and take care to limit the size of attachments (total < 10 MB) in any one email.

Kind regards, Ute Moniatte

Dr. Ute Moniatte | ESEB Office Manager| office@eseb.org

European Society for Evolutionary Biology | www.eseb.org ESEB <office@eseb.org>

ESEB ConferenceTravelAwards

**ESEB CONFERENCE TRAVEL AWARDS 2018*

The European Society of Evolutionary Biology (ESEB) is pleased to announce the call for applications for conference travel awards 2018.*

These stipends are for students and young scientists to attend the joint Evolution congress in Montpellier, France (http://evolutionmontpellier2018.org/). The stipend will consist of a waiver of the conference registration fee (early bird rate at registration and a contribution towards travel and living expenses (to be paid out as a reimbursement after the congress, based on specification of the expenses).

ELIGIBILITY: - Applicants must be ESEB members (for becoming an ESEB member, please visit www.eseb.org). - Applications can be submitted by scientists at various stages of their professional career (e.g., Masters and PhD students, postdocs, and lecturers). - Scientists working in a country with high GDP are not eligible (for the list of excluded countries see below). - People who received an ESEB travel stipend in the last five years are not eligible. - Applicants must submit to present either an oral communication or a poster to be eligible for the stipend. This will be verified before the reimbursement, but no proof that a poster or talk is accepted is necessary at the application stage.

PLEASE NOTE THAT THESE STIPENDS ARE GIVEN IN CONJUNCTION WITH ANALOGOUS STIPENDS OFFERED BY THE SSE (separate call), SO THERE IS NO NEED TO APPLY TO BOTH

HOW TO APPLY: Send your application by email to the ESEB Travel Bursary Committee, c/o Dr. Martijn

Egas, Email: egas@uva.nl

The application should be no more than 2 pages long and include:

- Name of the applicant; - Budget, including sources of additional support; - An explanation of how attendance to the meeting will support the attendant's professional goals; - and a CV.

Please submit the application as a single PDF-file. A support letter from the applicant advisor/mentor/senior colleague is also required. Support letters should be sent to the same email address (egas@uva.nl) by the applicant's mentor.

Deadline: 28 February 2018

Members professionally based in the following countries are not eligible for the travel stipend: Australia, Austria, Belgium, Canada, China, Croatia, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Israel, Italy, Japan, Luxembourg, Malta, Netherlands, New Zealand, Norway, Poland, Portugal, Singapore, Slovakia, Slovenia, South Korea, Spain, Sweden, Switzerland, United Kingdom, United States of America.

Dr. Ute Moniatte | ESEB Office Manager | office@eseb.org European Society for Evolutionary Biology | www.eseb.org ESEB <office@eseb.org>

ESEB outreachInitiative

ESEB Outreach Initiative Fund

The European Society for Evolutionary Biology (ESEB) welcomes applications to the ESEB Outreach Initiative Fund for projects that promote evolution-related activities. The goal of this initiative is to improve public knowledge about evolution globally.

Applications for funding will be accepted for educational initiatives that promote evolution, development of evolutionary material (books, films, web sites) intended for a general audience, public outreach seminars, public exhibitions, etc. While most projects will be financed for a sum between 1000-1500 Euro, exceptions can be made if a strong argument is provided for additional funds.

The application form can be found on the ESEB website (http://www.eseb.org/prizes-funding/outreach-fund/). Applications will be accepted twice yearly (deadlines March 15, September 15) and should be submitted by email to Ute Moniatte (office@eseb.org; Subject: Outreach).

Dr. Ute Moniatte | ESEB Office Manager| office@eseb.org European Society for Evolutionary Biology | www.eseb.org ESEB <office@eseb.org>

FieldMuseum Chicago NSF REU BiodiversityEvolution

NSF Research Experience for Undergraduates (REU) in the Evolution of Biodiversity across the Tree of Life

We are looking for 8 undergraduate students to participate in hands-on research in biodiversity science and receive training in cutting-edge techniques and analysis in evolutionary biology for 10 weeks during the summers of 2016-2018.

Students will learn research techniques that include DNA sequencing and computational analysis of genetic and genomic data, morphological measurements and phylogenetic analysis, and microbiology and next-generation microbial sequencing. Scientific projects to be conducted by the students include the morphological and ontogenetic variation in an African rodent, population genetics and blood meal identification of a parasitic catfish, coevolution of feeding morphology and taste receptors in fish-eating birds, Assessing genomic information to identify lichens, testing the causes of organismal diversification in the most species-rich lichenized fungi, wing morphology and dispersal ability in New Zealand water beetles, geographic variation in a widespread mullet fish, and diversity, evolutionary history and specificity of symbiotic microbes associated with turtle ants.

In addition students will receive career mentoring in a diversity of STEM fields, gain experiences in public outreach and science communication, receive training in ethics/responsible conduct of research, and participate in a diversity workshop to help overcome bias in science.

https://www.fieldmuseum.org/reu https://-www.fieldmuseum.org/2018-reu-program-offerings Students will be provided a stipend, dormitory housing, and assistance with travel costs.

Participants must be U.S. citizens or permanent residents, and an undergraduate during the entire period. We especially encourage students from groups traditionally underrepresented in science to apply.

To apply, please send complete the online application: https://www.fieldmuseum.org/reu Applications close April 22, 2016.

Please direct any questions to Emily Hallock (ehallock@fieldmuseum.org).

Please share widely.

Thank you, Corrie Moreau

Corrie Saux Moreau, Ph.D. Robert A. Pritzker Director of the Integrative Research Center and Associate Curator of Insects Department of Science and Education Field Museum of Natural History 1400 South Lake Shore Drive Chicago, IL 60605 USA Office: (312) 665-7743 Email: cmoreau@fieldmuseum.org Moreau Lab website: http://www.moreaulab.org/ FMNH website: http://fieldmuseum.org/users/corrie-moreau Field Museum Women in Science: http://fieldmuseum.org/-womeninscience Field Museum Integrative Research Center: https://www.fieldmuseum.org/integrative-research-center cmoreau@fieldmuseum.org

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GeorgetownU REUProgram EnvironmentalSciencePolicy

Dear Colleagues,

Please share this call for applications with interested students. Potential mentors work on a range of topics in areas of evolutionary biology, including behavior, evolutionary ecology, evolutionary genetics, mathematical and simulation modeling of biological systems, and extremophiles and exobiology.

Environmental Science and Policy in the Nation's Capitol

An NSF Research Experience for Undergraduates (REU) Program at Georgetown University

Summer 2018

Georgetown University's REU Site program in Environmental Science and Policy in the Nation's Capital is seeking talented and engaged undergraduate students. This ten-week program will bring a cohort of ten students to Washington, D.C. to conduct hands-on research in environmental science at Georgetown University and to take part in a mini-curriculum that builds research skills and also explores the intersections of science and public policy. Participating research mentors have expertise in fields including behavior, ecology, conservation biology, evolutionary ecology, evolutionary genetics, mathematical modeling of biological systems, statistics for environmental and biological studies, and earth science. See mentor research descriptions on the program web site. Interested students are encouraged to contact potential mentors directly.

The 2018 program will run from June 04 - August 12. Students will be housed on the Georgetown campus and will receive a $5500 stipend plus an allowance for travel and food. To be eligible, applicants must be U. S. citizens or permanent residents, a full-time student as of August, 2018, and available to participate full-time during the program. We are striving for a diverse group, so students from groups typically underrepresented in STEM fields are strongly encouraged to apply.

Review of applications will begin on February 19, 2018 and will be accepted on a continuing until all positions are filled.

For more information on the program and to apply, visit: http://reuenvscigeorgetown.weebly.com For inquiries, contact the principal investigator Dr. Matthew B. Hamilton (matthew.hamilton@georgetown.edu), or co-principal investigator Dr. Martha Weiss (weissm@georgetown.edu).

hamiltm1@georgetown.edu

Geum Primula RequestForSamples

Hello,

We need samples of two perennial wildflowers, the wood avens /Geum urbanum /(Fam. /Rosaceae/) and the oxlip /Primula elatior/ (Fam. /Primulaceae/). These species, common in most of Europe and parts of Asia, grow in damp shady habitat; they can be found in broadleaf woodlands and near/in hedgerows. Regarding the sampling protocol, this is simple. We only need one individual sampled per population. A population is here defined as any isolated individual or cluster of individuals which are distant of about 10m from the next isolated or cluster of individuals. To sample a population, just collect the 5 to 10 youngest leaves of a single rosette (individual) of /G. urbanum vs. P. elatior/ within the population. Collect only safe leaves (no hole or sign of herbivory, no chlorosis or virus attack). Put the fresh leaves in an envelope (standard small paper envelope) with GPS coordinates of that population written on the envelope or at least the name of the locality but lat/long coordinates is the best (one enveloppe per population). If you could then collect several populations (15 would be ideal, so 15 envelopes total) from the same forest patch but which are not too close from each others (cf. populations >10m away), this would be optimal. The idea is to collect several (when available) populations from a given forest patch so that the sample is representative of the sampled forest patch. For hedgerows (linear sampling) and especially for /G. urbanum/ which is most common and abundant than /P. elatior/, sampling can be done every 50m.

When finished, please put all collected populations from the sampled forest patch or hedge (cf. all envelopes with coordinates written on it) in another bigger envelope and send it to this address:

Prof. Annie Guiller

Edysan UMR 7058 CNRS - UPJV Laboratoire BIPE, Bâtiment des Minimes 33 Rue Saint-Leu, 80000 Amiens FRANCE

Thank you for your help.

Annie

Annie GUILLER EDYSAN UMR CNRS 7058 - UPJV 33 rue St Leu 80000 Amiens France Tel. : 33 (0)3 22 82 75 56

annie <annie.guiller@u-picardie.fr>

GlobalUrbanEvolutionProject Collaborators

Dear Evoldir community:

We are seeking collaborators to participate in the Global Urban Evolution (GLUE) Project, a large-scale study that seeks to understand whether urbanization drives parallel evolution in cities throughout the world. This project focuses on a single species (white clover, Trifolium repens), which is common in temperate environments globally. It is one of the few species where one could study the effects of urbanization on every inhabited continent.

We are inviting individuals subscribing to this list-serve to participate as collaborators on the project. You can learn more about the project, including what is involved for collaborators at www.globalurbanevolution.com. You can also find on this website whether your preferred city is already being sampled.

Please let us know if you have any questions about GLUE and how to get involved.

Sincerely

Marc Johnson James Santangelo Simon Innes Cindy Prashad Rob Ness

Marc T. J. Johnson, Ph.D. Director, Centre for Urban Environments (CUE) Associate Professor Depts. of Biology & EEB University of Toronto 'V Mississauga www.evoeco.org (lab) www.urbanenvironment.ca (CUE) www.globalurbanevolution.com (GLUE) twitter: @evoecolab twitter (CUE): @CUE_UofT

Marc Johnson <marc.johnson@utoronto.ca>

Hydra-2 0-GenomeProjectPortal

Hi, all 'V

In an effort to make genome-scale data resulting from the recent new assembly of the Hydra vulgaris genome widely and easily available, we are pleased to announce the launch of the Hydra 2.0 Genome Project Portal, available at http://research.nhgri.nih.gov/hydra . The web site features a customized, interactive genome browser that allows users to visualize multiple data sets at the same time, greatly facilitating the analysis of the genome. Users also have the ability to run BLAST searches against the Hydra genome, download complete sets of Hydra sequence data, and view individual gene wiki pages that contain additional information on each gene model. Transcriptomic data have also been provided by the laboratories of Celina Juliano (University of California, Davis) and Thomas Holstein (Centre for Organismal Studies, Heidelberg University), for download or visualization through the genome browser. In addition, a growing collection of in situ hybridization images are being added to individual gene pages, and we encourage members of the Hydra community to submit their own in situ images for inclusion on the site.

We hope that the availability of these data will be helpful to everyone with an interest in cnidarian biology, and we certainly welcome any comments or feedback you have regarding the site.

Best regards,

Andy Baxevanis, National Human Genome Research Institute, NIH Christy Schnitzler, Whitney Laboratory for Marine Bioscience, University of Florida Rob Steele, University of California, Irvine andy@mail.nih.gov

Interview blog

My name is Hari Sridhar and I'm a post-doctoral researcher at the Centre for Ecological Sciences, Indian Institute of Science. Since early 2016, I have been conducting a series of interviews of ecologists and evolutionary biologists. In each interview, I revisit an old "well-known" paper in ecology/evolution/behavior, with the primary author, to find out about 1. the making of the paper 2. the impact the paper had on the author's career and research and 3. the author's current stand on what was said in the paper. The idea is to construct, what one might call, 'shadow papers', which capture the past and future of the original published articles. This is an ongoing project, and I will post new interviews as and when they are ready. The interviews are now all available at https://reflectionsonpaperspast.wordpress.com/ This is an ongoing project and I will post new interviews as and when they are ready.

Thank you.

Regards, Hari

Hari Sridhar <harisridhar1982@gmail.com>

Manipal India SummerIntern EvolBiol

SUMMER RESEARCH INTERNSHIPS: (SRI2018)

Start Date: Monday 04^th June, 2018

End Date: Saturday 14^th July, 2018

Venue: Manipal Centre for Natural Sciences, Manipal Academy of Higher Education, Dr. TMA Pai Planetarium building, Madhav Nagar, Manipal 576 104, Karnataka, India

Applications are invited from outstanding students for the Summer Research Internship (SRI2018) Program at the Manipal Centre for Natural Sciences (MCNS), Manipal Academy of Higher Education, Manipal, Karnataka. MCNS carries out fundamental research in the natural sciences.

The SRI Program is an annual event which runs for 6 weeks over the summer.

Opportunities for SRI2018 are available in the following research areas:

- Paleontology and Stratigraphy
- Evolutionary Biology
- Computational Biology

Selections are highly competitive and only a limited number of supported internships are available.

Support for internships includes:

- A consolidated stipend of Rs. 15,000/-
- Free shared, on-campus hostel accommodation

Who can apply:

Highly motivated students currently enrolled or completed M. Sc./ M. Tech./ fourth year integrated M. Sc./ M. Tech. programs and highly motivated third or fourth year B. Sc./ B. Tech. students may apply.

How to apply:

- Application form is available from https://-manipal.edu/mu/academics/centers-of-excellence/mcns-manipal/mcn s-manipal-news/mcns-manipal-events-list/summer-research-internships-201 8.html.
- Filled Application form in a single PDF file must be sent by email to sri@manipal.edu on or before 29^th April 2018.
- Two letters of recommendation (to be sent to the above e-mail address) from referees, who have taught you or are familiar with your academic work.
- List of selected candidates will be uploaded to this website by 5^th May, 2018.

Contact: Dr. Ranajit Das

The Coordinator Summer Research Internship Program (SRI2018) Manipal Centre for Natural Sciences Dr. T.M.A. Pai Planetarium Building Manipal University, Manipal - 567 104, Karnataka

Email: sri@manipal.edu Telephone: +91 820 2923571

Mobile: +918582802871

"Ranajit Das [MAHE-MCNS]" <ranajit.das@manipal.edu>

MaxPlanckInst Seewiesen AvianMatingStrategies Volunteer

MaxPlanckInst_Seewiesen.AlternativeMatingStrategiesRuffsVolunteers

Where: Simon Fraser University, Burnaby, Canada When: 10 May - 10 August What: Volunteers Research Assistants

The Research Group of Behavioural Genetics and Evolutionary Ecology at the Max Planck Institute for Ornithology in Seewiesen, Bayern, Germany (see http://www.orn.mpg.de/3731861/Research_Group_Kuepper), is seeking a volunteer to assist with aviary work during the breeding season of captive Ruffs from 10 May until 10 August 2018. This work will be part of a project that aims to understand the proximate and ultimate mechanisms involved in alternative mating strategies in Ruffs.

The work will be conducted at Simon Fraser University, Burnaby, Canada. The position will suit undergraduate (or recent graduate) students with an interest in evolutionary and behavioural biology, endocrinology and/or developmental biology. The volunteer will have the opportunity to experience lekking Ruffs at close hands in a unique captive setting, gain experiences in handling animals, conducting experiments and learn about sexual selection, fascinating mating behaviour and aviculture.

The volunteer will assist with animal care (egg collection, feeding and weighing of chicks, occasional cleaning of the aviaries), blood and tissue sampling and data management and will help run mate choice trials.

Successful candidates should be highly motivated and well organized, with capabilities of working in a team and with task assigned independently. The volunteer will be included into the staff work rotation that consists of six working days per week that often start early in the morning and during the peak periods can continue until late at night. Experience with handling animals is desirable.

The working language is English, and we expect a good command of the language of all applicants. Eligibility is restricted to UK and EU students. We can only consider applicants who are willing to participate for the entire three months period in the project.

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 cover basic costs for food and accommodation and travel-related expenses to Canada.

If you are interested in applying for the volunteer positions as described above, please apply (including your CV and cover letter) via email to lgiraldo@orn.mpg.de.

Review of the applications will begin on 15 February 2018 until the position is filled.

Lina María Giraldo Deck Department of Behavioural Genetics and Evolutionary Ecology Max-Planck-Institute for Ornithology Eberhard-Gwinner-Straße, House 5 82319 Seewiesen Germany

"Giraldo Deck, Lina Maria" <lgiraldo@orn.mpg.de>

MolluscSystematics Grant

COA Academic Grants Program 2018 Deadline: February 28, 2018 Eligibility: please see the website: http://www.conchologistsofamerica.org/grants/ - Degree-seeking students and anyone engaging in malacological research is eligible. Typically, 80'V90% of applicants are degree- seeking students, and 80'V90% of award recipients are degree- seeking students. - Persons of any nationality and country of residence may apply. - Applicants from previous years may re-apply. - Recipients of previous years may re-apply, but must include a submitted manuscript to or published article in the American Conchologist based on the previous award. - Degree-seeking students must have a letter of recommendations by their advisor emailed to jannvendetti@yahoo.com by the Feb. 28th deadline with the applicant's name is the subject line.

Rules & Guidelines: - All submissions must be submitted via email as a .doc, or .pdf., preferably in one file. Keep file size under 3 MB. - The proposal must concern a malacological topic with any molluscan taxon or taxa as the focus, e.g., parasite studies should focus on the molluscan side of the interaction. All disciplines from autecology to zoogeography, including paleontology, are eligible. - The project must be self-contained. In other words, with the funding requested it must be possible to answer the question posed. However, the proposal may be a component of the applicant's overall research. - Permanent equipment is not an allowable expense. Time using a piece of permanent equipment (for example, SEM beam time) is allowable. - Institutional overhead is not permitted. - The maximum award is $2500 US. Smaller amounts can be requested and may be more likely to receive funding. Partial funding is possible at the discretion of the Academic Grants Committee. - If a grant is awarded, please consider options to avoid having to pay personal income tax on it (US citizens and residents must provide their social security number if given award and paid individually.). Many educational and non-profit organizations manage such grants; please inquire with such entities. COA and/or its representatives are not liable for any tax consequences of the award. - All recipients are expected to submit a summary of their work to American Conchologist within 12 months of receiving the award. - All applications are evaluated by the Academic Grants Committee composed of three professional malacologists appointed by the Chair of the COA Academic Grants program. - The decisions of the Committee are final.

Application: Must include 3 components: a proposal, budget, and CV. Proposal (2-4 pages): - title - abstract of project, not to exceed 150 words - body including background information necessary to understand the project and its significance, materials and methods, and proposed plan of research, and illustrations if necessary - literature cited - single-spaced, 12 point font Budget (1 page): - list of estimated expenses - list of grants applied to for same/similar project CV/Academic Biography (I page): - include address, phone number, email address of applicant, academic and/or relevant professional history

Suggestions: Keep the introduction short and relevant; consider that all committee members are broadly trained invertebrate zoologists. Provide justifications and details of analytical procedures including statistical analysis (which tests will be used and why those tests). Provide evidence that the techniques proposed are relevant and reasonably mastered. The inclusion of preliminary data is helpful, when applicable.

Applications are judged by the COA Grants Committee. Awardees will be notified via email in May, 2017, then announced at COA's annual convention (in Key West, Florida Aug. 13-19, 2017). Awardees need not be present at the convention.

THE DEADLINE FOR APPLICATIONS IS FEBRUARY 28 All application materials must be emailed as electronic documents to: jannvendetti@yahoo.com

Jann Vendetti, Ph.D. Assistant Curator & Twila Bratcher Chair in Malacology Natural History Museum of Los Angeles County 900 Exposition Blvd. Los Angeles, CA 90007 jannvendetti@yahoo.com

Jann Vendetti <JVendett@nhm.org>

Phyloseminar JosefUyeda Feb23

Next on http://phyloseminar.org/ :

On the need for phylogenetic natural history Josef Uyeda (Virginia Tech) Friday, February 23, 2018, 9:00 AM PST

The availability of phylogenetic trees based on molecular sequence data has revolutionized evolutionary biology by providing a map from which we can understand divergence and diversification across the tree of life. Numerous phylogenetic comparative approaches have opened up new avenues for testing macroevolutionary hypotheses regarding the drivers of the tempo and mode of trait evolution and lineage diversification. However, recent crises in the field have suggested that many of the methods we commonly use don't tell us what we would like them to. Specifically, I will show that unreplicated evolutionary events can break nearly every comparative method for testing associations from phylogenetically structured data. I will argue that one solution to this problem is to unite hypothesis testing with data-driven approaches, which I term "phylogenetic natural history", to disentangle the impact of singular shifts from replicated patterns of association. More generally, I will argue that we should abandon thinking of phylogenetic comparative methods as "corrections for statistical non-independence" and more meaningfully confront how our causal hypotheses map on to phylogenetically structured data.

– Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ Erick Matsen <ematsen@gmail.com>

Phyloseminar JoshuaSchraiber Jan17

Next up on http://phyloseminar.org/ ...

Applications of phylogenetic continuous trait models to gene expression Joshua Schraiber (Temple University) Wednesday, January 17, 2018, 10:00 AM PST

Historically, quantitative genetics was developed to understand macroscopic phenotypes, such as body mass.

However, with the advent of high throughput genomics technology, we now have access to extremely high dimensional molecular phenotypes. One of the most common traits analyzed is gene expression, measured via RNA sequencing in modern applications. I will attempt to put this work in historical context, highlighting some early work on building models of neutral gene expression evolution, which poses unique challenges in a phylogenetic comparative framework. I will also discuss some work, including my own, that attempts to leverage the dimensionality of gene expression data to increase power. Finally, I will conclude with some perspectives on future directions for analysis of molecular phenotypes in a phylogenetic context.

Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ Erick Matsen <ematsen@gmail.com>

PortlandStateU REU PlantGenomics

NSF Research Experience for Undergraduates (REU) in Plant Ecology and Genomics

We anticipate having funding for one or two enthusiastic students interested in enhancing their research skills and experience in plant ecology, genomics, and bioinformatics in the Cruzan lab at Portland State University in Portland, Oregon.

Successful applicants will become part of a research team working on dispersal and gene flow in upland prairie plants in Oregon and Washington under pressure from climate change. Dispersal is critical for colonization, gene flow, and range expansion 'V it is one of the most important but least understood aspects of the ecology of plants. Our research utilizes genomic techniques to detect the effects of dispersal over different spatial scales. This is an integrative research program that includes field work, wet lab preparation of genomic DNA for next-generation sequencing, bioinformatics processing of sequence data, and analysis of patterns of gene flow using GIS and landscape genetic methods. Students will be exposed to a wide range of methods and are expected to develop an independent research project within the scope of the larger research program. More information on our research is posted on our lab web site: https://cruzanlab.weebly.com/ . Students will be fully supported for 10 to 12 weeks during the summer of 2018. Funding is provided from an REU supplement to our National Science Foundation Macrosystems Biology grant. Housing will be provided on campus along with a daily allowance for food and a $500 weekly stipend. The start of the REU is negotiable with optimal start dates between May 1 and June 17.

To apply please email us an updated copy of your CV (including GPA) and a short (one page) statement of your research interests and experience, as well as goals for your education and career. Applicants should arrange to have one or two faculty members provide a letter of recommendation (email is fine). Students with experience in computer programming and/or bioinformatics are encouraged to apply. Application deadline is 29 February 2016. Feel free to email us with questions.

Pam Thompson, Postdoctoral Research Associate: thompson@pdx.edu

Mitch Cruzan, Principle Investigator: cruzan@pdx.edu

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Mitch Cruzan Professor of Biology Portland State University PO Box 751 Portland, OR 97207 USA Web: http://web.pdx.edu/~cruzan/

RockyMountainGroundSquirrel Intership

We are looking for 4 interns interested in taking part in a field ecology project on Columbian ground squirrels. Two interns will begin Apr 10, 2018 and two will begin May 1, 2018. All four internships will finish on Aug 31, 2018. The project investigates the ecology of Columbian ground squirrels. As a member of the study, interns will be involved with monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals. Fieldwork will involve live-trapping and handling of animals, radio-telemetry, behavioural observation and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. This is an excellent opportunity to gain training and experience working with a collaborative research team on a long-term study of a wild mammal. Opportunities for independent research projects are also available.

All fieldwork is carried out in the spectacular Rocky Mountains of southwestern Alberta, Canada, home to some of the most majestic wildlife in North America.

Interns will have the opportunity to interact with, and learn from, other researchers working with ground squirrels on a diversity of projects in behavioural and population ecology. Additionally, a number of other researchers in the area are studying a range of species, from insects to large mammals.

International applicants: If applicants are not Canadians or permanent residents, they will be required to apply to enter Canada as Visiting Research Students. This is a simple and straight-forward procedure and both current (graduate and undergraduate) and recently graduated (i.e. 'in between' degrees) students are eligible. Application forms and information are available at http://grad.usask.ca/admissions/alternate-applicants/visiting-research-student.php If you are interested in this program, please contact us (contact details below) and we will guide you through the process.

Skills Required: These positions are best suited to applicants with interests in ecology, evolutionary biology, wildlife, field biology, and/or physiological ecology. As evidence of this, applicants must either be enrolled in, or have graduated from, a relevant discipline. Successful applicants will need to be able to cope under these field conditions (including periods of time spent camping), enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team. Evidence of these abilities (gained, for example, through previous involvement on field projects or extended back-packing trips) is desireable.

Terms of Employment: These are volunteer positions and a salary is not provided. Accommodation and food are provided. Volunteers are required to provide for their own travel to Saskatoon, Saskatchewan. Travel between the field station and Saskatoon is provided.

If you wish to apply for one of these posts then please send a CV with a cover letter and contact details for three references (with e-mail addresses), by email to Jeff Lane (contact info below) by January 31, 2018.

Contact:

Dr. Jeff Lane

Department of Biology

University of Saskatchewan

usaskcgsproject@gmail.com

www.lanelab.ca "Lane, Jeffrey" <jeffrey.lane@usask.ca>

SMBE2018 ExtensionDealine

Dear All,

We are glad to have received numerous abstract submissions for SMBE 2018. Appreciating the strong interest, the deadline has been extended!

Final abstract submission closing date: Thursday, February 1, 2018

Don't miss this opportunity - be involved in the meeting's scientific program by submitting your abstract here. Please email us at smbe2018-p@jtbcom.co.jp for any questions.

SMBE 2018 Website < http://smbe2018.jp >

< http://smbe2018.jp/cf_abstract.html > | Call for Abstracts

< http://smbe2018.jp/awards.html > | Award

< http://smbe2018.jp/registration.html > | Registration

Professor Koichiro Tamura

Chair, Local Organizing Committee, SMBE 2018

"takezaki@med.kagawa-u.ac.jp" <takezaki@med.kagawa-u.ac.jp>

SMBE CallNominationsBestStudentPaper

Society for Molecular Biology & Evolution

Best Graduate Student Paper of 2017

Dear SMBE Members: SMBE is calling for nominations for Best Graduate Student Paper of 2017. These awards provide recognition for outstanding student papers in both SMBE journals. All articles published in the calendar year 2017 in the two SMBE journals, Molecular Biology & Evolution (MBE) and Genome Biology & Evolution (GBE), are eligible for nomination. This corresponds to papers published in the printed volume 34 in MBE and volume 9 in GBE. The best student paper winners will be given a certificate, a prize of $2,000 and a travel award to the next annual meeting. Best Regards, Bill Martin President, SMBE

Eligibility & Nomination 1. All articles published in the two SMBE journals, Molecular Biology & Evolution and Genome Biology & Evolution (one prize for each journal), in the calendar year 2017 are automatically eligible if the final publication date of the nominated paper is not more than two years later than the date of the nominee's PhD. 2. The nominated early-stage researcher must be the first author or joint first-author of the nominated paper. 3. An article and its first author can be nominated by anyone, including the first author. 4. A signed letter from the PhD advisor, MSc advisor, or equivalent, confirming that the paper was part of the nominee's thesis or graduate work is required. 5. The deadline for submitting nominations is March 11, 2018.

How to Enter Please send the name of the nominee, a scan of the signed advisor letter, and the name of the paper for which the award is to be considered as a SINGLE PDF to tleatherman@allenpress.com. If possible, please denote if the paper was published in MBE or GBE.

Society for Molecular Biology & Evolution smbe@allenpress.com

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

Smithsonian CollectionResearchGrants

Hello All,

We are pleased to announce a new graduate student fellowship available at the Smithsonian National Museum of Natural History (NMNH) - The Kenneth Jay Boss Fellowship. This fellowships provides financial support to graduate students to conduct collections-based research in the Department of Invertebrate Zoology (IZ) at SI-NMNH.

Eligibility Fellowships are available to currently enrolled graduate students engaged in collections-based research (e.g., systematics, phylogeny, biogeography, comparative morphology, species conservation). Students seeking support for conducting molecular studies at the museum should consider applying to other fellowship programs.

Both US and non-US citizens are eligible; applicants must write and converse well in English. Local investigators (based in the Washington, D. C. metropolitan area) are not eligible for these fellowships.

Applicants must contact an IZ research scientist to serve as the fellowship advisor well in advance of submitting their application (list here http://invertebrates.si.edu/-1IZstafflist.htm).

Resources The Department of Invertebrate Zoology can provide access to imaging facilities equipped with standard, low vacuum, environmental and field emission scanning electron microscopes, a microfocus X-ray computed tomography scanner, a compound fluorescent microscope, and digital microscopes with z-stacking capabilities; a histology lab equipped for paraffin sectioning and whole mount preparation; standard dissecting and compound microscopes. Fellows will also have access to the main NMNH Library and the specialized library collections in the department.

How it Works The fellowships are awarded preferentially to students investigating mollusks, although proposals focused on other invertebrate groups (exclusive of insects, arachnids, and myriapods) will also be considered and are encouraged.

Fellowship proposals are solicited biannually for projects ranging from one week to three months (no more than six months); the awards provide a stipend to cover housing and subsistence while visiting the museum.

The number of fellowships to be awarded each review cycle will depend on the quality of proposals and available funding.

Awardees must be in residence in the Washington, D.C. area and spend a significant amount of time working in the Department of Invertebrate Zoology during their fellowship tenure.

How to Apply All application materials should be sent to the Chairman of the Department of Invertebrate Zoology (Dr. Ellen Strong, stronge@si.edu) by email in pdf format. Applications that do not conform to the guidelines will not be considered.

For more information on how to apply please see https://www.smithsonianofi.com/kenneth-jay-boss-fellowship-in-invertebrate-zoology/ I am happy to answer any questions about this fellowship or contact Ellen Strong.

Cheers - Karen

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

Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163

P.O. Box 37012, Washington, D.C. 20013-7012 USA

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

"Osborn, Karen" <OsbornK@si.edu>

SocStudyEvol SmallOutreachGrants

Society for the Study of Evolution (SSE) < http://www.evolutionsociety.org/ > Small Grants Program for Local and Regional Outreach Promoting the Understanding of Evolutionary Biology

This is a call for proposals for support for local and regional educational outreach activities to take place during 2018. It is our hope that these projects will lead to ongoing outreach collaboration in future years. Preference will be given to new collaborations, but extensions of previous projects that have evidence of success are allowed. *Proposals will be accepted until January 25, 2018.*

Guidelines for applying for funds to support SSE 2018 outreach projects are as follows:

1. Proposal: Clearly but briefly state your plans in NO MORE THAN one single-spaced page. 2. Amounts requested may be up to $1000. Include a short justification for the use of the funds. Indicate any additional matching funds and include letters of commitment from collaborative partners. NOTE: Projects under $500 will receive funds upon award. Projects from $500 - $1000 will receive funds upon completion of the project and submission of receipts. 3. Send your request by email attachment (subject heading 'SSE Outreach 2018') to Robert Pennock [pennock5@msu.edu] no later than 25 January 2018.

Applications will be ranked by an SSE Education Committee working group according to the following criteria:

1. Clarity and quality of the proposed activity; 2. Expected impact in terms of reaching a critical or broad audience; 3. Evidence, in the form of matching funds, of partnership outside of your immediate academic department; 4. Indication as to how the project might lead to new or ongoing successful outreach collaborations.

We expect to fund in the range of 10-20 applications, with announcement of awards to take place by February 8, 2018.

Examples of past outreach activities have included public lectures, exhibits, student competitions, and professional development events for teachers. We especially encourage proposals that focus on discussing and implementing evolution education reforms recommended in the *Vision & Change in Undergraduate Biology Education: Chronicling Change, Inspiring the Future* (2013) report http://visionandchange.org/files/2015/07/VISchange2015_webFin.pdf or on dialogues between undergraduate instructors and K-12 teachers around the new emphasis on evolution in the *AP Biology Curriculum Framework* (2015) https://secure-media.collegeboard.org/digitalServices/pdf/ap/ap-biology-course-and-exam-description.pdf and the *Next Generation Science Standards * http://www.nextgenscience.org/next-generation-science-standards . We look forward to your applications!

Even if you are not interested in applying for funding from the SSE, we encourage you to engage through whatever means are at your disposal in opportunities to promote public understanding of evolutionary biology.

Sincerely,

Robert T. Pennock Chair, SSE Education Committee Outreach Grants Program

communications@evolutionsociety.org

SouthAfrica VolFieldResAssist SocialMoleRats

SouthAfrica.VolFieldResearchAssistant.SocialMoleRats

Cooperative breeding in Damaraland mole-rats (Fukomys damarensis).

We are looking for voluntary field research assistants to get involved with our research on the completely subterranean, highly social Damaraland mole-rat (Fukomys damarensis) in the Kalahari (South Africa). We are conducting a long-term capture-mark and recapture study, based at the Kalahari Research Centre, to investigate the life-history and social behaviour of Damaraland mole-rats (http://kalahari-meerkats.com/kmp/research-publications/damaraland-mole rats-group/). Entire groups of mole-rats will be captured and individually marked. Morphological measurements and tissue samples will be obtained before the release of the animals. The field work is physically demanding and weather conditions are challenging (heat during the day, cold during the night). Field work may make trapping during the night necessary. The assistants will mostly be working in teams of two but will be embedded in a large research community. This position requires working in a small team in a remote location on free ranging animals. The trapping season will start in Mid-March and last for 3 months. Research assistant will require a valid driving license.

Accommodation is provided, and research assistants are paid a monthly allowance to cover their personal costs and food.

We will review applications as they arrive. Please apply at latest the 8th of February. Please apply by email or contact for further information: Dr Markus Zottl, University of Cambridge, mz338@cam.ac.uk

Markus Zoettl <mz338@cam.ac.uk>

SouthAfrica Volunteers RiverPipefishConservation

Volunteer position: river pipefish conservation

We are looking for volunteer research assistants/interns to participate in a diving survey, genome screening and/or establishment of a captive breeding population of one of Africa's rarest coastal fish species, the critically endangered river pipefish, *Syngnathus watermeyeri*.

This small pipefish was believed to have become extinct at the end of the 20th century, but a small number of survivors has subsequently been found in some of the estuaries in its small range in the Eastern Cape Province, South Africa (https://en.wikipedia.org/wiki/-River_pipefish). However, it is presently hanging on by a thread, and the survivors are believed to be highly inbred, and at great risk of imminent extinction.

This position is particularly suited for, but not limited to, young researchers wishing to gain experience in a wide variety of conservation-related fields. Successful applicants can choose their level of involvement, which may include participation in diving surveys (including mark-and-recapture), DNA laboratory work and unix-based data analyses (at the University of Johannesburg), and the establishment of a captive breeding population (at uShaka Marine World in Durban).

The first field survey is expected to take place in late March 2018. The costs for food, accommodation and diving equipment during the fieldwork will be covered. Participants have to arrange travel to and from the study site themselves. Subsequent surveys will take place approximately every 6 months for the next 3 years.

If you are interested in this position, please send a letter of motivation and a short CV highlighting skills and interests relevant to the project to Prof. Peter Teske, University of Johannesburg (prteske@uj.ac.za). Please also provide contact details of at least 3 referees.

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Prof. Peter Teske

Department of ZoologyUniversity of Johannesburg, Kingsway CampusAuckland Park 2006South AfricaTel +27 (0)11 559 3373

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For courier shipments: D3 LAB 339 (D LAB building on the far right (seen from D RING), two floors up, turn right through the glass door, last entrance on the left) Department of Zoology University of Johannesburg, Kingsway Campus (APK) Corner Kingsway and University Rd. Auckland Park 2092 Email: pteske101@gmail.com Tel.: 011 559 3373

Lab website: http://sites.google.com/site/-drpeterteske/ Peter Teske <pteske101@gmail.com>

Spain VolunteerOrnithology Apr-Jun

Between April and June 2018 we will run our yearly intensive research campaign in our starling colony, 50 kms from Madrid. Around 250 nest boxes are almost daily followed through the two sequential broods that most nests obtain. Field work includes capturing adult birds for measuring and sampling, follow-up of reproduction (egg laying, hatching and fledging), ringing nestlings, setting-up of microchip readers to assess parental care..., as well as other activities related to the specific experiments running in each year.

The field site is a pleasant and undisturbed woodland, an hour from Madrid. Several researchers, PhDs and master students take part in the field work, but to be able to run it properly, we count with the help of a few volunteers every year. We provide free accommodation for volunteers in a nearby field station, transport to and from the field site, and a fantastic team-work atmosphere. We are happy to consider volunteers for any periods of time starting from a minimum of 2 months.

Please contact us asap if interested in taking part in the 2018 campaign, attaching your CV and a short personal statement of your interests, together with the emails of two academic or professional references that could support your application.

www.behavecol.es/en Please contact: diego.gil@csic.es

Dr. Raquel MonclÃºs

Departement d'Ecologie, Systématique et Evolution

Bât. 362, rue André Guinier

Université Paris-Sud

91400 Orsay

FRANCE

SystematicsResearchFund Deadline Feb15

The Councils of the Linnean Society (https://www.linnean.org/) and the Systematics Association (http://www.systass.org/) jointly administer the Systematics Research Fund (SRF) that provides grants annually for small-scale research projects in the field of systematics.

Typical activities supported include contributions to fieldwork expenditure, the purchase of scientific equipment or expertise (e.g. buying time on analytical equipment), specimen preparation (including the cost of temporary technical assistance), and contributions to publication costs. However, please note that it is unable to fund the cost of article publication charges. Projects of a more general or educational nature will also be considered, provided that they include a strong systematics component. Typical activities not supported include attendance at scientific meetings and contributions to student maintenance or tuition fees. The fund does not provide payments for Bench Fees. Projects already substantially funded by other bodies may be disadvantaged.Applications of all nationalities are welcome but applicants must be a current member of the Systematics Association or Linnean Society of London. Successful projects are selected by a panel of systematists who represent a wide range of conceptual interests and taxonomic groups. Generally, applications in the range of 500-1,000 are preferred, the value of any single award will not exceed 1500.

Deadline 15 February 2018

More information on SRF on the Systematics Association webpage: http://www.systass.org/awards/srf.shtml Questions about the application procedure can also be sent to the SRF Administrator (srf@systass.org)

Dr. Anne D. Jungblut Grants & Awards Secretary for SRF The Systematics Association

Anne Jungblut <a.jungblut@nhm.ac.uk>

TeachingEvolution VisuallyImpaired answers

Evoldir folks,

Many thanks to those who responded to my question regarding teaching material for blind students in General Biology. Below are ideas that we use/will try this semester here at Wichita State, followed by links provided by the EvolDir community. A general trend seems to be a lack of existing biology materials, even fewer for university level, and fewer still for evolution/ecology topics. There is an opportunity for someone with 3D printing design experience to really be an angel here. Not that I believe in angels.

Thanks and Happy New Year! James Beck Wichita State University www.becklaboratory.com/James —-

Quick Draw tactile Paper ($3.50 per page) raises up right along your pen lines. Its a good tool for relating graphs/microscopic images one-on-one with students: shop.aph.org/webapp/wcs/stores/servlet/Product_Quick-Draw%20Paper_38396074P_10001_11051

In a pinch, modeling clay is another option for making one-on-one tactile learning tools.

This book of tactile and brailled graphics is quite basic (designed for high school) but useful as a starting point for many general biology topics: http://shop.aph.org/webapp/wcs/stores/servlet/Product_Life%20Science%20Tactile%20Graphics%20-%20ON%20SALE_1-08840-00P_10001_11051 Were also going to attempt 3D printing of some items this semester. The thingiverse website has open access designs, but there appear to be relatively few for general biology, and most of these are cellular/molecular biology. Some examples: thingiverse.com/thing:1259352 thingiverse.com/thing:202079 thingiverse.com/thing:956013 thingiverse.com/thing:2695890 thingiverse.com/thing:1565917 hingiverse.com/thing:714312

Thingiverse also has an education section, but I havent explored it: thingiverse.com/education

Below are links provided by EvolDir users for various tips, exercises, and tactile teaching tools. Thanks everyone! perkinselearning.org/scout/teaching-biology-students-who-are-blind-or-visually-impaired researchgate.net/publication/234706180_Teaching_Biology_to_the_Visually_Impaired_Accommodating_Students'_Special_Needs researchgate.net/publication/309734090_Practical_work_in_science_with_visually_impaired_students teachingvisuallyimpaired.com/science-materials.html rnib.org.uk/insight-online/teaching-science-students-vision-impairment

"Beck, James" <James.Beck@wichita.edu>

Texas UndergradSummerRes PlantEvolution

Description: Switchgrass (Panicum virgatum) is emerging as an important biofuel candidate in the United States. Our labs (see website below) collectively study the evolutionary ecology, quantiative genetics, physiology and agronomy/plant breeding of Switchgrass. We are seeking a talented and diverse group of undergraduate students interested in conducting field research in Switchgrass biology across the US.

This program is an opportunity for undergraduate students to participate in a sustained mentored independent research on the biology of Switchgrass. 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. All science majors are encouraged to apply, but preference will be given to individuals with a strong background and/or interest in evolutionary ecology, environmental biology, quantitative genetics, and agronomy.

Application process: The application deadline is February 25, 2018. Please see our website for further details.

Questions: Bethaney Watson e-mail: bethaney.watson@austin.utexas.edu Subject: Switchgrass REU 2018

Website: https://sites.cns.utexas.edu/juenger_lab/summer-research-opportunities brandon.campitelli@utexas.edu

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UCalifornia Riverside Interns TrinidadGuppies

Research Internships - Evolutionary Biology

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

Qualifications: We seek interns who are entertaining the possibility of pursuing graduate studies in some area of ecology and evolution and who wish to gain some additional field research experience before doing so. Research will take place in semi-remote areas of Trinidad sometimes under bad weather conditions. Applicants must be able to live and work well with others. Research will involve carrying heavy packs over slippery and steep terrain. Applicants must be in good physical condition and be able to meet the demands of field research under these conditions. Ability to drive a standard transmission vehicle is desirable but not required. Applicants with first-aid/first responder training, skills in automobile maintenance, and construction skills are highly desirable. Please address these skills when applying.

Interns will be required to spend a minimum of 3-months in Trinidad, with possibility of extension. Starting dates are as early as January 2018. We will cover all travel and living expenses and provide housing.

Please see our website < www.theguppyproject.weebly.com > for more information on the project and access to reprints. Our video menu includes a "guppy censuses" submenu that details the main tasks associated with the internship.

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

Sincerely,

Ron Bassar

– Ron Bassar Assistant Professor Department of Biology Williams College 59 Lab Campus Drive Williamstown, MA 01267 Phone: 413-597-2119 College Webpage: https://biology.williams.edu/profile/rdb4/- Personal Webpage: www.ron-bassar.squarespace.com The Guppy Project: www.theguppyproject.weebly.com Ron Bassar <rdb4@williams.edu>

UKansas REUProgram ModelsInEvolution

The Models in Ecology, Evolution and Systematics Research Experiences for Undergraduates (REU) Program at The University of Kansas is now accepting applications. The NSF-funded program will occur over ten weeks this summer (May 20-July 26, 2018) in the Department of Ecology and Evolutionary Biology. In the program, students will participate in mentored, independent research. Students will receive a stipend, room and board, and course credit.

Projects available include, but are not limited to, theoretical disease ecology, biogeography of social spiders, butterfly genomics, lizard speciation, soil ecology, prairie communities, systematics of tapeworms, and insect behavior.

Applications are encouraged from biology majors and mathematics (or computer science) majors with an interest in biology. Students must be in good academic standing and enrolled at a community college, college or university. Members of underrepresented groups are strongly encouraged to apply. Students must be United States citizens or permanent residents. More information, including available projects, and an online application form are available at http://eebreu.ku.edu and inquiries should be directed to eebreu@ku.edu. The application deadline is February 15, 2018, but late applications will be considered.

Drs. Jennifer Gleason and Deborah Smith, Program directors Ecology and Evolutionary Biology University of Kansas

jgleason@ku.edu

UMinnesota REUPosition PeaAdaptations

Institution: University of Minnesota ’V Twin Cities

Principal Investigators: Dr. Ruth Shaw & Dr. Mason Kulbaba

Program Dates: 6/4/2018 ’V 8/10/2018

Description: Dr. Ruth Shaw’Âs Research Group in the Dept. of Ecology, Evolution & Behavior at the University of Minnesota is seeking applicants for an NSF Research Experience for Undergraduates (REU) position in summer 2018 to study the process of ongoing adaptation in experimental populations of partridge pea (Chamaecrista fasciculata) in prairie habitat. The student will work closely with Dr. Ruth Shaw and Dr. Mason Kulbaba to develop an independent project in the area of plant evolutionary genetics, with possibilities ranging from studies of heritability and phenotypic selection on plant traits to studies of pollination ecology and mating system variation. The student will gain invaluable experience in performing field work and in conducting an independent research project, from hypothesis formulation through oral and written dissemination of results, as grounding for future work in inquiry-based research. The student must be a U.S. citizen or permanent resident and enrolled as an undergraduate for Fall 2018. The ideal candidate should enjoy working outdoors and have an interest in learning about the evolution and ecology of plants in the Midwest prairies, and candidates planning to pursue a graduate career in evolution, ecology, or conservation biology are particularly well-suited for this position. The REU intern will receive a stipend of $5,500 and an allowance for room and board in the Twin Cities (with occasional overnight travel to field sites). Costs of travel to and from the Twin Cities will also be provided. The deadline to apply for this position is February 21, 2018, and the 10-week internship is expected to begin on Monday, June 4 and end on Friday, August 10. Please contact Mason Kulbaba (mkulbaba@umn.edu) for more information. The University of Minnesota provides equal access to and opportunity in its programs, facilities, and employment without regard to race, color, creed, religion, national origin, gender, age, marital status, disability, public assistance status, veteran status, sexual orientation, gender identity, or gender expression. Individuals of underrepresented groups are especially encouraged to apply. Please forward this advertisement to any interested and qualified undergraduates.

To apply, please e-mail the following application materials to Mason Kulbaba (mkulbaba@umn.edu) with the subject line "REU" no later than February 21, 2018: 1. A statement explaining the following: why you are interested in this position, what are your future plans, dates you are available to start and end this position, confirm eligibility for the REU program, the name and contact information of the person who will serve as your reference, your e-mail address and phone number. 2. Resume. 3. Transcript (unofficial is acceptable.) 4. One letter of recommendation (sent by your reference).

Mason Kulbaba <mkulbaba@umn.edu>

UNorthCarolinaGreensboro REU2018 MathematicsEvolBiology

REU Opportunity Summer 2018: "Research Experience for Undergraduates in Mathematics and Biology"

The University of North Carolina at Greensboro (UNCG) Department of Biology and Department of Mathematics and Statistics invite highly motivated undergraduate students to apply to our NSF-sponsored Research Experience for Undergraduates (REU) summer program.

Students will engage in one of multiple, co-mentored research projects at the interface of mathematics and biology. While exposure to both disciplines in desired, advanced expertise in both in not required because you will work in interdisciplinary teams.

Topics range from the evolutionary ecology of disease, to social evolution and the evolution of plant architecture. After a brief initial training period starting May 14, the students work on the research until July 20, 2018 and receive a stipend of $5000. Travel support and shared university housing will also be included.

For more information, visit https://www.uncg.edu/-mat/bio-math/REU/ or contact Dr. Jan Rychtar (rychtar@uncg.edu) or Dr. Olav Rueppell (olav_rueppell@uncg.edu).

Olav Rueppell <o_ruppel@uncg.edu>

UPittsburgh PymatuningLab EarlyCareerResearchFellowship

The University of Pittsburgh's Pymatuning Laboratory of Ecology (PLE) is pleased to offer the Frank J. Schwartz Early Career Research Fellowship of up to $10,000 plus up to three months of station fees and residency costs for the primary investigator (PI). PLE is a vibrant research and education facility located on Lake Pymatuning in Northwest Pennsylvania. PLE's research facilities are spread across 350 acres and include access to a variety of aquatic and terrestrial ecosystems. Its 10,000+ square feet of laboratory facilities include a field laboratory adjacent to an open field that can be used for large-scale replicated experiments, a modern molecular laboratory, and facilities for animal, plant and aquatic studies.

This opportunity is open to researchers holding PhD degrees in any science discipline that can benefit from PLE's resources (http://www.biology.pitt.edu/-facilities/pymatuning), and we look forward to receiving proposals on the topic of evolutionary biology. The purpose of the fellowship is to permit researchers to explore new projects or collect preliminary data. Fellowship funds can be used at the PI's discretion to facilitate the research but not for compensation. Preference will be given to individuals and projects with the potential to develop into long-term research activities at PLE. We especially encourage applications from individuals in the postdoctoral or early faculty phases of their careers working on projects involving fish, but researchers holding PhD degrees at all stages of their careers and working on projects involving other taxa are also encouraged to apply.

For more information about the fellowship program or research opportunities at PLE, please contact the Director, Dr. Cori Richards-Zawacki (cori.zawacki@pitt.edu).

Applicants should submit a single .pdf file including their

CV, a 2-3 page proposal outlining the proposed research, a budget detailing how the fellowship funds will be spent, and planned dates of residence to cori.zawacki@pitt.edu, placing the words "PLE Schwartz Early Career Fellowship" in the subject line of the email. Review of proposals will begin *February 19, 2018*.

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Corinne L. Richards Zawacki, Ph.D. email: cori.zawacki@pitt.edu <email%3Acori@tulane.edu> Associate Professor, Department of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

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

Cori Zawacki <cori.zawacki@pitt.edu>

UPittsburgh PymatuningLab ResGrants

The Pymatuning Laboratory of Ecology (PLE) invites applications for Pape/Darbaker/McKinley Grants in Aid of Research. Evolutionary biology is among the research topics suitable for these grants.

PLE is a vibrant research and education facility located on Lake Pymatuning in Northwest Pennsylvania. PLE's research facilities are spread across 350 acres and include access to a variety of aquatic and terrestrial ecosystems (http://www.biology.pitt.edu/-facilities/pymatuning/research). Its 10,000+ square feet of laboratory facilities include a field laboratory adjacent to an open field that can be used for large-scale replicated experiments, a modern molecular laboratory, and facilities for animal, plant and aquatic studies.

Pape/Darbaker/McKinley Grants are intended to support researchers in the early stages of their ecological and evolutionary research programs at PLE. Grant proposals are submitted each year in February and several awards are made, generally not exceeding $3,500. Most awards go to graduate students, but consideration will be given to recent Ph.D.'s and more senior researchers interested in initiating new work at PLE. *The due date for grant proposals is February 19, 2018. *

Please visit our website for further details about the application process: http://www.biology.pitt.edu/-facilities/pymatuning/research-grants –

Corinne L. Richards Zawacki, Ph.D. email: cori.zawacki@pitt.edu <email%3Acori@tulane.edu> Associate Professor, Department of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

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ArizonaStateU EvolutionAndMedicine

https://evmed.asu.edu/news/evolution-and-medicine-postdoctoral-research-fellowship The Center for Evolution & Medicine (CEM) at Arizona State University (ASU) invites applications for the Evolution & Medicine Research Fellowship. The Fellowship brings talented researchers with a recently awarded M.D. or Ph.D. to the ASU campus to develop and extend their own independent research agendas with opportunities to collaborate with CEM faculty and other members of their laboratories. Additionally, fellows will spend time working with their mentor to develop skills in the areas of outreach, education and grant writing. Possible research areas include, but are not limited to, co-evolution and infectious diseases, regulation of inflammation and other defenses, autoimmune disorders, cancer, genomics, reproductive health, lactation, and factors that influence disease susceptibility. The proposed research project must advance evidence based science for evolution and medicine.

Salary: $60,000 Job #12228 Full-time

The successful fellow(s) will be an outstanding scientist with a specific independent research plan, wide-ranging interests in evolutionary biology related to disease and health, and an appreciation for interdisciplinary research. Selections are based on academic achievement, creativity, overlap of interests with multiple CEM faculty, and the likely success and impact of the research project. Fellows cannot have had more than five years of previous postdoctoral experience, nor have been employed previously as an assistant professor, associate professor or professor on the tenure track. Nominees who are non-US citizens are encouraged to apply, and will need to be eligible for a J-1 Scholar visa status for the duration of the Fellowship. CEM does not support H1B visa status. A background check is required for employment.

Fellows will receive a salary of $60,000 and will have access to funding of up to $10,000 per annum to support their research, of which $1500 may be allocated for moving expenses. The initial closing date for receipt of complete applications is February 1, 2018; applications will be reviewed weekly thereafter until the search is closed. The earliest anticipated start date is July 2018, the latest is January 2019. This is a full-time (1.0 FTE) benefits-eligible, fiscal year (July 1 - June 30) appointment. The fellowship is granted for a period of two years, with a possible third year. Renewal for the second and possible third year is contingent on performance and the availability of resources. For additional information and policies regarding postdoctoral scholars at ASU, please see http:// provost.asu.edu/postdoc . By the start date, candidates must have completed a Ph.D. in anthropology, biology, psychology or another natural science field that provides an extensive background in evolutionary biology, or an MD, DVM, DrPH or equivalent level health professional degree. Minimum qualifications include demonstrated proof of advanced degree listed above and research experience in the field of evolutionary medicine by the time of the appointment. Preference will be given to applicants interested in furthering their own research agenda in a multidisciplinary environment and prior research experience in co-evolution and infectious diseases, regulation of inflammation and other defenses, autoimmune disorders, cancer, genomics, reproductive health, lactation and factors that influence disease susceptibility. To apply, please email a single pdf document to evmedsearch@asu.edu that contains:

A one-page statement explaining your interest in this position, which faculty members you would like to work with (and to have act as your postdoctoral sponsor/advisor(s)), and how it could advance your career plans A one or two-page statement that describes the research you will pursue at CEM if awarded a fellowship. The ability to clearly articulate a research plan that can be understood by faculty from other disciplines is an important selection criterion, so please minimize jargon and technical language. The names and contact information for three references A curriculum vitae

Please use 11 point Times font with 1 inch margins and 1.5 line spacing for all items except the CV. The Center for Evolution & Medicine is a university-wide Presidential Initiative directed by Randolph Nesse. Its mission is to improve human health by establishing evolutionary biology as an essential basic science for medicine, worldwide. It supports research that demonstrates the power of evolutionary biology to advance the understanding, prevention, and treatment of disease, as well as teaching and outreach initiatives. See http://evmed.asu.edu for details and information on Core Faculty. As an interdisciplinary unit,

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ArizonaStateU EvolutionaryGenomics

Postdoctoral positions are available in Susanne Pfeifer's group at Arizona State University, Tempe (US). Research in the Pfeifer Lab is focused on analysing high-throughput sequencing data to learn about genetic and evolutionary—processes, with a particular interest in:

(i) Mutation rate variation in primates A better understanding of the basis of evolutionary variation as generated by mutation will improve both insights into the genetic basis of disease as well as our understanding of the chronology of human evolution. Germ line mutations depend on several biological processes that are well known to vary between different primate species, yet only a limited number of studies has focused on directly estimating mutation rates in non-human primates. Projects will involve computational method development as well as the analysis of large-scale genomic pedigree data to characterize variation in mutation rates—across the primate clade.

(ii) Genomic mechanisms underlying links between evolutionary shifts In many species, coloration is an important phenotypic trait, involved in a range of different biological processes ranging from sexual signalling to crypsis to mimicry to thermoregulation. Building upon our results in recently evolved cryptically colored populations, we are extending this work to consider the co-evolution of coloration phenotypes with other evolutionary signals.

Successful candidates are expected to have a strong computational and statistical background (programming proficiency in R, Perl, or Python, and shell scripting is essential; experience with analysing high throughput sequencing data is highly desired) along with a genuine interest in genetics and evolution. Preference will be given to candidates with a strong publication record, evidence of research productivity, and an ability to successfully communicate scientific information. Funding is available for three years, contingent on annual renewal based on progress. The start date is flexible.

The Pfeifer Lab offers a vibrant work environment with excellent opportunities for collaborative efforts as well as independent accomplishments. The Lab is integrated within a diverse bioinformatics, evolution, and population genetics research community at ASU

(ASUpopgen.org), as well as the Center for Evolution and Medicine (evmed.asu.edu) and the Center for Mechanisms of Evolution (biodesign.asu.edu/mechanisms-evolution). Additional information about the Lab and research can be found at: http://spfeiferlab.org . Interested applicants should send a short summary of research interests, CV, and contact information for two references to susanne.pfeifer@asu.edu. The evaluation of applications will begin on January 15th, 2018, and will continue until one or more suitable candidates has been found. Informal inquiries are welcome.

Susanne Pfeifer <spfeife1@asu.edu>

BielefeldU EvolutionaryBiology

For our newly funded collaborative research center 'A Novel Synthesis of Individualization across Behavior, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3)' that proposes to combine behaviour, ecology and evolution in an etho-eco-evo approach to develop a novel synthesis of individualisation we search candidates with a background in evolutionary ecology, evolution of behaviour or behavioral ecology for a 3+ Years Postdoc position in Meta-analysis of Individualized Niches at Bielefeld University, Germany A Postdoc position with a duration of about 40 months for working on meta-analysis of individual niche specialization is immediately available at the Faculty of Biology at Bielefeld University in Northern Germany. The position is funded by the German Research Foundation (DFG) within the recently granted collaborative research center (SFB/TRR 212).

The project: The behavioural ecology of individualized niches in light of meta-analyses will use quantitative methods to synthesize the current knowledge on individual niche specialization. Meta-analyses offer the formal framework, a framework that is growing in popularity and importance in all fields of quantitative research. Meta-analyses allow a formal assessment of the generalizability of research findings and an exploration of context dependencies. This involves a thorough reading of the published literature and will thus strengthen both conceptual and quantitative thinking. Specifically, we will explore the extent to which factors like environmental complexity, assortative mating, ecological inheritance, temporal variation, niche inheritance, condition dependence and others lead to between individual variation concerning individualized niches. The project will collaborate intensely with various empirical projects within the SFB. It promises strong training in statistical analyses, deep conceptual understanding and advances in several of subfields of ecology and evolution concerned with individualization.

The collaborative research center: The position will be embedded within a larger collaborative research center (SFB) comprising 18 principle investigators, 8 postdocs and 16 PhD students based at Bielefeld University, the University of Münster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualization across behavior, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programs. For more information, visit the SFB website (www.uni-bielefeld.de/biologie/crc212).

Main responsibilities - compilation of results on individualized niche ecology from the published literature - analysis of published effects using modern meta-analytic methodology - collaboration with other research groups in the collaborative research center - writing scientific publications for international peer- reviewed journals

Applicant's profile We seek a bright and highly motivated candidate with - a PhD in a relevant field like evolutionary or behavioral ecology or statistics - solid knowledge in basic statistics, including experience with statistical software such as R or SPSS - interest in both biological and statistical questions - motivation to read deeply into the scientific literature on specific topics - excellent oral and written communication skills in English - documented experience with publishing scientific results

Remuneration Salary will be paid according to Remuneration level E13 of the Wage Agreement for Public Service in the Federal States (TV-L), the standard payment scale for scientists and lecturers. Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programs. Employees have the opportunity to use a variety of health, counselling, and prevention programs. Bielefeld University places great importance on a work-family balance for all its employees.

Application procedure The deadline for application is February 14, 2018 and interviews will take place shortly thereafter. To apply, please provide (i) a letter of motivation, including a statement of your research interests, skills and experience relevant to the position, (ii) a CV including publication list, (iii) names and contact details of two referees willing to write confidential letters of recommendation. All materials should be sent, preferentially as a single pdf file by email, to the address below. For further information on the projects and the department, please contact Klaus Reinhold (klaus.reinhold@uni-bielefeld.de). Please note that a twin project within the collaborative research center has

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CharlesU CzechRep PollinationEcology

REMINDER OF A COMING DEADLINE

A postdoctoral position - Changes of pollination networks characteristics along various environmental gradients

We are seeking a highly motivated postdoc to join a project assessing studies of plant-pollinator relationships in tropical and temperate environments. The research is focused on changes of general characteristics of pollination networks with environmental gradients, as well as on case studies of selected pollination systems. All the new team members will process already collected data and material, as well as actively participate on field sampling (at least two larger expeditions during the job) of data and their subsequent processing in collaboration with international specialists. The length of the postdoc is two and half years.

The successful applicant will become a part of the multidisciplinary team (www.insect-communities.cz) at the Faculty of Science, Charles University, Prague, Czech Republic, with a close collaboration with the Institute of Entomology and Institute of Botany, Czech Academy of Sciences. The fieldworks will be performed in Cameroon and/or Czech Republic. We have more than ten years continuous experience with various field projects in Cameroon. All senior members of our team have also worked in field in the Czech Republic since their studies.

Offered for all positions

- attractive scientific topic in an established international team

- sufficient financial and logistical sources for the projects (currently we hold three large projects for pollination research)

- 360,000 CZK net annual income for the post-doc (salary), plus various employee bonuses; the income sufficiently covers living expenses in the Czech Republic (the national average net income is ca. 260,000 CZK annually)

Required for all positions

- enthusiasm in nature and ecological science

- ability to work as a team member, but also being independent

- fluency in English, both written and spoken

Desirable (but not necessary) for all positions

- previous experience of collaboration in scientific projects evidenced by a (co)authorship of research papers or conference contributions

All applicants will send a structured CV, contacts for three referees, and a cover letter stating their previous work, qualification (especially all field experience and less usual field/laboratory techniques) and motivation to our group email insectcommunities@gmail.com. Any questions should be sent to the same email as well. The review of applications will begin on 20th February 2018 and will continue until the position has been filled. Selected applicants will be interviewed through Skype in the first ten days of March 2018. The postdoctoral position will start from early summer 2018.

The postdoc will be collaborating on several our projects from both tropical and temperate regions. She/he should be mainly responsible for the network analyses and comparisons of various datasets of plant-pollinator interactions on the community level. Nevertheless, she/he is expected to join also other aspects of our pollination research based on her/his skills, including field sampling, samples identification, measuring and analyses etc. She/he will have an opportunity to join our field sampling in both Cameroon and Czechia. The postdoc will be jointly led by Dr. Robert Tropek and Dr. Â©tÃán Janeèek.

Specific requirements for this position

- a Ph.D. degree in the relevant field (in early spring 2018 at the latest)

- advanced skills in ecological networks statistical analyses

- enthusiasm for statistical revealing of ecological enigmas

- reasonable publication record

Desirable (but not necessary)

- reasonable knowledge of insects or plants
- experience with trophic interactions research

Robert Tropek <robert.tropek@gmail.com>

CharlesU Prague SpeciationGenomics

A postdoctoral position in Genomics of speciation at Charles University in Prague

Position available: from June 2018 to December 2020

Application deadline: 18^th February 2018

We are looking for a motivated post-doc to join our group working on genomics of speciation in two hybridizing songbirds, the Common Nightingale and the Thrush Nightingale. These species hybridize in a secondary contact zone and produce viable hybrid progeny. In accordance with Haldane's Rule, hybrid females are sterile, while hybrid males are fertile, allowing gene flow to occur between the species. The two species also show marked differences in sperm morphology, which could contribute to post-mating prezygotic isolation. The main goal of the project aims at identifying genetic basis and molecular mechanisms of both hybrid female sterility and postmating prezygotic isolation. The project will combine QTL mapping experiments and population genomic analyses of transcriptomes and whole genome sequences of both species. The successful applicant will be mainly responsible for the bioinformatic part of the project. The position requires experience in analysis of large-scale next-generation sequence data and the ideal candidate should have background in quantitative or population genetics. Programming skills are desirable.

Salary:

The candidate's monthly income will be 1,500 EUR (ca 37,500 CZK) with the possibility of increase up to 2,000 EUR (ca 50,000 CZK). Note that living expenses in the Czech Republic are generally lower than in Western European countries.

How to apply: If interested, please, send (1) CV including a list of publications, (2) copy of PhD diploma, (3) motivation letter, and (3) contact details for 2-3 references to Radka Reifova (radka.reifova@natur.cuni.cz) by 18th February 2018.

Contact: Further information about the position can be obtained from Radka Reifova (radka.reifova@natur.cuni.cz).

You can also find further information about our group at our web page: http://web.natur.cuni.cz/~radkas/ "RNDr. Radka Reifová, Ph.D." <radka.reifova@natur.cuni.cz>

ClemsonU SnakeVenomEvolution

Postdoctoral opportunity: venom as a key innovation in snakes.

The laboratory of Christopher Parkinson, recently relocated to Clemson University, is looking for a highly motivated postdoctoral associate to join a vibrant research team. This position is funded for 2 years by our NSF Dimensions of Biodiversity award and Clemson University. Our NSF Dimensions award is a collaboration among Lisle Gibbs at Ohio State, Darin Rokyta at Florida State and in Brazil- Ignacio Azevedo, Ana Moura, Erika Hingst-Zaher at Butantan Institute and Hussam Zaher at USP. We will be investigating the evolution of venom in the traditionally classified venomous snakes as well as studying several lineages of "nonvenomous" snakes to quantify links between functional diversification of the complex trait of venom and the speciation process in snakes. This project involves work at the intersection of population genomics, transcriptomics, quantitative biochemistry, phylogenomics and comparative phylogenetics. The selected individual will be responsible for facilitating sample collection in several Latin American countries and will be involved in downstream genomic and proteomic analyses as well as venom functional assays.

Qualifications: Candidates should have completed or be within 6 months of completing their Ph.D.'s in an appropriate related field. We are seeking a scientist with field experience, who is creative & talented, has an excellent publication record, is organized, and possesses excellent communication skills. As this positon requires field work in several Latin American counties the ability to speak Spanish and/or Portuguese is desirable. Additionally, the successful candidate should have a strong computational background and previous experience working with NGS data sets and phylogenetics. The candidate is expected to secure funding through submission of fellowships and grant applications, which will help further prepare them for a successful academic career.

The position is located in Clemson, SC at Clemson University, though there will be opportunities to work with, and at, collaborating institutions. Interested candidates should send their CV, a research/motivation statement for this position and contact information for three references to Chris Parkinson (viper@clemson.edu). Review of applications will begin immediately and continue until the position is filled. For more information on the Parkinson lab see: https://www.parkinsonlab.com/ Department of Biological Science and

Department of Forestry, and Environmental Conservation 190 Collings St., 157b Life Sciences Facility,

Clemson University, Clemson, SC 29634 (864) 656-3058

emailsigpict

Christopher L Parkinson <viper@clemson.edu>

GuangxiU Phylogenomics

Two postdoctoral fellowships available immediately in Plant Phylogenomics.

Two Postdoctoral Fellowships are available immediately at the Plant Ecophysiology and Evolution Group of Guangxi University (Nanning, China). We are seeking highly motivated and productive postdoctoral fellows to engage in 2-year projects in the following field:

- Plant Phylogenomics (2 funded fellowships available)

Plant Ecophysiology and Evolution Group at Guangxi University (Nanning, China) http://www.plant-ecophysiology-evolution.com/ http://www.plant-ecophysiology-evolution.com/person/joeri-sergej-strijk/ 1 Plant Phylogenomics Two fellowships are available in the Biodiversity Genomics Team, led by Associate Prof Joeri S. Strijk. We focus our research efforts on understanding the origin, rise and persistence of tropical plant biodiversity by combining the latest NextGen sequencing techniques and advances in genomics with molecular systematics, taxonomy, ecology and historical biogeographical reconstruction. Our study area covers the greater tropical Australasian zone and extends to include the flora of the Madagascar and Indian Ocean Island Biodiversity Hotspot. Members of the team address a wide range of research topics, ranging from understanding the effects of palaeogeographic changes in landmass configuration on patterns of plant genome evolution and divergence, studying community assembly and in-situ plant diversification patterns on oceanic islands, to using genomic data to clarify the links between gene divergence, diversification and distribution, and employing the latest NGS techniques to resolve longstanding botanical and evolutionary questions typical for amorphic, speciose and widespread tropical tree families.

-REQUIREMENTS: Prospective candidates, (younger than 34 years at the contract starting date), should have a PhD with a strong background in plant genomics and/or systematics, bioinformatics, molecular dating and/or biogeographical reconstruction, and should have a proven track record of successful publication in peer-reviewed journals. Additional experience in botanical collecting and fieldwork, taxonomy and herbarium experience are considered a major advantage when applying. The candidate will join a dynamic and international team that uses the latest advances in genomics to push the boundaries of our knowledge on plant biodiversity and plant divergence. Within the team's programs, a number of topics are available for discussion following a successful application.

Fellowship details Opportunities for the development of individual research projects as well as collaborative work exist within the Plant Ecophysiology and Evolution Group.

The postdoctoral tenure will be two years and renewable for one more year upon evaluation. The fellowship covers an annual salary, a furnished apartment on campus and medical insurance. A small research fund (30,000 Yuan RMB) is provided by the university and the host supervisor will cover the rest of the initial research expenses. Prospective candidates are required to take part in external funding applications to support the joint research work. In addition, the selected candidate will be eligible to apply for a National Postdoctoral Scholarship through Guangxi University.

General information Guangxi University The Plant Ecophysiology and Evolution Group is part of the College of Forestry, under the State Key Laboratory of Conservation and Utilization of Subtropical Agro-bioresources, and the newly proposed Guangxi Key Laboratory of Forest Ecology and Conservation, which houses a wide range of laboratories and research teams. We are centrally located on the large green Nanning City campus, with easy access to on-campus housing and day-to-day facilities for life on campus. Visit our website for a picture impression: http://www.plant-ecophysiology-evolution.com/contact-us/ Postdoctoral Fellows will be part of a growing and multidisciplinary team of Chinese and foreign researchers, providing a creative and stimulating research environment. Group members (students and faculty) represent over fifteen different nationalities, spanning a wide range of research backgrounds and experiences. Knowledge of Chinese for application is not mandatory, but opportunities exist to attend weekly courses in Mandarin if desired. The working language in our research group is English.

Guangxi University (>25,000 students) in Nanning is part of China's National 211 University Scheme (http://en.wikipedia.org/wiki/Project_211), and is rapidly becoming a major research hub in Southern China. The city forms the natural gateway to South-East Asia, with Vietnam only

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Ifremer France Biodiversity eDNAanalysis

Post doctoral position : Improving marine biodiversity inventories through eDNA analysis

Context

The knowledge and understanding of the ecology and evolution of the marine realm requires an enhanced appraisal of marine biodiversity and of the biotic and abiotic drivers of its distribution and evolution. Yet the very first step, that of inventory, appears stumbled: considering the pace of taxonomic description in 2015, an estimated 10,000 years would be required to complete the taxonomic descriptions and inventory of the majority of the existing biodiversity, provided it would be accessed and sampled. The recent improvement and unprecedented acceleration of sequencing techniques and the development of environmental genomics open promising avenue for the development of methods allowing the rapid and reliable characterization of biodiversity and ecosystems status (Valentini et al. 2009, Creer et al. 2010, Hajibabaei et al. 2011), including in the deep sea (Pawlowski et al. 2011, Sinniger et al. 2016) . Previous studies have shown good evidences for the potential of metagenomics in support of monitoring surveys(Ji et al. 2013, Cowart et al. 2015, Pawlowski et al. 2015, Aylagas et al. 2016, Cordier et al. 2017) and ultimately leading to new tools and/or indicators to assess potential impacts from industrial operations (Bista et al. 2015, Lejzerowicz et al. 2015).

During a previous collaboration, Total and Ifremer developed protocols of metabarcode and compared their efficiency with classical morphological inventories (Cowart et al. 2015). Their aim in the EU H2020 project "Atlas: A Trans-AtLantic Assessment and deep-water ecosystem-based Spatial management plan for Europe" is to go one step beyond using constantly upgraded protocols (taking into account the evolution of molecular and bioinformatics tools) in deep sea ecosystems including Atlantic habitats among which potentially impacted ones.

The post-doc is hired to contribute analyzing deep sea sediment samples with the objective of comparing and if necessary improving existing protocols based on metabarcoding and capture methods. This will be performed to fulfill the needs of operational sites surveys and feed comparative approach between eDNA based and conventional taxonomic approaches. The objective is to develop standardized molecular and bioinformatics protocols and indicators for environmental impact assessments, and consider the definition of new indicators.

Skills:

*Good background in community ecology, genomics and bioinformatics

* eDNA analysis and interpretation

*Team work

*Rigorous laboratory methods and practices

*Good redaction skills

**

*Contact * Sophie Arnaud-Haond sarnaud@ifremer.fr <mailto:sarnaud@ifremer.fr>

http://wwz.ifremer.fr/ *Duration of the contract—:*18 months

*Starting dates—:*between March 1^st and June 1^st *2018*

*Candidatures (CV, a letter and two contacts for references) sent by email before 08/02/2018—:*Interviews between February 1^st and 15

*Lab—: *Ifremer, UMR MARBEC (Marine Biodiversity, Exploitation and Conservation), Bd Jean Monnet, BP 171, 34203 Sète Cedex

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Sophie Arnaud-Haond Ifremer UMR MARBEC (Marine Biodiversity, Exploitation and Conservation) Bd Jean Monnet, BP 171, 34203 Sète Cedex - France Tel: +33 4 99 57 32 61

Sophie Arnaud Haond <Sophie.Arnaud@ifremer.fr>

IndianaU BeetleEvoDevo

Postdoctoral Fellow in Host-Microbiome Evo Devo of Horned Beetles

One full-time postdoctoral position is available in Armin Moczek's lab, Department of Biology, Indiana University, Bloomington. Our lab conducts research in the evolutionary developmental (evo-devo) and ecological developmental (eco-devo) biology of insects. Additional information about research in the Moczek lab can be found at http://ecoevodevo.com/ . The position will explore the relative significances of - and interactions among - dung beetles, their microbiome, and niche construction behaviors of larvae and adults in the ecological radiation of horned beetles. This work will combine genomic, transcriptomic, and candidate-pathway approaches alongside behavioral and ecological manipulations in both beetles and their symbionts. Long term objectives are to characterize the role of co-development and reciprocal niche construction in the ecology and evolution of dung beetles. The successful candidate would have opportunities to develop additional independent lines of research in these and related areas.

The position is initially available for 12 months.

We seek a collegial, self-motivated, independent, and intellectually curious individual. A PhD in Evolutionary Biology, Developmental Biology, or related field is required. Applicants for this position must have strong bench skills, and familiarity with techniques such as RNA interference, qPCR, cloning, immunohistochemistry, and the bioinformatic analyses of next-gen sequencing data is strongly desirable (though training in these techniques will also be provided as necessary). In addition, candidates must have demonstrated written and oral communication skills. Experience working with insects is helpful but not required.

For questions about the position, contact Armin Moczek (armin@indiana.edu).

Commensurate with experience, full benefits included

To apply, please submit a letter of application, a CV, a statement of research interests, and the contact information for three references to http://-indiana.peopleadmin.com/postings/4871 . Armin P. Moczek Professor of Biology, Indiana University Fulbright Distinguished Chair for Research, Innovation, & Technology Australian National University and CSIRO, Canberra http://ecoevodevo.com/ http://www.iu.edu/-~biosim "Moczek, Armin P" <armin@indiana.edu>

Istanbul EvoDevo

Postdoctoral position at the Institute of Life Sciences and Biotechnology in Istanbul

We are looking for highly motivated enthusiastic scientists with PhD degree in Health or Biological sciences. International research experience is highly preferred. In general, research experiences of molecular biology, cell culture, and Immunofluoresnce microscopy are desired. Excellent communication skills in English are necessary.

Multiple positions are sought to be filled in the following fields:

1) Molecular and Cellular Microbiology.

The candidate will be working with rodent models and mosquitoes. Prior experience with rodent models is preferable.

2) Evolutionary Developmental Biology, endosymbiosis, and microbiome research.

The candidate will be working with ant and mouse models. Prior knowledge of development is preferable.

The salary is competitive and depends on the qualification and experience of the candidate. The institute is located on a beautiful hill overlooking the Bosphorus on the Anatolian side of Istanbul. It is fully equipped with state of the art facilities.

The institute is an equal opportunity employer and does not discriminate based on gender, religion or nationality.

Review of applications will start immediately.

For applications and enquiries, please contact: m.rafiqi@bezmialem.edu.tr

Ab. Matteen Rafiqi (PhD)

Assistant Professor | Bezmialem Vakif University | Adnan Menderes Bulvarı |Vatan Caddesi | 34093 |

Fatih, Istanbul, Turkey | Phone +90 (538) 555-7580

Matteen Rafiqi <m.rafiqi@bezmialem.edu.tr>

KAUST SaudiArabia MarineEvolutionaryGenomics

Postdocdoctoral fellowship available immediately at the Integrative Systems Biology Lab to study coral reef fish adaptation to climate change.

One postdoctoral position in Marine Evolutionary Genomics is available at the Integrative Systems Biology Lab (http://systemsbiology.kaust.edu.sa) at the King Abdullah University of Science and Technology (KAUST) in Saudi Arabia (www.kaust.edu.sa). This is part of a large and funded collaborative project with the laboratory of Prof. Phil Munday at the ARC Centre of Excellence for Coral Reef Studies, James Cook University (www.coralcoe.org.au).

Background

Anthropogenic activities are leading to global Climate Change at an unprecedented rate. Understanding the mechanisms of how coral reef fish cope with environmental shifts is imperative to understand their fate in a changing planet. Little is known about the mechanisms of rapid evolution/phenotypic plasticity to the adaptive response of coral reef fish to changing ocean conditions.

We are seeking for a highly motivated postdoctoral fellow to work on a long-term project that aims to understand the effects of climate change stressors (i.e. ocean acidification and warming) on coral reef fishes, specifically the damselfish (*Acanthochromis polyacanthus*) and the clownfish (*Amphiprion percula*). Our main goal is to understand acclimation to climate change at the genomic level by using a set of unique multi-generational experiments. These studies combine Next-Generation Sequencing approaches such as genome and transcriptome sequencing to understand the molecular mechanisms that underline fish responses to climate stressors. The successful candidate will be able to look at a variety of data including physiological responses, but will mainly be working on the computational analysis of comparative genomics and transcriptomics.

About the successful applicant

To be successful in this role you will have:

- PhD (completed or soon to be completed) in marine biology, biology, ecology & evolution or computational biology and genomics. - Research and publication track record in a relevant field, commensurate with opportunity. - Expertise in the analysis and interpretation of Next-Generation Sequencing datasets. - Demonstrated programming skills in a Unix/Linux environment (e.g. Python, Perl, R etc.)

We offer a very competitive compensation package, as well as free on-campus housing and health benefits. Applications should include a CV and contact information of at least three referees.

For further information, or to submit your application, please contact Prof. Timothy Ravasi (timothy.ravasi@kaust.edu.sa) and please visit the Employment section at the KAUST Website < http://-www.kaust.edu.sa/employment/employment.html > for further information about opportunities and benefits available at the KAUST.

Celia Schunter <celia.schunter@kaust.edu.sa>

KULeuven ComparativeGenomicsYeast

Job description:

We are looking for a highly motivated and talented postdoctoral researcher, specialized in comparative genomics and sequence analysis. In your role, you will work on exciting research projects - you will be directly collaborating with our team of wet-lab scientists who are generating novel data (whole-genome sequences, RNAseq transcriptome data, Illumina, 454, PacBio,). These collaborations also allow your computational results to be experimentally validated.

Who we are:

The lab for Systems Biology of Kevin Verstrepen is a research team at VIB & University of Leuven. Our team focuses on genomics, genetics, epigenetics, transcriptomics and evolution, using yeast as a model. We combine wet-lab and computational research to investigate how biological systems work and evolve. The lab is located at Leuven University, one of the oldest and most prominent universities in Europe, consistently ranked within the top 50 worldwide universities. Leuven is located 10 miles from Brussels, with frequent direct train connections to Brussels airport.

Example publications include:

o Domestication and Divergence of Saccharomyces cerevisiae Beer Yeasts.

Gallone B, Steensels J, Prahl T, Soriaga L, Saels V, Herrera-Malaver B, Merlevede A, Roncoroni M, Voordeckers K, Miraglia L, Teiling C, Steffy B, Taylor M, Schwartz A, Richardson T, White C, Baele G, Maere S, Verstrepen KJ. Cell (2016).

o Origins, evolution, domestication and diversity of Saccharomyces beer yeasts.

Gallone B, Mertens S, Gordon JL*,* Maere S, Verstrepen KJ, Steensels J. Curr Opin Biotechnol. (2017).

o Adaptation to High Ethanol Reveals Complex Evolutionary Pathways.

Voordeckers K, Kominek J, Das A, Espinosa-CantÃº A, De Maeyer D, Arslan A, Van Pee M, van der Zande E, Meert W, Yang Y, Zhu B, Marchal K, DeLuna A, Van Noort V, Jelier R, Verstrepen KJ. PLoS Genetics (2015)

We offer:

——— The ability to work on scientifically exceptional and high-impact research topics ——— Fulltime appointment as postdoctoral fellow at VIB / KU Leuven, a highly-ranked research institute with competitive payscale and benefits (health insurance, sports facilities,...) ——— A stimulating and supportive international research environment (with English as main language) ——— Various training opportunities within VIB and KU Leuven to broaden your expertise and skills ——— State-of-the art infrastructure ——— Job is available immediately, starting date is negotiable

Profile:

——— You have a PhD degree in Bioinformatics, Computational Biology, Computational Biology, (Bio)-Engineering or related. ——— You have a strong research output (peer-reviewed publications) ——— You have hands-on experience with or a strong interest in bioinformatics programming, including linux, scripting) and R ——— You have experience with the analysis of next-generation sequence data such as whole-genome sequencing, CNV, Structural variation and RNA- Seq. ——— You are fluent in English, for both written and oral communication ——— You are enthused about scientific research and have a strong interest in studying biology using genomics and systems biology approaches. ——— You must have good, open communication skills and be willing to collaborate with multiple other researchers from our team.

How to obtain more information and apply?

Motivated candidates are asked to apply online. Applicants are invited to send their CV (including a list of your scientific publications) and motivation letter. For every formal application, please arrange for at least 2 letters of reference sent to Kevin Verstrepen (direct email from mentor to Kevin) - Tel : +32 (0)16/751393.

More information: http://www.kuleuven.be/verstrepen https://vibvzw.jobsoid.com/j/11076/postdoc-position-in-bioinformatics-comparative-genomics Brigida Gallone <brgal@psb.vib-ugent.be>

MasseyU ComputationalGenomics

Postdoc in Computational Genomics Massey University, New Zealand

I am looking for a motivated postdoctoral fellow to explore the evolution of genome structure in filamentous fungi. My group is interested in interactions between genome structure and gene expression, epigenetic modification and 3D conformation. A key focus of this postdoc will be on how interactions like these change over evolutionary time. This research program will build on a growing set of genomic data for the genus Epichloe, an increasingly important model system for studying the genome evolution of haploid and polyploid fungi.

The postdoc will be expected to help develop her/his own research program, with an emphasis on addressing novel hypotheses rather than data description. This analytical position requires solid quantitative and computational skills, with the ability to develop and apply new bioinformatic applications to genome analysis. At a minimum, some confidence in bioinformatics and a programming language is required. Training in fungal biology or genomics can be provided as needed, and candidates from non-standard research backgrounds with a clear fit to the position are encouraged to apply.

Funding is guaranteed for two years and three months, but may be extendable. Salaries are extremely competitive, starting at NZ$69,000, considerably higher than comparable salaries in the US and Europe. Items considered benefits in some other countries, such as healthcare coverage, are a standard right in New Zealand.

My research group aims to achieve work-life balance within a productive scientific environment. The team is firmly embedded in the international scientific community, with extensive collaborative links to Australia, Asia, Europe and the United States. Ongoing training is a key focus for postdocs. As a computational biology group, I offer a supportive environment for computationally-inclined postdocs to work towards independence. The successful candidate will not be a lone bioinformaticist isolated in a bench biology group.

My group is highly international, and applicants from all countries and backgrounds are actively encouraged to apply. Members of underrepresented groups are welcome, as are postdocs with families.

The position will be based in my computational biology research group at Massey University in the city of Palmerston North, New Zealand. This offers a rare opportunity to experience New Zealand's unique natural and cultural environment, while still undertaking world leading research. Palmerston North, a university town with a large international community, offers a full range of social and cultural amenities. The city is located between mountains and the sea, and presents regular opportunities for hiking, skiing, surfing and adventure sports. It also has a good café scene for those of a more cosmopolitan bent.

For further information, please visit my group's website (http://massey.genomicus.com) and the website of our funder, the Bio-Protection Research Centre (http://bioprotection.org.nz). Please contact me directly if you have any further questions (m.p.cox@massey.ac.nz).

To apply for this position, upload the following documents at the official Massey University job website: http://massey-careers.massey.ac.nz/10118/postdoctoral-fellow-in-computational-genomics 1. A brief statement of research interests and experience, focusing on short to mid-term career goals. 2. A curriculum vitae, including qualifications and scientific publications. 3. The names and contact details of three referees willing to provide a confidential letter of recommendation upon request.

APPLICATION DEADLINE: Saturday 24 February 2018

Prof Murray Cox Statistics and Bioinformatics Group Institute of Fundamental Sciences Massey University Palmerston North New Zealand

http://massey.genomicus.com m.p.cox@massey.ac.nz

murray.p.cox@gmail.com

MaxPlanck Jena Germany PopulationGenetics

Postdoc position (E13 100%) Max Planck Institute for the Science of Human History, Jena, Germany

The department for Archaeogenetics at the Max Planck Institute for the Science of Human History in Jena, Germany, is offering a position for a Postdoc in Population Genetics (E13 100%) for up to four years, starting in spring/summer 2018.

The overarching research topic in the department of Archaeogenetics is the use of novel scientific approaches from high throughput sequencing of ancient DNA from human populations and their pathogens to explore research questions related to human history, gene-culture coevolution, and adaptation to infectious disease.

The candidate's job will be the analysis of human genomic data from ancient and modern samples to reconstruct population history. The goal is to understand genetic diversity and substructure of Neolithic and Bronze Age populations, with a particular emphasis on West-Eurasia. To this end, the candidate will use statistical methods to quantify ancestral relationships, such as PCA, admixture, and f-statistics. We will also develop explicit tree- and graph-based population-genetic models for common ancestry and admixture between different groups of samples to understand order and timing of historical events.

The ideal applicant should have completed a PhD in genetics, bioinformatics, and computer science or relevant neighboring disciplines, worked with large high-throughput sequencing or SNP datasets, and a profound interest in human history. Prerequisites also include evidence of strong oral and written communication skills and the ability to complete tasks in a timely and structured fashion.

For detailed information on the institute please visit our website: http://www.shh.mpg.de/en . The Max Planck Institute for the Science of Human History promotes women and encourages especially women to apply. Handicapped candidates will be given

priority in case of the same professional qualification.

Please submit a letter of interest detailing how you meet the qualifications, curriculum vitae (indicating previous academic performance indicators, publication history, and prior research experience), and contact information for three references to:

E-mail: dag-jobs@shh.mpg.de

For more details on the research program please contact

Prof. Johannes Krause, E-mail: krause@shh.mpg.de

Dr. Wolfgang Haak, E-mail: haak@shh.mpg.de

Dr. Stephan Schiffels, E-mail: schiffels@shh.mpg.de

richter@shh.mpg.de

MichiganStateU eDNA Metabarcoding

Postdoctoral Research Associate: Environmental DNA metabarcoding

Department of Fisheries and Wildlife, Michigan State University

A postdoctoral research associate position is available in the labs of Dr. John Robinson and Dr. Kim Scribner in the Department of Fisheries and Wildlife at Michigan State University. The successful applicant will join a collaborative project between university and Michigan Department of Natural Resources researchers applying environmental DNA metabarcoding approaches to basic and applied community ecological questions in Michigan waters of the Great Lakes and their tributaries. This project will develop and apply sensitive and rapid molecular approaches for detecting aquatic invasive species, while also more broadly characterizing associations among aquatic community biotic components (fish, mollusks, invertebrates, plants) with physical properties of lakes and streams. The successful candidate will regularly participate in (and eventually, lead) field eDNA sampling. The postdoc will lead laboratory, bioinformatic, and statistical analyses. The postdoc will also have op portunities to collaborate on future and ongoing research in both labs.

Applicants must have a Ph.D. in Genetics, Evolutionary Biology, or a similar field. Applicants should also have experience with genomic library preparations, data base management of large sequencing data sets, and basic bioinformatic and statistical skills. Programming experience in R, UNIX, or other languages is preferred, as is experience with high performance computing.

The start date is on or before June 1, 2018 but can be somewhat flexible. Initial appointment is for a period of 19 months, with the potential for additional support contingent on performance and funding. Interested applicants should apply through www.careers.msu.edu, search posting number 483503. Questions about the position can be directed to Dr. John Robinson, jdrob@msu.edu, or Dr. Kim Scribner, scribne3@msu.edu.

Review of applications will begin February 1, 2018 and will continue until the position is filled.

“jdrob@msu.edu” <jdrob@msu.edu>

New Zealand StickInsectGenomics

A three year post-doctoral position is available at Manaaki Whenua - Landcare Resesarch in New Zealand to contribute to a newly funded Marsden Fund project “Evolution thermal performance in stick insects”. We are seeking to recruit a post-doctoral researcher with experience in genomics or transcriptomics and an interest in using genomic data to test hypotheses on thermal biology, adaptation, plasticity and evolution.

Project summary

This project is led by Thomas Buckley at Manaaki Whenua - Landcare Research, Auckland, New Zealand. Key collaborators are Brent Sinclair (University of Western Ontario, Canada) and Hester Roberts (Manaaki Whenua - Landcare Research, Auckland, New Zealand). The goal of this research programme is to determine whether tropical species that colonize temperate environments shift their thermal performance, or rely on inherent plasticity. This post-doctoral project will integrate genomics, physiology, and phylogeny to address this question using the well-studied clade of New Zealand and New Caledonian stick insects. The successful candidate will be tasked with collecting and analysing a variety of -Omic data sets from New Zealand and New Caledonian stick insects. The techniques employed will include whole genome data, RNAseq, miRNA sequence and bisulfite sequence data. The candidate will perform the bioinformatic analysis of the data and use it to test evolutionary hypotheses. The candidate will also have the option of being involved in field work and thermal performance experiments, and integrating these results with the genomic data. These analyses will help to reveal the genomic basis of thermal performance and reconstruct its evolution across a group of stick insect species inhabiting a subtropical to cool alpine environmental transect.

The successful candidate will ideally: - hold a PhD in biology with proven publication track record and conference presentations - have laboratory experience with DNA and RNA extraction, quality control, and sequencing library preparation - have experience with the bioinformatic analysis of genomic data sets such as RNAseq, whole genome assembly and annotation, and bisulfite sequencing data - have an understanding of thermal biology and its evolution - have an understanding of evolutionary biology, processes of adaptation and associated models and methodology - have the ability to relate to people in all circumstances and to work well in a team - be versatile, demonstrates initiative in solving problems - work well under pressure, self motivated - be well organised, capable of independently and effectively planning time and resources - have the ability to mentor students

The three year, full time position will be based at Manaaki Whenua-Landcare Research in Auckland.

If you would like to take advantage of this great opportunity please view the position description and apply online. Applications must include a cover letter, CV and evidence of the required skills as per the position description.

For further details about our organisation and the relevance of our science please visit our website: www.landcareresearch.co.nz Applications close on Tuesday 13 February 2018 at 5.00pm.

https://careers.sciencenewzealand.org/jobdetails/-ajid/RlTr8/26385-Postdoctural-Fellowship-Marsden-,26385.html Thomas Buckley Research Leader, Invertebrate Systematics Manaaki Whenua 'V Landcare Research

Associate Professor, University of Auckland T +64 9 574 4116

E buckleyt@landcareresearch.co.nz

www.landcareresearch.co.nz Thomas Buckley <BuckleyT@landcareresearch.co.nz>

NHGRI-NIH Bethesda BioinformaticsEvolutionaryGenomics

Computational and Statistical Genomics Branch National Human Genome Research Institute National Institutes of Health

Postdoctoral Fellowship in Bioinformatics and Evolutionary Genomics

A postdoctoral training position is currently available in the Computational and Statistical Genomics Branch (CSGB) of the National Human Genome Research Institute (NHGRI). The position is located in the laboratory of Andy Baxevanis, Ph.D., whose research group uses comparative genomics approaches to better-understand the molecular innovations that drove the surge of diversity in early animal evolution. The overarching theme of Dr. Baxevanis' research program is focused on how non-traditional animal models can be used to convey critical insights into human disease research, in line with the NIH Intramural Research Program's renewed emphasis on developing new animal models for the study of basic biology.

With this translational context in mind, Dr. Baxevanis' group is currently leading an international effort to sequence two cnidarian species: Hydractinia echinata and Hydractinia symbiolongicarpus. The regenerative abilities of these colonial hydrozoans make them excellent models for the study of key questions related to pluripotency, allorecognition, and stem cell biology, work that will be significantly advanced by the availability of high-quality whole-genome sequencing data from these organisms. In addition, and in collaboration with colleagues at the Whitney Marine Laboratory of the University of Florida, the group is also now focusing on polychaete species that show particular promise for advancing our understanding of regeneration and early developmental processes. The successful applicant will have the opportunity to develop and apply bioinformatic approaches to these and other large-scale genomic data sets, focusing on the evolution of specific protein families and biological pathways that have putative roles in disease causation.

Candidates should have or be close to obtaining a Ph.D. or equivalent degree in bioinformatics, computational biology, computer science, molecular biology, or a closely related field. Candidates with a background in evolutionary biology are particularly encouraged to apply. Programming skills and experience in the application of computational methods to genomic data are highly desirable. Applicants must possess good communication skills and be fluent in both spoken and written English. The ability to learn how to use new software and quickly become expert in its use, critical thinking, problem-solving abilities, and the ability to work semi-independently are required.

The NIH Intramural Research Program is on the Bethesda, Maryland campus and offers a wide array of training opportunities for scientists early in their careers. The funding for this position is stable and offers the trainee wide latitude in the design and pursuit of their research project. The successful candidate will have access to NHGRI's established and robust bioinformatics infrastructure, as well as a 'Top 100' high-performance computing resource made available through NIH's Center for Information Technology (CIT).

Interested applicants should submit a curriculum vitae, a detailed letter of interest, and the names of three potential references to Dr. Baxevanis at andy@mail.nih.gov.

For more information, please visit https://irp.nih.gov/-pi/andy-baxevanis . The NIH is dedicated to building a diverse community in its training and employment programs.

"Baxevanis, Andy (NIH/NHGRI) [E]" <andy@mail.nih.gov>

NHM London EvolutionFrogVision

The Natural History Museum, London (NHM)

Postdoctoral Researcher - Frog Vision

Starting date: July 2018 (preferred)

The Herpetology Group (embedded within the Department of Life Sciences, Division of Vertebrates) is a research-active group with four permanent staff members and multiple honorary Scientific Associates, postdoctoral researchers and postgraduate students. The group specializes in systematics, phylogenetics, and the biology of amphibians and reptiles. The NHM Herpetology group fosters a supportive and positive environment for research training and highly values diversity.

We seek a full-time postdoctoral researcher for a 28-month research-intensive position. This position is funded through a Natural Environment Research Council - National Science Foundation award The evolution of visual systems during major life history transitions in frogs. The project integrates morphological, molecular, and physiological data to investigate the evolution of vision systems in frogs at both broad and recent timescales - from across the frog tree of life to recently-diverged lineages. Molecular evolutionary studies will provide a genomic perspective on vision evolution to test hypotheses about natural selection, gene duplication, and retention of vision genes. The overall project runs for four years and tackles several sub-projects, including: (1) characterizing the physiology and molecular underpinnings of vision in species with varying early life-history modes, (2) testing whether the evolution of bright coloration in frogs is associated with visual system diversity that maximizes species recognition, and (3) determining how transitions to burrowing ecologies have shaped the morphological and genetic components of visual systems.

The successful candidate will be based at the Natural History Museum in London and will participate in multiple aspects of the research and broader impacts of the project, with a particular focus on analyses of museum specimens, studies of burrowing frogs (especially Microhylidae), and outreach through the NHM. There will also be opportunities to interact with our partner researchers at the Smithsonian National Museum of Natural History (Washington, D.C., USA) and The University of Texas at Arlington (Texas, USA). The postdoc will be provided with career planning assistance and opportunities to learn and refine skills designed to increase their professional aptitude in research, professional communication, and public outreach. Further enquiries may be emailed to Dr Jeff Streicher at j.streicher@nhm.ac.uk and/or to Dr David Gower at d.gower@nhm.ac.uk .

How to apply

Please complete your application online in our recruitment portal before 9am (GMT) 7 February 2018.

You should upload the following documents:

A comprehensive curriculum vitae giving details of relevant achievements in recent posts as well as your education and professional qualifications.

A covering letter that summarises your interest in this post, providing evidence of your ability to match the criteria outlined in the role competencies.

To access the recruitment portal please use the following link:

https://careers.nhm.ac.uk/templates/CIPHR/-jobdetail_405.aspx A detailed job description (job profile document) is available for download on the

NHM website.

J.Streicher@nhm.ac.uk

NorthCarolinaStateU InsectPlantInteractions

POSTDOCTORAL POSITION ON INSECT VECTORS OF PLANT VIRUSES

In support of a large multi-investigator initiative to develop vectored plant viruses that could edit plant genomes, a postdoctoral position is available in the Scott lab at North Carolina State University. The main aim is to develop transgenic strains of plant vectors carrying conditional lethal genes.

The vectors are aphid and leafhopper species that transmit viruses that impact corn. The engineered strains would not survive in the absence of a small chemical regulator such as an antibiotic. The modified insects would thus have a limited lifespan in proposed greenhouse trials but in the future could also potentially be used for genetic control programs.

The position is suitable for recent PhD graduates in entomology or genetics. Experience in molecular genetics and knowledge of insect vectors of plant viruses is desirable.

For more information contact Max Scott at mjscott3@ncsu.edu and apply online at https://jobs.ncsu.edu/ The posting number is PG160203PD

"coby@ncsu.edu" <coby@ncsu.edu>

NortheasternU GenomicsComputationalBiology

A postdoctoral position is available in the laboratory of Dr. K. E. Lotterhos at Northeastern University. The postdoc will also be mentored by Sam Yeaman at the University of Calgary. The successful candidate will be part of an NSF-funded project to develop and evaluate multivariate methods for analyzing genomic data.

Qualifications Applicants will be expected to develop and lead projects. Candidates are required to have a Ph.D. in Biology, Evolutionary Genetics, Statistics, Computational Biology (bioinformatics), or related disciplines. A computing background is required, especially experience with Unix, and knowledge in one or several programming languages (R/BioConductor, Python, C/C++, etc). Candidates should demonstrate a strong track record of publication; have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team.

Additional Information The appointment is for 24 months. Start time is flexible, with a desired start before May 2018.

The Lotterhos Lab is based at the beautiful in Nahant campus north of Boston (NUMSC). The NUMSC has a strong research presence in evolution and ecology research, and there are many opportunities for interaction and collaboration both there and in the greater Boston area. More information about the lab's research can be found here: https://sites.google.com/site/katielotterhos/home. The successful candidate will also have opportunities to travel to Calgary for extended periods of time for collaboration, and to manage a diverse team of collaborators. We welcome applications from candidates with diverse educational backgrounds.

To apply, please prepare a CV, cover letter, references, and one peer-reviewed publication and upload them at this site: https://neu.peopleadmin.com/postings/49443 Please contact Dr. Lotterhos with any questions at k.lotterhos@neu.edu

K. E Lotterhos Assistant Professor Department of Marine and Environmental Sciences Northeastern University Marine Science Center, Room 113 430 Nahant Rd Nahant, MA 01908 Phone: 781.581.7370 ext 304

Katie Lotterhos <k.lotterhos@northeastern.edu>

NYU AbuDhabi MangroveGenomics

Deadline for applications: 10 January.

New York University Abu Dhabi (NYUAD) is seeking a Post-Doctoral Researcher who will apply genomics to study the locally abundant, pan-tropical gray mangrove, Avicenna marina. NYUAD is located on the shores of the Persian/Arabian Gulf, an area that is at the northern margins of this species range and where environmental conditions (temperature ranges, salinity, aridity) are extreme. The core focus of the Post-doctoral

Researcher'Âs role will be to use a population genomics approaches to identify regions of the mangrove genome under positive selection in response to extreme temperatures and highly saline conditions using various populations in the Arabian Gulf, Arabian Sea, and Red Sea. As part of a larger integrated research project, the Post-doctoral Researcher will also work closely with researchers who will be developing a reference genome for Avicenna marina and investigating the influence of abiotic stress at the transcriptomic and metabomic level. The candidate would be encouraged to expand this core research to address broader evolutionary/ecological questions.

The Post-Doctoral Researcher will work in the NYUAD marine biology laboratory (https://-nyuad.nyu.edu/en/research/centers-labs-and-projects/-marine-biology-lab.html) under PI John Burt with day-to-day supervision by Research Scientist Ed Smith, and will closely collaborate with researchers in the NYUAD Laboratory of Algal, Systems, and Synthetic Biology headed by PI Kourosh Salehi-Ashtiani (https://lassb.abudhabi.nyu.edu/index.php).

To be successful in this role you MUST possess the following essential traits: - PhD in Biology or equivalent [only those with PhDs completed on/before April 2018 can be considered]. - A strong publication record with first-author experience - Research experience in population genetics - Strong interpersonal skills with the ability to liaise with external stakeholders, employees, management and students.

DESIRABLE experience/qualifications: - Experience in population genomics - Experience with other 'Vomics - Experience linking genomics and ecological performance - Experience working on mangroves - Boat operator certification (e.g. powerboat skipper, etc) - Dive certification from an accredited agency (PADI, BSAC or similar organization) - Ability to conduct multiple, possibly divergent, research projects simultaneously - Ability to train and mentor undergraduate students - Ability to plan, allocate, and monitor research budgets for projects - Experience leading permit requests for research collections (nationally and internationally) - Valid driver'Âs license in home country - International research experience

The position begins September 2018. This will be a two-year fixed-term contract position, potentially renewable for a third year based on successful performance. Salary is competitive and the position will come with an attractive salary and benefits package including a housing allowance, annual flights, and tuition for children (if relevant), and medical insurance. Salary is free from income tax in the UAE. Hiring is contingent on successful clearance of security, health, and reference checks, among other HR-related parameters.

APPLICATION INSTRUCTIONS: The closing date for applications is 10 January 2018. Applicants should create a single PDF file that includes a cover letter (max 2 pages) that specifically refers to qualifications/experience related to the lists above, a curriculum vitae that includes the names and contact information for three research-related references, as well as copies of recent relevant lead-author publications. Please email this application file to John.Burt@nyu.edu with the text MANGROVE APPLICATION in the subject line. Only short listed candidates will be contacted for an interview.

John Burt <john.burt@nyu.edu>

OldDominionU MarineBiodiversity

Graduate Research Assistant (PhD) - Marine Molecular Ecology at Old Dominion University

The Department of Biological Sciences at Old Dominion University, a "Doctoral Research - Extensive" state university, has an opening for a PhD Graduate Research Assistant in marine molecular ecology. The appointment will begin in the summer or fall semester of 2018. This position involves participation in an NSF-funded PIRE (Partnerships for International Research and Education) Project to examine genetic and species-level changes in marine biodiversity over the past century of intense fisheries exploitation and habitat degradation in the Philippines. The successful candidate will be expected to live in the Philippines during summer sessions to conduct research in the field and laboratory in a collaborative, multinational setting. Applicants must have a bachelor's or master's degree at the time of employment, and demonstrate interest or experience in molecular ecology, population genomics, marine phylogeography, or a closely related field. Competitive applicants will have some experience conducting molecular ecology research in the field and/or laboratory; AAUS Scientific Diver certification is desired. Underrepresented minorities are particularly encouraged to apply.

Interested applicants should send an email to Kristene Parsons (kparsons@odu.edu) that includes (1) a cover letter describing your interest in the position, prior research, and future career goals, (2) your curriculum vitae, (3) a copy of your college transcript(s), and (4) the names, telephone numbers, and addresses (postal and email) of three references. Review of applications will begin in February, 2018 and will continue until a suitable candidate is found. For more information about the department, other faculty and students, please see the websites of the Department of Biological Sciences (http://www.odu.edu/biosci) and Kent Carpenter (http://www.odu.edu/directory/people/k/kcarpent). Additional information on the Philippine PIRE Project can be found at https://sites.wp.odu.edu/PIRE/. AA/EOE/M/F/Disability/VETS/Drug Free

Kristene T. Parsons NSF PIRE Project Administrator Department of Biological Sciences Old Dominion University Norfolk, VA 23529-0266 USA

kparsons@odu.edu | 757-683-3481

“Parsons, Kristene” <kparsons@odu.edu>

Prague EvolGenomicsOlfactionFishes

LAST CALL: We are offering a postdoc position in the Laboratory of Fish Evolution in Prague, Czech Republic.

The topic: Sensory genomics of the olfactory system in fishes

The selected candidate will become part of a research team within the framework of the project entitled: “Genomics of sensory adaptations: evolution of vision, smell and taste in fishes” funded by Swiss National Science Foundation (SNSF, Switzerland). The main focus of the lab is on the evolution of the sensory systems (vision, olfaction, gustation) in several groups of fishes (including crater-lake cichlids, deep-sea fishes, elephant fishes). The research in the lab is currently substantially covered by two research grants.

We search for a highly motivated postdoc candidate who would be responsible for the analysis of the olfactory receptors in the whole-genome and transcriptome data leading to the large-scale comparative analysis, as well as a small-scale focus on evolution of the olfactory receptors during speciation. The general research project further aims to integrate the findings of molecular genetics with trophic ecology, developmental stages and other sensory abilities (mostly vision) in different species.

We offer: 24-months postdoc position in a dynamic research team with several PhD and MSc students, access to fascinating fish samples from the tropics, European rivers, as well as the deep sea, possible (not required) participation in the field work in Africa. We offer substantial salary (360’000 CZK annually, equal to the average national salary in the Czech Republic; guaranteed), the candidate will then immediately apply for a very competitive salary of 746’000 CZK annually (more than 2x the average salary in the Czech Republic).

We require: postdoctoral candidate with at least moderate bioinformatics skills (experience with molecular genetic data highly desired), with the PhD title received no longer than 7 years ago (extension due to maternity leave applicable), at least two research publications in the last three years, the applicant must have resided outside the Czech Republic at least for 2 of the last 3 years. All nations applicable.

Start: July 2018, Duration: 2 years.

Deadline: 24th January 2018 (the candidate should be ideally assigned to the position by the end of January).

All questions and applications (CV + half-page motivation letter + contact details for two persons who can be asked for a reference) should be sent directly to Zuzana Musilova (zuzmus@gmail.com - preferred, zuzana.musilova@natur.cuni.cz). More info about the Division of Animal Evolutionary Biology, and Department of Zoology: http://web.natur.cuni.cz/zoologie/biodiversity/index.php?page=3Dmusilova zuzmus@gmail.com

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PUCE Ecuador AmphibiaReptiliaSystematics

Museo de Zoologia QCAZ

Pontificia Universidad Catolica del Ecuador

Quito - Ecuador

Post-doctoral Fellowships in Systematics of Amphibians and Reptiles

Starting date: May 1st, 2018

The Zoology Museum at Pontificia Universidad Catolica del Ecuador (http://bioweb.puce.edu.ec/QCAZ/inicio) invites applications for post-doctoral research fellowships in Systematics of Amphibians and Reptiles with a start date of May 1st, 2018. These positions will be part of the “Arca de Noe” initiative, a long-term research project (2009-present) funded by the Ecuadorian government.

The "Arca de Noe" initiative has produced 80 scientific publications including the description of more than 70 species of amphibians and reptiles from Ecuador and Peru. This project is led by Professors Santiago Ron (curator of amphibians) and Omar Torres-Carvajal (curator of reptiles), and it has a strong field component that has resulted in large collections of specimens and tissue samples.

We seek candidates with a strong research background and publication record in phylogenetic systematics of amphibians and reptiles. Experience in molecular genomics and bioinformatics is preferable. Candidates should have completed their PhD anytime during the last 10 years. The post-doctoral fellows will help with the description of new species of amphibians and reptiles, as well as with projects on molecular systematics, phylogenomics and biogeography of Neotropical taxa. Candidates willing to develop their own research projects that match the goals of the "Arca de Noe" initiative are welcome. Fellows will be provided with office space, computer facilities, funding for laboratory work, and a one-year contract. We encourage international applicants to review all regulations and requirements for applying for jobs in Ecuador (see links below).

Applications should include: (1) curriculum vitae, (2) letter of intent, and (3) contact details of two academic referees. Applications should be submitted electronically as a single PDF file to <santiago.r.ron@gmail.com> or <omartorcar@gmail.com> before February 15th, 2018.

Visa information: http://www.consuladovirtual.gob.ec/servicios/2017_req_vis2_temCienti_ing.html For citizens of MERCOSUR countries:

http://www.consuladovirtual.gob.ec/servicios/2017_req_vis2_temMercos_ing.html Omar Torres Carvajal <omartorcar@gmail.com>

SLU Sweden EvolutionaryEcology

A POSTDOC POSITION in Evolutionary Ecology is available in The Strawberry Lab at SLU, SWEDEN.

Plant resistance and tolerance to herbivores often show high complexity that results from interactions with multiple selective agents. Understanding the complex nature of plant defences against multiple herbivores, as well as the evolutionary and ecological consequences of attack by multiple herbivores, adds not only to our knowledge of the evolutionary ecology of plant-herbivore interactions, but is also likely to benefit attempts to find sustainable plant protection strategies.

THE AIM of this postdoc project is to gain knowledge about the evolutionary and ecological consequences of attack by multiple herbivores. Woodland strawberry, Fragaria vesca L., will be used as a model plant. Since non-domesticated plant species in general are more resistant and tolerant to herbivores, and show higher variation in their traits, studying woodland strawberry provides useful information about traits that contribute to improved resistance and tolerance. The postdoc will have access to a large number of strawberry genotypes that show high genetic variation in several traits. For example, we already have some knowledge on genetic variation in plant resistance against the strawberry leaf beetle (Muola et al. 2017) as well as some preliminary data on plant resistance and tolerance against several other herbivores. The postdoc is expected to expand this knowledge through experimental work. Woodland strawberry shares substantial sequence identity with garden strawberry (Fragaria Ã ananassa). The genome of woodland strawberry has been sequenced and it serves as model plant for cultivated strawberries. Thus, understanding the different defence strategies of woodland strawberry provides useful information for plant breeders.

QUALIFICATIONS: We are looking for a highly motivated candidate with a PhD degree in Evolutionary Ecology or similar subject. Scientific qualifications within the area are necessary. Good collaborative ability is also necessary. The ranking of candidates will be made based on proven scientific competence within the subject of the position. Priority will be given to applicants who have been awarded their PhD degree at most three years before the application deadline. The candidate should have the ability to work independently, take own initiatives, and have an interest in Integrated Pest Management.

SPECIFIC DOCUMENTS to attach: CV including a list of publications, max. five publications, description of previous research and current research interest (max. two pages), contact details to at least two reference persons.

MENTORS: Anne Muola & Johan A. Stenberg

STARTING DATE: Flexible, but we would like to fill the position before field season 2018.

FORM OF EMPLOYMENT: stipend, 1+1 year(s)

EXTENT: 100%

MORE INFORMATION: anne.muola@slu.se; johan.stenberg@slu.se

HOW TO APPLY: Send your application to Muola and/or Stenberg using the above email addresses. There is no formal deadline - the position is open until we find a suitable candidate.

Johan A. Stenberg Associate Professor

Sveriges lantbruksuniversitet Swedish University of Agricultural Sciences

Department of Plant Protection Biology PO Box 102, SE-230 53 ALNARP Visiting address: Sundsvägen 14 Tel: +46 40 41 53 78 johan.stenberg@slu.se, www.slu.se/stenberg "Johan A. Stenberg" <Johan.Stenberg@slu.se>

StockholmU EvolutionaryEcologyThermalAdaptation

Postdoc position in Evolutionary Ecology at Stockholm University

APPLICATION DEADLINE: MARCH 1, 2018

A 2-year postdoc position is available in Rhonda Snook's group, recently relocated to the Department of Zoology, Stockholm University. The project is focused on the genetic architecture of reproductive performance in response to thermal stress using Drosophila. The work will include collection and analysis of male and female reproductive phenotypes under different thermal regimes, analysis of population genomic data, and the use of forward and reverse molecular genetics techniques. You will be expected to have a PhD in evolutionary biology, population genetics or a similar—subject with a strong interest in thermal ecology, and a molecular genetic and bioinformatic background.

Stockholm University's Department of Zoology is a vibrant international and interactive community. Working language in the lab is English.

For informal queries, contact Rhonda on rhonda.snook@zoologi.su.se

Details to apply, including more about the project, are available here:

https://www.su.se/english/about/working-at-su/jobs?rmlang=UK&rmpage=job&rmjob=4655 Rhonda Snook <rhonda.snook@zoologi.su.se>

StockholmU EvolutionaryGenomics

Postdoc position in Evolutionary Genomics at Stockholm University

We have an opening for a highly motivated postdoctoral fellow to work on the ERC-funded project SuperGenE. The position is for two-years, with possibility for extension, in the group of Dr. Tanja Slotte at Stockholm University and Science for Life Laboratory in Stockholm. Deadline for applications is February 15, 2018.

The complete ad with information on how to apply is available on the Stockholm University webpage: http://www.su.se/english/about/working-at-SU/jobs?rmpage=3Djob&rmjob=3D4587&rmlang=UK Project description: In this project, we will investigate evolutionary processes at a classic supergene, the distyly S-locus. We will conduct these studies in Linum, where the dynamic nature of distyly presents an outstanding opportunity to study supergene evolution. To do so, we will first generate multiple de novo genome assemblies of Linum species, and then use this genomic framework to comprehensively test hypotheses on the evolution and breakdown of the distyly supergene.

Responsibilities: The postdoctoral fellow will be responsible for de novo genome assembly based on long reads, and comparative and evolutionary genomic analyses.

Infrastructure and environment: The postdoctoral fellow will join a group of postdocs and PhD students led by Dr. Tanja Slotte. For recent examples of our work, see e.g. Laenen, Tedder et al. 2018 PNAS, Steige, Laenen et al. 2017 PNAS, Steige et al. 2015 MBE, or Slotte et al. 2013 Nature Genetics. The postdoc will be based in the Slotte lab (http://tanjaslottelab.se), a part of the Dept. of Ecology, Environment and Plant Science, Stockholm University. We are located at the Science for Life Laboratory in Stockholm (http://www.scilifelab.se), which holds considerable expertise in high-throughput sequencing technology and bioinformatics. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both genomicists, evolutionary biologists and ecologists at SciLifeLab and Stockholm University.

Qualification requirements: Applicants are expected to hold a PhD, preferably in evolutionary genetics, genomics, bioinformatics, or a related subject. The degree should have been completed no more than three years before the deadline for applications. Experience of de novo assembly and annotation of eukaryotic genomes is a very strong merit. Experience of evolutionary genetic analyses, comparative genomics, genetic mapping and/or gene expression analyses is highly meriting. Strong coding/scripting skills and ability to work on a high-performance computing cluster are required. A strong interest in evolutionary genetics is beneficial.

Assessment: In the appointment process, special attention will be given to research skills, in particular pertaining to analyses of large-scale genomic data. The applicant should have proven expertise in genomics and be used to handle large genomic data sets. Experience of de novo genome assembly of eukaryotic genomes is especially meriting. Documented scientific qualifications within the research field, such as first, or joint-first author publication(s) are desirable. Excellent proficiency in English (the working language of the group) is required. The postdoctoral fellow needs to be able to work well in a collaborative environment, as well as independently. Finally, creativity and drive are personal characteristics that are desirable.

Terms of employment: The position involves full-time employment for a maximum of two years, with a possibility of extension. Start date per agreement.

Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Application: Apply for the positions through Stockholm University's recruitment system: http://www.su.se/english/about/working-at-SU/-jobs?rmpage=3Djob&rmjob=3D4587&rmlang=UK Contact: For further information about the position, please contact Dr. Tanja Slotte directly at tanja.slotte@su.se

“tanja.slotte@su.se” <tanja.slotte@su.se>

StockholmU PopulationGenomics

Postdoc position in Population Genomics at Stockholm University

A two-year postdoctoral position in population genomics of plant mating system shifts is currently available at Stockholm University and Science for Life Laboratory in the research group of Dr. Tanja Slotte. Deadline for applications is February 15, 2018.

The complete ad for this position is available on the Stockholm University webpage: http://www.su.se/-english/about/working-at-SU/jobs?rmpage=-3Djob&rmjob=3D4585&rmlang=UK Project description: Plant mating systems, such as shifts from outcrossing to selfing, have profound effects on levels and structuring of genetic variation, and are expected to have a marked effect on the impact of natural selection. We are looking for a highly motivated postdoctoral fellow to work within a project concerning the population genomic consequences of plant mating system shifts and the impact of selection on linked sites on plant genomic variation. Whole-genome and whole-transcriptome sequence data sets from multiple species are already available, and more are currently being generated in the lab.

Responsibilities: The position involves research on the population genomic effects of plant mating system shifts, and will include analysis of large-scale population genomic data and population genomic simulations. The position may also include sampling of natural plant populations in the Mediterranean region.

Infrastructure and environment: The postdoctoral fellow will join a group of postdocs and PhD students led by Dr. Tanja Slotte. For recent examples of our work, see e.g. Laenen, Tedder et al. 2018 PNAS, Steige, Laenen et al. 2017 PNAS, or Steige et al. 2015 MBE. The postdoc will be based in the Slotte lab (http://-tanjaslottelab.se), a part of the Dept. of Ecology, Environment and Plant Science, Stockholm University. We are located at the Science for Life Laboratory in Stockholm (http://www.scilifelab.se), which holds considerable expertise in high-throughput sequencing technology and bioinformatics. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both genomicists, evolutionary biologists and ecologists at SciLifeLab and Stockholm University.

Qualification requirements: Applicants are expected to hold a PhD, preferably in population genetics, evolutionary genetics, bioinformatics, or a related subject. The degree should have been completed no more than three years before the deadline for applications. Experience of analyses of large-scale population genomic data is required. Experience of population genetic simulations is beneficial. Excellent coding skills and ability to work on a high-performance computing cluster are required. Experience of sampling of plant populations in the field is beneficial. A strong interest in mating system evolution, in particular transitions from outcrossing to self-fertilization, is beneficial.

Assessment criteria: In the appointment process, special attention will be given to research skills, in particular pertaining to analyses of large-scale population genomic data. The applicant should have proven expertise in genomics and be used to handle large genomic data sets (i.e. "next-generation sequencing" data). Documented scientific qualifications within the research field, such as first or joint-first author publication(s) are desirable. Excellent proficiency in English (the working language of the group) is required. The postdoctoral fellow needs to be able to work well in a collaborative environment, as well as independently. Finally, creativity and drive are personal characteristics that are desirable.

Terms of employment The position involves full-time employment for a maximum of two years, with a possibility of extension. Start date per agreement.

Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Application Apply for the position through Stockholm University's recruitment system: http://www.su.se/-english/about/working-at-SU/jobs?rmpage=-3Djob&rmjob=3D4585&rmlang=UK Contact For further information about the positions, please contact Dr. Tanja Slotte directly at tanja.slotte@su.se

"tanja.slotte@su.se" <tanja.slotte@su.se>

TuftsU MicrobialEvolution

Post-doc position in *plant microbiome ecology/evolution in the Wolfe Lab @ Tufts University (Boston Area) *https://sites.tufts.edu/wolfelab/join-the- wolfe-lab/

The Wolfe lab in the Department of Biology at Tufts University (https://sites.tufts.edu/wolfelab/) is seeking a post-doc to start in April 2018 (start date flexible). Our lab studies the ecology and evolution of microbial communities, using tractable microbial communities isolated from food (cheese, kimchi, fermented tea) as model systems.

This position is funded by a grant from the NSF/USDA Plant-Biotic Interactions program to study the assembly of microbial communities on cabbage leaves (https://-goo.gl/CAuXkn). Using field experiments across New England and lab experiments with gnotobiotic cabbages, the post-doc will identify the ecological and evolutionary processes that shape the diversity of the cabbage phyllosphere microbiome. The project also seeks to identify links between cabbage phyllosphere microbiome assembly and fermentation outcomes.

The ideal candidate will be a creative, independent, and integrative scholar with interests in discovering the ecological and evolutionary processes that generate microbiome diversity. She/he will have the following:

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a PhD in microbiology, ecology/evolution, plant pathology, or biology

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experience in plant microbiomes or plant-microbe interactions -

experience generating and analyzing next-generation sequencing datasets -

a track record of supporting an engaging, thoughtful, and collaborative lab environment

This position also provides ample opportunities for the post-doc to develop teaching/outreach skills. Our accessible and engaging model systems provide powerful tools to promote microbial literacy in the college classroom as well as in our local communities (https://sites.tufts.edu/-wolfelab/open-lab/). Members of the lab communicate their science through social media, writing for online publications, and by developing novel public outreach experiences.

The Wolfe lab is based in a newly renovated lab space associated with the Tufts University Medford Campus. In addition to diverse research being conducted in the Department of Biology that spans the entire breadth of biology (http://ase.tufts.edu/biology/), the Sackler School of Graduate Biomedical Sciences at the Tufts Medical School has an outstanding group of microbiologists (http://bit.ly/WDvgqA). There are also numerous potential collaborators and resources at the Tufts Friedman School of Nutrition and the Cummings School of Vet Medicine. The academic community in the Greater Boston Area has an unprecedented collective wealth of resources in microbiology, ecology, and evolution.

To apply, email Dr. Benjamin Wolfe (benjamin.wolfe@tufts.edu) with: 1) a short description of why you are interested in and qualified for the position, 2) a CV listing peer-reviewed publications, skills, and research experiences, and 3) the names and contact information for three references. Applications will be considered as they are received. For full consideration, apply on or before March 1st, 2018.

Benjamin Wolfe <benjamin.wolfe@tufts.edu>

UAlgarve Portugal EvolFunctionalDifferentiation

A postdoctoral position is available at CCMAR (Univ. Algarve, Portugal) to work on the functional differentiation of thermal traits in kelp species (large forest-forming brown algae), focusing on both intra- (between population) and inter-specific levels. The position requires bioinformatic expertise for the analysis of RNA-seq data from completed and ongoing experiments. The successful candidate would be proficient in UNIX command line computing, and preferably additional scripting languages (perl, python or other). Previous experience in bioinformatic analysis of transcriptome data in non-model organisms (de novo assembly, expression analysis and annotation) are desirable, but not essential. The candidate will be joining a dynamic and productive team of molecular ecologists and evolutionary biologists whose current major focus is on the biogeography and conservation of brown algal forests worldwide. Additional credit will be given to candidates with a strong background in independent research and proven publication record.

For details on the project please contact: — gpearson@ualg.pt Gareth Pearson (Research Associate) Centre of Marine Sciences (CCMAR), Universidade do Algarve, 8005-139 Faro Portugal

If interested, please send to gpearson@ualg.pt your CV, contacts of three referees and a letter of motivation explaining how you meet these evaluation criteria:

Evaluation criteria: - proficiency in UNIX command line computing, and preferably additional scripting languages (perl, python or equivalent). - Previous experience in bioinformatic analysis of transcriptome data in non-model organisms (de novo assembly, expression analysis and annotation) - Independent research experience and proven publication record in bioinformatics (expected: at least one paper as first author per year since the PhD).

The position can start anytime and will remain open until we find a suitable candidate. The contract will be initially for 6 months and can be renewed for up to two years depending on performance.

Ester Serrāo <eserrao@ualg.pt>

UArizona ProteinEvolutionBioinformatics

Postdoc position: long-term trends in protein evolution

A postdoc position is available with PI Joanna Masel (http://eebweb.arizona.edu/faculty/masel) at the University of Arizona in Tucson. A popular tourist destination surrounded on all four sides by mountainous national and state parks, Tucson is a vibrant city of nearly a million people with an attractive climate. The EEB department was ranked in the top 10 by US News & World Report.

We recently found that genes of different ages encode proteins with different computationally predictable structural properties, forming an extraordinarily long-term trend (see https://doi.org/10.1101/176867). This project will use bioinformatics techniques to discover whether these long-term trends are really a consequence of evolution by descent with modification that continues for long periods of time in a consistent direction. It will also provide a major new annotation of genes based on homology, in order to begin removing the problem of phylogenetic confounding within gene families from “correlomics”.

Techniques used may include phylostratigraphy (assigning ages to gene families), ancestral sequence reconstruction, and porting macroevolutionary techniques for studying speciation and extinction to the study of gene duplication and loss. A high level of statistical sophistication is required throughout.

Excellent computer programming skills are strongly preferred, ideally with bioinformatics / genomics and statistics experience. Exceptionally strong candidates who come from a more experimental background within evolutionary biology, and who now wish to retrain as bioinformaticians, will also be considered. A background in evolutionary biology is also strongly preferred, although again, exceptionally strong computational scientists from highly quantitative backgrounds outside evolutionary biology will also be considered. Statistical knowledge, and knowledge about protein structure and folding, are advantages. Start date is negotiable, and the position is renewable, with funding secured through July 2020.

Contact Joanna Masel at masel@email.arizona.edu for more information and to apply.

masel@email.arizona.edu

UBarcelona EvoDevo

We seek EvoDevo Postdoctoral candidates for 2-year-BP-fellowship call (ASAP, deadline Feb 28th 2018) to work on #EvoDevoGenomics #GeneManipulation #Transcriptomics #HeartMuscleDevelopment #UrochordateOikopleura #GeneLoss (more info in https://goo.gl/uCBBSp) Call info: https://goo.gl/0ZaDm0 Cristian Cañestro's lab (canestro@ub.edu) Department of Genetics, University of Barcelona

oikocris@gmail.com

UBath SpeciationGenomicsMice

Postdoc available on SPECIATION GENOMICS in House Mice

Leslie Turner's lab, Milner Centre for Evolution, University of Bath, UK I am recruiting a postdoctoral research associate to work on a German Research Foundation (DFG) funded project focused on genetics and genomics of hybrid male sterility in house mice. The project combines genome and transcriptome sequencing with detailed phenotyping to identify genes and gene networks contributing to this reproductive barrier trait. Postdoc will contribute primarily to transcriptomic analysis, but will have the opportunity to contribute to molecular genetics research. The position also offers the successful candidate flexibility to pursue related questions, and I will encourage development of an independent research project.

The recently established Milner Centre for Evolution is a vibrant community of 18 labs working on diverse evolutionary questions. The successful candidate will join an academically stimulating, research-intensive environment with many opportunities for interaction and collaboration. We are located in a brand new building on the lovely University of Bath campus.

The successful candidate will have a strong background in evolutionary biology, quantitative genetics and/or computational genomics. Strong data analysis skills, including programming and statistical analysis, are essential. Bioinformatics or molecular genetics experience is a plus. Candidates should have a demonstrated ability to publish high quality science as well as good interpersonal and communication skills.

The position is for 24-30 months. Starting date: as soon as convenient (preferably by Jun 1st 2018).

For more information about the lab see http://leslieturner.net Email me with informal enquiries (l.m.turner@bath.ac.uk) Apply by January 29th here: https://www.bath.ac.uk/jobs/Vacancy.aspx?ref=SF5480 Leslie Turner <L.M.Turner@bath.ac.uk>

UBritishColumbia GeneticBasisAdaptation

Postdoctoral position at University of British Columbia and the University of Calgary in methods to measure the genetic repeatability of local adaptation.

Michael Whitlock at UBC and Sam Yeaman at the University of Calgary have a post-doctoral position available to develop and test methods to measure the repeatability and constraints on the genetic basis of local adaptation. We seek to develop genomic methods that will quantify the extent to which the genetic basis of local adaptation is shared among evolutionarily distinct lineages, based on inference from gene-environment correlations and genome-wide association studies.

This project is part of a larger initiative called CoAdapTree (http://coadaptree.forestry.ubc.ca), funded by Genome Canada. CoAdapTree aims to uncover the genetic basis of adaptation to climate and fungal pathogens for several economically-important conifer species. This will include large population-scale sequencing efforts in four species (lodgepole pine, Douglas fir, western larch, and jack pine).

The ideal candidate will have a strong background in both evolutionary biology and statistics. Experience with bioinformatics, phylogenetics, or evolutionary genomics would be desirable but not required.

In addition to the core project of methods development, this post-doc has the possibility of collaborating on further projects, including other analyses of the larger CoAdapTree project or the development of theory on mechanisms of convergent evolution.

Funding is available for two years with salary of 0,000 Canadian per year plus benefits.

For more information, please contact Michael Whitlock at UBC (whitlock@zoology.ubc.ca) or Sam Yeaman at University of Calgary (samuel.yeaman@ucalgary.ca). To apply, please send a CV and a contact list of people who could be contacted for letters of reference.

Michael Whitlock <whitlock@zoology.ubc.ca>

UCalifornia LosAngeles Conservation

The UCLA La Kretz Center for California Conservation Science (http://www.environment.ucla.edu/lakretz/) invites applications for its annual Postdoctoral Fellowship in California Conservation Science. Consistent with our mission, we seek one or two postdoctoral scholars who simultaneously conduct innovative research and interface with the conservation and management agencies that direct and lead California conservation. For our 2018 competition, we are specifically seeking one, or possibly two postdoctoral candidates who will lead a broad, conservation genomics analysis of multiple co-distributed species across Los Angeles and Southern California. Our goal for this targeted call is to determine such issues as the contribution of protected lands to the conservation of genetic diversity, the ability of species to traverse the urban landscape of Los Angeles and surrounding regions, and genetic resilience to future climate change. Work on any taxa can be appropriate. We are particularly interested in fellows who develop a taxonomically broad, multi-species approach to comparative landscape genomics. The fellows will be co-funded by the La Kretz Center and the UCLA Sustainable LA Grand Challenge (https://grandchallenges.ucla.edu/sustainable-la/-), working together to conduct molecular lab work and GIS-intensive analyses. We will consider candidates who have recently completed their PhD, or will have completed it by summer, 2018.

These La Kretz Fellowships are for two years, subject to review after the first year. Our expected start date is summer, 2018. Successful applicants will be expected to identify and work with at least one UCLA faculty member La Kretz affiliate (http://www.environment.ucla.edu/lakretz/people/-affiliates.php) and one off-campus agency partner. The position has an annual salary of approximately $49,000 plus full benefits as well as funds for molecular lab work. Fellows have the option to reside at the newly renovated La Kretz Field Station (https://www.ioes.ucla.edu/-santa-monica-mountains-research/), located in the Santa Monica Mountains about 25 miles from campus, should it fit with their research objectives.

Several of our partner agencies have expressed particular interest in this conservation genomics call. We encourage candidates to contact our key partners in developing this project, including:

Sophie Parker The Nature Conservancy sophie_parker@TNC.ORG Jann Vendetti LA Natural History Museum JVendett@nhm.org Robert Fisher U.S. Geological Survey rfisher@usgs.gov Mike Westphal US Bureau of Land Management mwestpha@blm.gov Cat Darst US Fish and Wildlife Service cat_darst@fws.gov Katy Delaney National Park Service katy_delaney@nps.gov Seth Riley National Park Service seth_riley@nps.gov Danielle Lefer CA State Parks danielle.LeFer@parks.ca.gov

Interested candidates should submit 1) cover letter, 2) current CV, 3) maximum 2-page description of their research and management accomplishments, 4) 2-page proposal describing their proposed research including potential faculty and agency mentors (single spaced, 2 page limit includes figures but not references), and 5) copies of two research publications, all as a single PDF file to Will Zou, Administrative Assistant, at lakretz@ioes.ucla.edu You should also have three letters of recommendation, including one from your Ph.D. advisor and one from your UCLA and agency co-mentors, sent under separate emails with the subject line 'La Kretz Postdoc letter for XXX (your last name)'. The deadline for completed applications is 10 February 2018.

E-mail questions to to Brad Shaffer (Director of the La Kretz Center) at brad.shaffer@ucla.edu

Brad Shaffer <brad.shaffer@ucla.edu>

UCalifornia Riverside PlantBacterialSymbiosis

The Sachs Lab at UC Riverside is recruiting a postdoctoral scholar to join our team. We are looking for a highly motivated, independent, postdoctoral scholar to study the evolution and population genomics of plant-bacterial symbioses.

We use field studies, greenhouse experiments, in vitro evolution, and next-generation sequencing to investigate nitrogen-fixing symbioses between rhizobia and legumes. In the legume-rhizobia symbiosis, soil bacteria trigger the formation of nodules on legume roots and fix nitrogen for their host in exchange for carbon. This mutualism generates much of the fixed nitrogen for our biosphere, promotes plant growth and carbon sequestration, and accelerates ecosystem development. But among rhizobial genotypes there is significant variation in nitrogen fixation, including ineffective strains (non-nitrogen fixing) that can be common in some habitats. Ineffective rhizobia persist in natural and agricultural soils, but scant is known about the forces that drive variation in the key mutualist service of nitrogen fixation.

We work on wild, model, and crop legume species that interact with multiple bacterial symbiont lineages. The postdoc can propose research or can choose their primary research foci once they join the lab. Major projects in our lab include i) investigating the evolution and mechanisms of 'host control' traits in legumes that constrain exploitation in rhizobial symbiont populations, ii) uncovering competitive interactions among rhizobia in soil communities to explain the genomic and phenotypic drivers of rhizobial strain dominance, and iii) using greenhouse and in vitro experiments to generate novel applications to improve crop growth. Our group is broad and has included students focusing on plant biology, microbiology, genetics and genomics, and evolutionary ecology.

Candidates should have a Ph.D. in evolutionary biology, genetics, genomics, population biology, or related disciplines. Solid bacteriology skills and some computational competence are both a plus for this position. A strong background in evolutionary and or molecular genetics would also be useful. Finally, the ideal candidate would have experience with next-generation sequencing techniques, which might include RADseq and highly-multiplexed-whole genome sequencing. Irrespective of experience, the postdoc must be able to learn new techniques and quickly and easily troubleshoot protocols. She or he will likely work closely with graduate students and the PI to manage multiple research projects and thus we seek a team player with excellent leadership skills.

The start date is flexible. The position will be available as early as March 2018, but can begin later if necessary. The position is initially for a one-year period, with possible extension of another two years, dependent upon satisfactory performance. Salary is commensurate with experience and qualifications.

Application for the position requires three documents:

1. A cover letter describing your interest in the position and that details 2 projects that you would like to do in our lab.

2. Contact details of three referees

3. A CV

Interested individuals should send these materials to joel.sachs@ucr.edu by February 15, 2018. Also, feel free to e-mail me to ask any questions about the position or our lab.

The University of California, Riverside has an active career partner program, and is an Affirmative Action equal opportunity employer committed to excellence through diversity.

Recent publications from the lab

Lotus japonicus alters in planta fitness of Mesorhizobium loti dependent on symbiotic nitrogen fixation K.W. Quides, G.M. Stomackin, H.Lee, J.H. Chang, J.L. Sachs. 2017 PLoS One

Cell autonomous sanctions in legumes target ineffective rhizobia in nodules with mixed infections J.U. Regus, K.W. Quides, M.R. O'Neill, R. Suzuki, E.A. Savory, J.H. Chang, J.L. Sachs. 2017 American Journal of Botany 104 (9):1-14

Nitrogen deposition decreases the benefits of symbiosis in a native legume J.U. Regus, C.E. Wendlandt, R. M. Bantay, K.A. Gano-Cohen, N. J. Gleason, A. C. Hollowell, M. R. O'Neill, K. K. Shahin, J.L. Sachs. 2017 Plant and Soil 414:159-170

Metapopulation dominance and genomic-island acquisition of Bradyrhizobium with superior catabolic capabilities A.C. Hollowell, J.U. Regus, D. Turissini, K.A. Gano, R. Bantay, A. Bernardo, D. Moore, J. Pham, J.L. Sachs. 2016. Proceedings of the Royal Society of London. 283: 20160496

Epidemic spread of symbiotic and non-symbiotic Bradyrhizobium genotypes across California A.C. Hollowell, J.U. Regus, K.A. Gano, R. Bantay, D. Centeno, J. Pham, J.Y. Lyu, D. Moore, A. Bernardo, G. Lopez, A. Patil, S. Patel, Y. Lii, J.L. Sachs. 2016 Microbial Ecology, 71 (3) 700-710

Lotus hosts delimit the mutualism-parasitism continuum of Bradyrhizobium Regus, J. U., K.A. Gano, Holllowell, A.C., V. Sofish, J. L. Sachs . 2015 Journal of Evolutionary Biology. 28, 447-458

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UCalifornia SantaCruz PlantSpeciation

Postdoc in Plant evolution at University of California, Santa Cruz

DESCRIPTION

The Ecology and Evolutionary Biology Department (https://www.eeb.ucsc.edu/) at the University of California, Santa Cruz (UCSC) invites applications for the position of Postdoctoral Scholar under the direction of Associate Professor Kathleen Kay under a five-year NSF Dimensions of Biodiversity grant ("Biotic and abiotic drivers of Neotropical plant speciation"). The scholar will investigate the phylogeny, population genomics, and quantitative genetics of the spiral gingers (monocot genus Costus). The project is a collaboration among PIs Kathleen Kay (UCSC), Jennifer Funk (Chapman University), Carlos Garcia-Robledo (University of Connecticut), Santiago Ramirez (UC Davis) and Dena Grossenbacher (Cal Poly SLO) to uncover patterns and mechanisms of speciation in a recent, rapid radiation throughout Central and South America. The first years will be focused on phylogenetics and population genomics, whereas later years will be focused on QTL mapping and field testing of key traits and loci involved in adaptive divergence and reproductive isolation. Primary responsibilities include experimental design, coordinating and conducting sequence data collection, managing and analyzing large datasets, mentoring undergraduate and graduate students, coordinating research collaborators, and contributing to the dissemination of results through manuscripts, presentations, public outreach, and agency reports. Applicants with the following preferred qualifications are strongly encouraged to apply: experience generating and analyzing next gen sequence data from non-model plants, excellent bioinformatics skills, a strong interest in plant speciation and adaptation, and a track record of publishing in leading journals. The position requires excellent time management and written/oral communication skills. The scholar will be based at UCSC, with opportunities for lab exchanges and fieldwork in Costa Rica and Panama. More information on the Kay Lab can be found at https://kay.eeb.ucsc.edu/ ACADEMIC TITLE

Postdoctoral Scholar

SALARY

Minimum annual salary of $48,216, commensurate with qualifications and experience. Minimum annual salary rates are made based on the individual'Âs Experience Level, which is determined by the number of months of postdoctoral service at any institution. See current salary scale for Postdoctoral Titles at https://apo.ucsc.edu/compensation/salary-scales/index.html

BASIC QUALIFICATIONS

- Ph.D. or foreign equivalent in Biology or related field
- A minimum of two years experience in phylogenetic and/or population genetic laboratory research.

POSITION AVAILABLE

April 1, 2018. Start date could be as late as October 1, 2018. Ph.D. must be in hand at time of the initial appointment.

MAXIMUM DURATION OF SERVICE IN A POSTDOCTORAL TITLE

Postdoctoral Scholar appointments are full-time; the initial appointment is for two years, with the possibility of reappointment. Reappointment will be contingent upon positive performance review and availability of funding. The total duration of an individual'Âs postdoctoral service may not exceed five years, including postdoctoral service at any institution. Under limited circumstances, an exception to this limit may be considered, not to exceed a sixth year.

APPLICATION REQUIREMENTS

Applications should be emailed to Kathleen Kay kmkay@ucsc.edu. All documents and materials must be submitted as PDFs. Please refer to Position # EEB Postdoctoral Scholar-18T in all correspondence. Informal inquiries may be sent to kmkay@ucsc.edu

Documents/Materials

- Cover letter describing past research experience and qualifications for this position (required)

- Current curriculum vitae (required)

- A list of three references that includes their contact information (required)

- Up to three copies of published manuscripts-submitted as separate pdfs (required)

RECRUITMENT PERIOD

Full consideration will be given to applications completed by January 29, 2018. Applications received after this date will be considered only if the position has not been filled. The position will remain open until filled, but not later than 9/30/2018.

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. UC Santa Cruz is committed to excellence through diversity and strives to establish a climate that welcomes, celebrates, and promotes respect for the contributions of all students and employees. Inquiries regarding the University'Âs equal employment

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UColoradoBoulder PlantEvolutionaryEcology

A postdoctoral research position is available in the Emery lab in the Department of Ecology & Evolution Biology at the University of Colorado Boulder. Our lab studies plant evolutionary ecology with an emphasis on understanding plant adaptation in variable environments and the ecological and evolutionary drivers of species' distribution patterns. Additional information can be found at http://www.colorado.edu/lab/emery/ This opening is for one full-time postdoctoral researcher who will contribute to an NSF-funded project investigating the evolutionary feedbacks between dispersal and habitat specialization. The primary responsibilities include establishing and monitoring field and greenhouse experiments, managing and analyzing data, and contributing to the dissemination of results through manuscripts and presentations. The position requires travel to California for several weeks each spring and fall to establish and maintain field experiments at the Jepson Prairie Reserve.

Candidates must have PhD in Ecology, Evolutionary Biology, Botany, or a related field, and experience conducting field experiments with plants. Candidates are also expected to have a background in quantitative and statistical methods, a strong work ethic, and excellent interpersonal, communication, and time management skills. A clear track record of publications and independent research experience are also required. The expected duration of the position is 30 months.

TO APPLY: Please submit a single PDF that includes (1) a cover letter describing past research experience and qualifications for this position, (2) a current CV, and (3) contact information for 3 references, as well as separate PDFs of up to 3 published manuscripts, to Dr. Nancy C. Emery (nancy.emery@colorado.edu).

– Nancy C. Emery Assistant Professor Department of Ecology & Evolutionary Biology Campus Box 334 University of Colorado Boulder Boulder, CO 80309-0334 Phone (office): (303)735-7548 Website: http://www.colorado.edu/lab/emery Nancy.Emery@Colorado.EDU

UEdinburgh EvolEcolMalariaCircadianRhythms

Position: Postdoc

Location: Reece lab, Institutes of Evolution, Immunology and Infection Research, University of Edinburgh, UK

Topic: Parasite offence or host defence? The ecology and evolution of biological rhythms in malaria infection

Details and application info at: https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id=042288 Biological rhythms allow activities to be coordinated with the consequences of the Earth's daily and seasonal rotation. The mechanisms underpinning the clocks that drive daily rhythms are well understood. In contrast, the costs and benefits provided by daily rhythms - including how rhythms shape interactions between organisms - are poorly understood. One of the most fundamental interactions between organisms is that between hosts and parasites. Why parasites - that exclusively live within the bodies of other organisms - exhibit biological rhythms and how they are regulated are longstanding questions. Examining the roles of rhythms in disease is a new arena for studying host-parasite-vector coevolution. Also, integrating disease control interventions into an evolutionary chronobiology framework offers innovative approaches to improving health. This includes the development of drugs to disrupt parasite rhythms, harnessing circadian systems to enhance immune responses, or precisely timing drug administration to make treatment more effective.

We are offering a postdoctoral position as part of a Wellcome Trust funded project to investigate the role of circadian rhythms in malaria infection. The project will integrate a novel mix of disciplines (evolutionary ecology, chronobiology, and parasitology) to determine why and how timing matters for interactions between parasites, hosts and vectors, the severity and transmission of disease, and fitness of all parties. This is a very broad topic and so the successful candidate will be encouraged to develop their own niche. Growing evidence that the daily rhythms of malaria parasites can confer tolerance to antimalarial drugs, and that the use of bed nets is changing the biting time of the mosquitoes that transmit malaria makes understanding how and why parasites exhibit daily rhythms increasingly urgent.

This interdisciplinary Wellcome Trust funded project will break new ground by elucidating the evolutionary ecology of biological rhythms for parasites. It will integrate a novel mix of disciplines (evolutionary ecology, chronobiology, and parasitology) and open up novel avenues for disease control. The post holder will plan, conduct and write up research that they have led and support the research of others in the lab. The project will focus on a rodent malaria, murine host, and mosquito vector model system.

This post is full time and fixed term for 3 years.

Salary: 32,548 - 38,833 per annum

Closing Date: Friday 02 February 2018 at 5pm (GMT)

Professor Sarah Reece Chair of Evolutionary Parasitology

[Note - I am part time and do not (usually) work on Thursdays]

Centre for Immunity, Infection & Evolution, Institutes of Evolution, Immunology and Infection Research, School of Biological Sciences, Ashworth Laboratories, University of Edinburgh, Edinburgh EH9 3FL Scotland, UK

Tel +44 131 650 5547 Fax +44 131 650 6564

sarah.reece@ed.ac.uk www DOT reecelab DOT science

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

Sarah.Reece@ed.ac.uk

UGothenburg Sweden PlantSpeciationGeonomics

Project description

Although parallel speciation is a well-recognized phenomenon in animals, it is poorly evidenced in plants. This project aims to address the following general questions: Does ecology affect population structure in plants to the degree that it can cause ecological speciation? Does ecological speciation occur parallel in continental systems? Can evidence of ecological speciation support a model of sympatric speciation, where new species arise in overlapping geographic distributions? These questions will be applied to a model system that has been developed in an Amazonian palm (Listabarth 1993; Roncal et al. 2006, 2007; Borchsenius et al. 2016; Bacon et al. in preparation).

We are looking for a highly motivated and skilled person to work with statistical approaches, phylogeonomics and phylogeography, and species occurrence data to develop a framework to test for parallel ecological speciation. The work is focused on palms, specifically on *Geonoma macrostachys,* but data is also available for comparative phylogeographical work with the palm, *Mauritia flexuosa*, and other Amazonian taxa across the tree of Life. This four-year project is funded by the Swedish Research Council.

*Job assignments *The tasks envisioned will include some or all of the following:

-

Field work in the western Amazon (e.g. Colombia, Ecuador) -

DNA extraction -

Bioinformatics and phylogeographical analyses -

Use fossil pollen to infer ancestral population sizes through time

- Quantify adaptability to climate using outlier SNP loci

*Eligibility *The applicant must hold a PhD in an area relevant for the tasks at hand (molecular phylogenetics, molecular ecology, phylogeography, biostatistics, bioinformatics, or related fields). The PhD exam must be finished prior to the closing date of this announcement.

Other required qualifications:

- Documented capacity to work in groups and independently - Advanced skills in R, python or another analytical platform - Advanced skills in phylogeography and/or phylogenomics - Excellent written and spoken communication skills in English

* Assessment (other desirable qualifications)*

- Experience with manipulative experiments related to common gardens and/or reciprocal transplants - Experience with phylogenetic diversity metrics, molecular dating, biogeography, comparative phylogenetic analyses, ancestral trait evolution, and/or next-generation sequencing data - Language capacity in Spanish

The employment

The employment is a full-time position for 24 months. The physical placement will be decided upon agreement, but should be at the University of Gothenburg.

The application should be written in English, compiled into a single .pdf file, and must include:

-

A cover letter with the applicant's motivation for application, describing how the applicant meets the selection criteria (max. two A4 pages) -

A list of qualifications (CV) -

Complete list of publications, including submitted and accepted manuscripts -

Certificate of PhD exam and other relevant education -

Contact information for at least two referees that are familiar with the applicant's qualifications

The top ranked candidates will be selected for an interview, which will be held in English, and will be performed by phone /skype.

In order to apply for a position at the University of Gothenburg, you have to register an account in our online recruitment system. It is the responsibility of the applicant to ensure that the application is complete in accordance with the instructions in the job advertisement, and that it is submitted before the deadline.

Complementary documents, such as publications/books should be sent to the following address: University of Gothenburg, Department of Biology and Environmental Sciences, Att: Ingela Lyck, Box 463, 405 30 Gothenburg. Reference number should be clearly stated when sending complementary documents.

Closing date 2018-03-15

For further information please contact

Christine D. Bacon, Assist. Prof. Phone: +46 076 618 5167

Email: christine.bacon@bioenv.gu.se

Webpage: http://antonelli-lab.net/ Henrik Aronsson, Professor and Head of Department Phone: +46 31 786 48 02

Email: henrik.aronsson@bioenv.gu.se

https://www.gu.se/english/about_the_university/job-opportunities/vacancies-details/?id=1834 – Christine D. Bacon

Assistant Professor University of Gothenburg Gothenburg, Sweden

Gothenburg Global Biodiversity Centre Box 461, SE 405-30 Göteborg, Sweden

Associate Researcher Universidad CES Medellin, Colombia

Christine Bacon <christinedbacon@gmail.com>

UMaryland StatModelingMicrobiomes

Postdoctoral Researcher in Statistical Ecology / Spatial Distribution Modeling of Microbiomes

Bill Fagan's ecology lab at the University of Maryland in College Park, MD, has a new opening for a Postdoctoral Researcher in the Statistical Ecology / Spatial Distribution Modeling of Microbiomes. This dynamic lab group, which currently includes one associate research scientist, seven postdocs, four graduate students, and numerous undergraduates, is pursuing a wide variety of research projects in ecology. Much of this work is explicitly spatial in nature, drawing upon GIS, mathematical modeling, and statistical analyses. For examples, see http://www.clfs.umd.edu/biology/faganlab/ This advertisement is for a postdoctoral position on a DoD / MURI-funded project in collaboration with Johns Hopkins Applied Physics Lab, Johns Hopkins School of Medicine, and Duke University. The project focuses on the analysis of the human skin microbiome, with a particular emphasis on developing multi-scale models for understanding and predicting spatial variation in microbiome composition. The candidate should have expertise in species distribution modeling and/or the statistical analysis of spatially structured presence/absence and abundance data. In addition, very strong computational skills with knowledge in various programming languages (e.g., R, Python, Matlab) are required. Experience in microbial ecology and familiarity with sequencing data are highly desirable. Experience working with large datasets and/or hierarchical spatial models would be particularly helpful.

The successful candidate will have a PhD at the time of appointment, likely in quantitative ecology, microbial ecology, statistics, or a related field. Prior postdoctoral experience is beneficial, but not required.

The initial appointment will be for one year, but funding is already in place for up to two additional years pending good performance. Efforts to secure substantial long-term support via collaborative grant proposals would be encouraged and, when successful, could lead to appointment at the level of assistant/associate research scientist. Benefits are included and pay will be commensurate with experience. The start date is negotiable, but could be as early as March 2018.

Review of applications will begin immediately and will continue until the position has been filled. To apply for the position, please email a CV, reprints, and the names and email addresses of three references to:

Bill Fagan

Professor and Chair

Department of Biology

University of Maryland

College Park, MD 20742

bfagan@umd.edu

Eleanor Brush <eleanor.brush@gmail.com>

UMichigan NextProf DiversifyingAcademia

NextProf Science - Future Faculty Workshop @ University of Michigan

We would like to invite interested evolutionary biologists, ecologists, and organismal biologists to the NextProf Future Faculty Workshop at the University of Michigan. NextProf Science will be held April 30 - May 3, 2018 and is a workshop designed to encourage talented scientists and mathematicians with a demonstrated commitment to diversity to consider academia as a career. The workshop is aimed at helping participants develop strategies that will strengthen their ability to pursue academic careers. The workshop is targeted at scholars ready to take the next step –postdoctoral fellows and very advanced doctoral students. Underrepresented minorities and women are especially encouraged to apply. Travel, lodging, and meals will be provided for those selected to participate. Deadline for submission of all application materials is February 14, 2018. Learn more at: sites.lsa.umich.edu/nextprof-science/ Application information: sites.lsa.umich.edu/nextprof-science/how-to-apply/

˜ U-M EEB NextProf Organizing Committee (Dan Rabosky & Hernan Lopez-Fernandez)

“drabosky@umich.edu” <drabosky@umich.edu>

UMinnesota EvolutionaryBiology

Grand Challenges in Biology Postdoctoral Program

College of Biological Sciences

University of Minnesota

Application deadline: February 1, 2018

Position start date: May-August 2018 (specific date negotiable)

Rationale

Understanding and predicting the behavior of complex biological systems requires a framework that can integrate across levels of biological organization, can capture nonlinear feedbacks in dynamical systems, and can incorporate and facilitate mechanistic understanding. This is the challenge of the future of biology. Meeting this challenge requires a multidisciplinary approach that relies heavily on innovations in quantitative fields such as mathematics, computer science, statistics, and engineering. It also requires strong integration (or re-integration) of molecular biology with organismal biology. Meeting the food, water, and energy needs of a growing human population, while minimizing adverse impacts of habitat alteration, climate change, invasive species, overexploitation, and pollution on human health and ecological systems - operate at scales from molecules to ecosystems, and there is a pressing need to develop the science that can cross these scales. The University of Minnesota is developing research and curricular initiatives focused on addressing grand challenges, and this program is part of CBS’ contribution to the university-wide programs.

Program Aims

The overall aim of the Grand Challenges in Biology (GCB) Postdoctoral Program is to stimulate synergistic interactions between faculty and postdoctoral associates interested in collaborating on multidisciplinary research that addresses societally relevant problems. Postdoctoral projects are for two years (assuming satisfactory progress toward research goals in year one). Postdoctoral associates will be encouraged to participate in grant proposal development workshops and other professional development activities offered at UMN and CBS and are permitted to serve as Principal Investigators on grant proposals. While in residence, the postdoctoral associates will be expected to be visible members of CBS, actively engaging with faculty, undergraduate- and graduate students and contributing to furthering the collaborative culture of CBS.

Application Process

To apply:

Visit http://humanresources.umn.edu/jobs Click the appropriate maroon link in the center of the page

Enter 320761 in the Keywords box

Click "Search"

Applications must be submitted through the UMN employment site.

Applicants should develop a 2-year research project under the guidance of two or more faculty advisors, at least one of whom must be a faculty member in the College of Biological Sciences (CBS). The other advisor(s) may be from a different department within CBS, from any other College at UMN or from a local entity external to the university (e.g., private company, government agency, NGO). Since an important aim of the program is to jumpstart the formation of new teams, the faculty advisors should not have an already established record of collaboration with each other (as evidenced by jointly authored publications).

Uploaded applications materials must include:

CV

1-page description of previous or current research

3-page (maximum) description of proposed research containing: a statement of the problem to be addressed; methods/approach; relevance of the work in relation to grand challenges in biology; contributions of the collaborating partners; literature cited (does not count toward the 3-page limit)

letters of support from each of the proposed faculty advisors who will be involved in the project as well as the names and contact information for two external persons (not from UMN) who may be asked to submit letters of recommendation

The expected salary will be $47,500 plus benefits. In addition, the postdoctoral scholar will receive $5,000 per year for research supplies and research-related travel. It is expected that necessary office and laboratory space, access to large equipment and any other research needs will be provided by faculty advisors.

Additional Details

Positions are initially for two years with the possibility of renewal for a third year pending progress review.

Early-career scientists with a high potential to springboard their careers to future faculty positions are especially encouraged to apply.

Applications will be evaluated by a search committee representing CBS's disciplines. This same committee, or a subset thereof, will also be responsible for evaluating postdocs' performance at the end of the first year and in connection with eventual renewal for a third year.

Applicants should have completed all of the requirements necessary to attain a Ph.D. degree and be able to be on campus to start employment by the agreed start date.

Graduates of UMN are eligible to apply for these positions, but we also hope to recruit a strong pool of external applicants.

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UMinnesota EvolutionaryGenomicsOfSleep

Cave tetras experience vastly different selection pressures than do conspecifics living in surface waters, and there are multiple, independent origins of cavefish in separate caves, providing a naturally replicated experiment. Distinct phenotypes and behavioral differences have evolved and are maintained in the cavefish populations, while in some caves, substantial gene flow between surface and cavefish is ongoing. Thus, Mexican cave tetras offer a unique opportunity to study how recombination, selection, drift, and introgression shape genomic divergence.

Cavefish have repeatedly evolved loss of total sleep duration relative to surface fish, providing a unique opportunity to examine the genetic basis of sleep in naturally evolved populations.

The McGaugh lab is recruiting a postdoc to: 1) analyze resequenced genomes for outlier loci involved in sleep loss (including modeling complex demography, admixture, and local adaptation in repeatedly evolved cavefish) and 2) construct multiple high-resolution QTL maps of sleep loss and circadian deregulation in repeatedly evolved cavefish.

This is a collaborative project with the Keene lab at Florida Atlantic University and the Rohner lab at Stowers Institute.

Applicants with a strong computational, population genomic, or functional genetic background are encouraged to apply. Please send a CV and references to smcgaugh@umn.edu Salary follows the NIH stipend recommendations. Start-date is flexible.

The initial contract is for one year with renewal for additional years pending performance.

Principal Duties and Responsibilities 90% Computational genomics, sample collection, writing manuscripts, animal husbandry and DNA extraction Analyzing next-generation sequencing data, keeping detailed notes and logs of the analyses, and keeping well-annotated code that was written for those analyses to ensure future replication of the work.

Conduct phenotyping, genotyping, and analyses of fish for a large-scale QTL experiment.

Submit permits, conduct field-work, and extract DNA for population genomic analyses.

Maintain fish and basic molecular lab work to confirm results of next generation sequence analysis.

Participate in projects that may or may not be directly related research, but aid in other's projects in the lab and help generate preliminary data for grant submissions. This may also include mentoring of undergraduate and graduate students.

Write and submit manuscripts that present results of the analysis conducted in the McGaugh lab. Help in the preparation of other lab-wide manuscripts and analyses for those manuscripts.

5% Lab maintenance, safety, supplies and systems administration In charge of daily function and operation of the McGaugh lab including the purchasing of supplies, maintenance of a safe and productive physical and computational environment.

5%- Lab citizen Attend lab meetings, relevant lectures, and training sessions. Assist other lab/community members.

Minimum Qualifications A PhD in genomics, evolution, genetics, or related fields.

Experience with next-gen sequence data and a unix/command line interface.

Experience with scripting/programming languages including R, python, and/or C++ Demonstrated ability to produce high-quality publications.

A desire to help lead an integrative and motivated group of young scientists.

Patience, dedication, flexibility, and enthusiasm.

Excellent communication skills.

Preferred Qualifications Strong knowledge of population genetics, genomics Interest in aging, stress, and recombination.

Experience with international fieldwork and caving At least minimal understanding of Spanish or willingness to learn basics prior to fieldwork.

The Twin Cities offer a range of arts and entertainment, and an amazing restaurant scene. The University of Minnesota also houses one of the most comprehensive computing environments (Minnesota Supercomputing Institute) and abundant bioinformatics training opportunities.

The UofM is a collaborative atmosphere and with a concentration of population, quantitative, and evolutionary geneticists which make up a vibrant scientific community.

Suzanne McGaugh <smcgaugh@umn.edu>

UNebraska PopulationBiology

Population Biology Postdoctoral Research Fellowship

THE UNIVERSITY OF NEBRASKA-LINCOLN is seeking applications for a 2-year postdoctoral position in the Population Biology Program of Excellence.

The goal of the Population Biology-POE Postdoctoral Fellowship is to stimulate synergistic interactions between faculty and postdoctoral scholars interested in the broad area of Population Biology. We are seeking applications from recent PhDs who show promise of conducting cutting edge research related to, and expanding upon, faculty research areas in the Ecology, Evolution & Behavior (EEB) section in the School of Biological

Sciences (http://biosci.unl.edu/research-specializations). The POE also seeks to identify potential postdoctoral fellows who will enhance graduate education, serve as a model for graduate students in career development, and promote interactions among faculty at UNL. Qualified candidates are required to submit a 2-3 page research proposal detailing the two-year program of research to be completed under the guidance of a faculty member in the Ecology, Evolution & Behavior (EEB) section in the School of Biological Sciences. Applicants are encouraged to reach out to potential faculty mentors before developing a proposal for additional guidelines and suggestions. The position does not include research funds so the extent of contributions from the faculty sponsor should be addressed in the proposal. While in residence, the postdoctoral fellow will be expected to lead a seminar, symposium or outreach project that will appeal to Population Biologists across campus. Applications must include a CV, a 1-page description of previous or current research and the description of proposed research. In addition, the applicant must arrange for two recommendation letters from non-UNL faculty, and one from the UNL faculty sponsor (a total of 3 letters) to be emailed to the address below. The expected salary will be $45,000 per year with a start date of August 19, 2018. Priority will be given to applicants who have completed their degree and are new to UNL. Research descriptions for past and current POE postdoctoral fellows can be viewed at http://biosci.unl.edu/population-biology/ Application materials should be emailed to: Dr. Johannes Knops at: jknops2@unl.edu. The subject line should read Population Biology Post-doc application. Applications should be received by March 1, 2018. We anticipate notifying the successful applicant by April 1, 2018, with a starting date of August 19 or later in 2018. We strongly encourage applications from women and members of minority groups. The University of Nebraska is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers. We assure responsible accommodation under the Americans with Disabilities Act.

Dai Shizuka <dshizuka2@unl.edu>

UOregon PopulationGenomics

The Singh lab at the University of Oregon invites applications for a Postdoctoral Researcher position in population genomics. This project focuses on the causes and consequences of natural variation in recombination frequency in D. melanogaster and is supported by multiple NSF grants.

http://careers.uoregon.edu/cw/en-us/job/521721/-postdoctoral-research-scholar

nsingh@uoregon.edu

UPadova Italy CircularRNABioinformatics

*Post-doc position in Bioinformatics available at the University of Padova, Italy *

TOPIC: Circular RNAs in leukemias.

Tentative deadline for applications: January 30 2018

- The post-doc will be recruited in the frame of a 5 year AIRC project (2018-2023) on normal hematopoiesis and leukemias.

- The planned activity comprises both NGS (RNA-seq) data analysis, using software tools available in the lab to discover and quantify circular RNAs, and development of new methods for the functional characterization of circular RNAs in silico (miRNA binding, coding potential, protein binding motifs). Experience in RNA-seq data analysis, statistic background and programming abilities are required.

- Opportunity to work in team with computer scientists, experimental researchers, and clinicians in a stimulating group with several national and international outstanding collaborations.

- Padova is a pleasant city in the north of Italy, close to great outdoors, such as Venice and Dolomiti mountains, and harbors one of the top ranking Science universities in Europe.

*PLEASE CONTACT:Prof. Stefania Bortoluzz*i Computational Genomics Laboratory, Department of Molecular Medicine, University of Padova, Italy *stefania.bortoluzzi@unipd.it* ++39 049 8276502

Stefania Bortoluzzi Associate Professor of Applied Biology Department of Molecular Medicine University of Padova

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stefania bortoluzzi <stefania.bortoluzzi@unipd.it>

UPittsburgh EBV-cancer evolution

POSTDOCTORAL FELLOW POSITION Laboratory of Dr. Kathy Shair University of Pittsburgh

University of Pittsburgh UPMC Hillman Cancer, Center Cancer Virology Program PA, 15213. U.S.A.

Post date: Jan 3rd, 2018 Position: Full time, immediate start date Experience: Entry-level to 2 years post-doc preferred Epstein-Barr virus-associated cancers A postdoctoral position is immediately available to study the oncogenic mechanisms of Epstein-Barr virus (EBV). The ideal candidate should have a Ph.D in the field of molecular virology or cancer biology. The project will study EBV pathogenesis in nasopharyngeal carcinoma and elucidate how virus evolution impacts pathogenesis and host cell oncogenic mechanisms. Opportunities also exist to work with mice. Experience in tumor virology is preferred, but candidates with independent thinking, experimental rigor and evidence of scientific writing and presentation will be the most highly ranked.

Current projects in the Shair lab include: 1) oncogenic signaling mechanisms of EBV latent membrane proteins (LMP) 1 and LMP2A, 2) determinants of EBV latency and persistence, and 3) mouse models of EBV-associated cancers. The Shair lab at the University of Pittsburgh is housed in the Cancer Virology Program, Hillman Cancer Center, where our common interest is to elucidate the molecular basis of cancer and translational medicine.

To be considered, please submit a C.V. and names of 3 references to Dr. Shair (kas361@pitt.edu). Applicants will be continually reviewed until the position is filled.

vaughn.cooper@pitt.edu

UPittsburgh EvolutionPolymicrobialInfections

The Cooper and Bomberger laboratories seek a motivated colleague who shares our interest in defining evolutionary dynamics of bacterial populations during polymicrobial infections and advancing this emerging field. We are focused on dynamics within infections of the upper and lower airway of persons with cystic fibrosis (CF), where we are following patient cohorts to study how viral infections or antibiotic treatments influence Pseudomonas aeruginosa and Staphylococcus aureus evolution. Opportunities also exist to study pathogen dynamics within pediatric, non-CF patients with chronic sinusitis. A representative NIH-sponsored project is described here: https://projectreporter.nih.gov/-project_info_description.cfm?aid=9304418&icde=-37479658&ddparam=&ddvalue=&ddsub=&cr=-2&csb=default&cs=ASC&pball= . Responsibilities include: to analyze metagenomic data to identify patterns and processes of bacterial evolution during infections, define reproducible workflows for these studies, identify and implement state-of-the-art methods, developing algorithms, writing manuscripts and progress reports. This position also includes opportunities for studying bacterial genotype-phenotype relationships in vitro and in vivo. Our goal is to provide excellent training to the postdoctoral fellow to establishing his/herself as an independent investigator or senior research staff.

Qualifications: Ph.D in Computational Biology, Evolutionary Biology, Microbiology, or Genetics/Genomics. Publications in these fields.

Highly desirable: Experience in Computational Biology, high-throughput genomic data analysis. Ability to write scripts and proficiency at the command line.

Candidates with a computer science background also can apply but basic knowledge of genetics is a requirement.

School / Department: University of Pittsburgh School of Medicine / Microbiology and Molecular Genetics Classification: Postdoctoral Associate Funding source: NIH and Gilead grants. Start Date: 2/1/2018 Send letter of interest and CV to vaughn.cooper@pitt.edu. See also: http://micropopbio.org "Vaughn S. Cooper" <vaughn.cooper@pitt.edu>

Uppsala PopulationGenomics

Researcher in population genomics at Uppsala University

We have an opening for a researcher in a project investigating local adaptation in dogs. The position is for one year, with possibility for extension, in the group of Dr. Erik Axelsson at Uppsala University. Deadline for application is February 15, 2018.

Project description: Thanks to the rapid and recent changes accompanying domestication, comparisons of wild and domestic life forms represent an ideal system for characterizing the genetic basis of phenotypic diversity. Based on whole genome sequencing we recently compared patterns of genetic variation in dog and wolf to provide an initial understanding of the genetic basis of adaptations during dog domestication. We found that selection had targeted the entire pathway responsible for starch digestion and glucose absorption in the small intestine of dogs, indicating that a shift from a meat based to a starch rich diet constituted a crucial step during the domestication process. Combined with evidence that this change was accompanied by selection for mutations that also affected the ability to store glucose as fat, these findings argue that dogs underwent a general shift from a protein to a more carbohydrate based energy metabolism. Dog domestication may thus represent a unique and unexplored natural model for studying metabolism arguing that a detailed characterization of the genetic basis of adaptations during dog domestication represents a novel perspective on the molecular components of nutrient absorption and carbohydrate and lipid metabolism. To benefit from this new perspective and to understand how dogs coped with the fundamental changes associated with the agricultural revolution this project combines large scale population genomic analyses, transcriptomics and analyses of existing comparative genetics resources to localize mutations that are likely to underlie metabolic adaptations in dog, followed by physiological experiments in genetically modified cell lines to test the effect of the indicated genes on metabolic processes.

Job description: Research in the project described above. The successful applicant will mainly analyse population scale whole genome resequencing data and transcriptome data.

Qualifications: To be eligible to apply you must have a Ph.D. in evolutionary biology, population genetics, genomics, bioinformatics or another relevant field. The position requires documented experience in large-scale next- generation DNA sequencing analysis and the ideal candidate is highly motivated with a strong background in statistical, quantitative or population genetics. Candidates must have good communication skills, both in written and spoken English. Programming skills are desirable. We will put great emphasis on your personal qualities and interpersonal skills such as ability for collaborative work and flexibility.

Uppsala University finds that gender balance and diversity brings a higher quality to the organization. We therefore welcome applicants of any gender and with different birth background, functionality and life experience.

Pay: Individual salaries

Starting: As soon as possible for a period of one year with eventual possibility to extension.

Type of employment: Temporary position.

Working hours: 100 %

Application: Apply for the position through Uppsala University's recruitment system: https://www.uu.se/-en/about-uu/join-us/details/?positionId=187891 For further information about the position please contact: Erik Axelsson, mailto: erik.axelsson@imbim.uu.se

Erik Axelsson <erik.axelsson@imbim.uu.se>

UppsalaU 2 BacterialEvolution

EVOLVABILITY OF ANTIBIOTIC RESISTANCE GENES, POST-DOC Lionel Guy and Diarmaid Hughes are looking for a post-doctoral fellow with, ideally, experience of both bacterial genetics and molecular evolution to tackle a collaborative project on the evolvability of ancestral antibiotics resistance genes.

PROJECT The mains goals are (i) to better understand how different antibiotic resistance genes evolved before the clinical use of antibiotics, and to assess (ii) their evolutionary potential and (iii) the predictability of the mutations providing antibiotic resistance. We will focus on four classes of genes providing resistance to four classes of antibiotics: beta-lactams, aminoglycosides, tetracycline and the last-resort antibiotic colistin. First, the successful candidate will reconstruct the evolutionary history of each class of genes, trying to infer what they are derived from. Second, they will evaluate the resistance potential of ancestors, by reconstructing them, cloning them into E. coli MG1655 and assessing their minimal inhibitory concentrations (MIC). Third, the reconstructed ancestors will be evolved in sub-MIC conditions, to examine evolutionary paths and time necessary to reach present-day MICs. By comparing the mutations obtained in experimental evolution to the ones found in actual modern sequences we'll be watching how "replaying the tape of life" mimics the actual evolutionary pressures experienced by sequences in vivo, and may predict the potential emergence of antibiotics resistance in clinical settings.

FORM Two-years post-doctoral fellowship (SEK 276 000, circa USD 32 400, per annum), free of tax. Fellowship rules exclude candidates with a PhD from the host institution (Uppsala University). The candidate has to be approved by the funder. Starting date: to be discussed

BASIC SKILLS AND QUALIFICATIONS - A PhD in molecular evolutionary biology, microbial genetics or a related topic. - Experience with microbiology and bacterial genetics. - Experience of bioinformatics, ability to run basic molecular evolution software. - A documented experience of team work and collaborative projects.

DESIRED QUALIFICATIONS - Extended experience of molecular evolution tools. - Programming experience. - Skills in molecular genetic tools in E. coli and Salmonella.

APPLICATIONS To be sent by email to lionel.guy@imbim.uu.se, latest on February 18th, 2018. Applications (in one single document) should include: - Letter of motivation. - Resume. - Publication list. - Names and contact information of two references or two letters of reference.

HOST INSTITUTION The project is a collaboration between the research groups of Lionel Guy and Diarmaid Hughes, Department of Medical Biochemistry Microbiology, Uppsala University. The host department is a very strong and stimulating research environment, counting over 250 researchers in over 30 groups, and is conducting world-leading research in antibiotic resistance. Uppsala University is a comprehensive research-intensive university with a strong international standing. Our mission is to pursue top-quality research and education and to interact constructively with society. Our most important assets are all the individuals whose curiosity and dedication make Uppsala University one of Sweden's most exciting workplaces. Uppsala University has 40,000 students, 7,000 employees and a turnover of SEK 6.5 billion.

CONTACT Lionel Guy, M: lionel.guy@imbim.uu.se, P: +46 18 471 42 46, W: http://www.imbim.uu.se/-Research/Microbiology-immunology/guy-lionel/ Lionel Guy, PhD Assistant Professor Department for Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden lionel.guy@imbim.uu.se

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POSTDOCTORAL FELLOW IN EVOLUTIONARY MICROBIOLOGY, BIOINFORMATICS We are recruiting a new postdoctoral fellow to Lionel Guy's research group at Uppsala University.

PROJECT Our group is studying the evolution of host-adaptation in bacteria. We are currently focusing on the Legionellales order, which contains representatives at several stages of host adaptation. We are gathering a number of novel genomes through extended sampling, metagenomics and data mining. The goal of this project is to extend the current dataset, analyze it, to shed light on the evolution of Legionellales in particular, and on the evolutionary transitions in host adaptation in general.

FORM One-year post-doctoral fellowship (SEK 288 000, circa USD 34 000, per annum); extension for a second year possible. Candidates who are employees of Uppsala University, or have been in the two years before the start of the fellowship, are not eligible.

Starting date: to be discussed.

BASIC SKILLS AND QUALIFICATIONS - A PhD in evolutionary biology, molecular evolution, microbiology or related topic. - Experience with high-throughput sequencing data, metagenomics, comparative genomics, and molecular evolution tools.

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URochester EvolutionaryGenetics

Postdoctoral fellow in evolutionary genetics/genomics Department of Biology, University of Rochester

The Fay lab in the Biology Department at the University of Rochester is seeking candidates for a postdoctoral fellow position. The lab works broadly on the genetic basis of evolutionary change, utilizing both high-throughput experimental approaches combined with statistical and computational models. Our main experimental system is yeast, focusing on the Saccharomyces species with occasional forays into Candida and other species that commonly show up in our field collections. However, we also have active collaborations working on domestication in barley, preterm birth in humans, and testing theories of diversity using experimental evolution. These interactions both stimulate project cross-fertilization and create opportunities to develop novel approaches to long-standing problems of interest to the lab.

Candidates will have the opportunity to expand on current projects or explore new areas through the development of a creative and independent project. Our current projects focus on the evolution of gene expression dynamics and when changes in gene expression matter, the genetic basis of interspecific differences in thermotolerance, and domestication and diversification of S. cerevisiae, including wine, beer and other industrial strains. We have extensive resources in population genomics through our collection of over 4,000 wild yeast strains, probabilistic models of cis-regulatory sequences, as well as our recent acquisition of high-throughput robotics paired with both natural and constructed collections of strain, plasmid and synthetic reporter libraries.

Candidates should have a clear vision of their research interests along with expectations for training and mentorship. While there are no strict requirements for the position, strong quantitative skills, programming experience, and a population or evolutionary genetics background are desirable.

The Fay lab is located in the Biology Department, which has a strong research group in evolutionary genetics and genomics that has recently grown, providing a stimulating and interactive environment. The Department is located on the top floors of Hutchinson Hall, adjacent to the Goergen Institute for Data Science, Computer Science and Biomedical Engineering Departments. We also benefit from an excellent group of yeast labs originally built up through the vision of Fred Sherman. Genomics and proteomics cores are available across the street at the Medical center. Finally, the Center for Integrated Research and Computing provide state of the art facilities for both parallel and large memory computing jobs.

Applicants for the position should send a curriculum vitae, a statement of interest and contact information for three references via email. Applications will be reviewed starting in February, 2018 and will continue until the position is filled.

Justin Fay Associate Professor Biology Department University of Rochester justin.fay@rochester.edu http://labsites.rochester.edu/faylab/ Justin Fay <fayjustin@gmail.com>

USDA Colorado GenomicsBioinformatics

1-year Post-doc position in genomics/bioinformatics

We are seeking a dynamic individual to work on a study of invasive, island mice genomes. This is part of a broader effort to develop genetic biocontrol methods for invasive rodents in island ecosystems. Our specific goal for this position is to characterize the genomes of mice from different island systems and identify regions that are unique to each population. These regions will be chosen as sites for genome editing in order to have potential biological specificity for target populations. The role of the individual we seek will be to help select the best next-generation sequencing approach for identifying unique genomic regions in wild mouse genomes, laboratory work, and bioinformatics analyses. We expect experience in one or preferably more next-generation sequencing methods such as whole genome sequencing, Pool-seq, RAD-seq, RNA-seq, and Genotype-by-sequencing and some bioinformatics experience. We expect a candidate to have strong laboratory bench skills including a clear understanding of the potential biases of the data introduced at each step of the laboratory process. Candidates must be enthusiastic about the project and process to achieve study goals. This study is part of a larger collaboration between multiple universities and federal level agencies within multiple countries. Thus, candidates must have strong interpersonal skills, professional presentation capabilities, and scientific writing proficiency.

This position will be housed at CSU under the supervision of Dr. Zaid Abdo and will be co-advised by Dr. Toni Piaggio, USDA-APHIS-NWRC and Dr. John Godwin at North Carolina State University.

For full position announcement and to apply go to: http://jobs.colostate.edu/postings/52464 CSU is an EO/EA/AA employer and conducts background checks on all final candidates.

Toni Piaggio, Ph.D. Research Scientist, Wildlife Genetics National Wildlife Research Center 4101 LaPorte Ave. Fort Collins, CO 80521 (970)266-6142 toni.j.piaggio@aphis.usda.gov

"Piaggio, Antoinette J - APHIS" <Toni.J.Piaggio@aphis.usda.gov>

UUppsala EvolutionSexualDimorphism

Title of project: Evolution of sex differences in life histories despite a shared genome

I am seeking a highly motivated postdoc to join the Bolund lab at the Dept. of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, Sweden. The project is funded by the Carl Tryggers Foundation and the Swedish Research Council, VR.

Project: Females and males often have different phenotypic optima for important life history traits, but their shared genome causes conflict. Such sexual conflict is a dominating theme in evolutionary studies. Different selection pressures in the two sexes can decouple the genetic basis of the trait, allowing the resolution of conflict through sexual dimorphism. However, traits are seldom independent and covariances between traits can strongly influence evolutionary trajectories.

This project aims to understand how the strength of intra-locus sexual conflict over multiple life history traits constrains or facilitates the evolution of sexual dimorphism. You will use the nematode Caenorhabditis remanei, a powerful model system, and study lines that have been subjected to experimental evolution under increased/decreased sexual conflict. Within this framework, there are several possible lines of enquiry to pursue depending on the interests and background of the successful candidate. These include the study of:

-The evolution of genetic variances and covariances (represented statistically by the G matrix) within males (GM), within females (GF) and between traits between the sexes (B and its transpose BT). The stability of G and B over evolutionary time remains an open question. Estimations of GF, GM and B and their stability over time is essential to our understanding of both long-term constraints on the independent evolution of the sexes and of how different populations are expected to evolve under sex-specific selection.

-The relative importance of pre- and post-copulatory sexual selection on the evolutionary dynamics of sexual conflict.

You will join the lab of Dr. Elisabeth Bolund, and be part of the well-equipped nematode lab, led by two PI-s (Dr. Bolund and Dr. Lind). In the Bolund lab, we are interested in the evolutionary dynamics of life histories, sexual dimorphism and sexual conflict, using nematodes and humans as model organisms. Within the lab, we encourage a dynamic collaborative atmosphere.

Qualifications: The successful candidate will have a Ph.D. in evolutionary biology, ecology, genetics, or a related field. A background in or experience of some of the following areas is desirable: evolutionary biology, life history evolution, sexual conflict/sexual selection, quantitative genetics, statistics (experience in Bayesian analyses is a plus), basic R programming, and the running of large-scale lab experiments (with nematodes or other species). Further, good team work and communication skills are valued.

The environment:

EBC hosts one of the largest aggregations of evolutionary biologists in the world and Uppsala University was recently ranked 7th in the world in evolutionary biology (CWUR 2017). The Department of Ecology and Genetics is a highly international working environment and our research spans the scope from evolutionary ecology and genetics to studies of ecosystems. A number of high-profile projects address natural and sexual selection, local adaptation, speciation, molecular evolution, microbial diversity, and ecosystem processes. For more information, see ieg.uu.se. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant college town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm.

Position: The postdoc is funded by a tax-free 2-year scholarship from the Carl Tryggers Foundation, amounting to 23,000 SEK per month. It is a requirement from the funding agency that you are an incoming postdoc (in other words that your Ph.D. is not from Uppsala University).

How to apply: Application deadline: January 31, 2018.

Submit an e-mail to elisabeth.bolund@ebc.uu.se with the subject heading 'POST-DOC APPLICATION', with the following documents combined into ONE pdf file:

- A cover letter describing your research interests and suitability for the position - A detailed CV including a publication list and other achievements - Contact details of two to three references 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 February 2018.

Informal inquiries can be directed to elisabeth.bolund@ebc.uu.se

Lab home page: http://bolund.wix.com/homepage I am looking forward to your application!

Elisabeth Bolund <elisabeth.bolund@ebc.uu.se>

UUppsala ExpEvolutionInheritanceSystems

Title of project: Experimental evolution of inheritance systems

I am seeking a highly motivated postdoc to join the Lind lab at Dept. of Animal Ecology, Evolutionary Biology Centre (EBC), Uppsala University in a project funded by Carl Tryggers Foundation and the Swedish Research Council VR.

Project: The belief that the genetic code is the sole basis for biological inheritance has been challenged by phenotypic plasticity and more recently by the discovery of trans-generational epigenetic inheritance, where environmentally induced phenotypes are inherited for several generations by factors that determine how DNA is read. However, the adaptive significance of complementary inheritance systems that is induced by the environment is enigmatic.

The project aim is to investigate the evolution of adaptive plastic, epigenetic, trans-generational and genetic inheritance during adaptation to new environments that differ in heterogeneity, using the powerful laboratory model system of the nematode Caenorhabditis remanei. We will use a combination of experimental evolution and trans-generational phenotypic assays of life history traits, including analyses of already existing lines. For the experimental evolution part, the postdoc will work in close collaboration with an already recruited PhD student. Within this overall framework, there are several possibilities to explore related areas in life history evolution and environmental influences on phenotypes, depending upon the interests and background of the candidate.

You will join the lab of Dr. Martin Lind, and be part of the well-equipped nematode lab, led by two PIs (Dr. Lind and Dr. Bolund). In the Lind lab, we are interested in life history evolution in its broad sense, with special emphasis on local adaptation, the evolution of inheritance systems, life-history trade-offs and the evolution of lifespan and ageing. We encourage an open and collaborative atmosphere in the lab, and many projects are collaborative by design.

Qualifications: We are seeking a highly motivated and collaborative candidate with and with a background in evolutionary biology, especially life-history evolution. It is desirable if you have basic R programming knowledge and experience of large-scale laboratory experiments of nematodes or other organisms. The candidate will have a Ph.D. in evolutionary biology, genetics, ecology or a related field.

Working place: EBC hosts one of the world's largest aggregations of evolutionary biologists and Uppsala University was recently ranked 7th in the world in evolutionary biology (CWUR 2017). The Department of Ecology and Genetics is an international environment with staff and students from all over the world. Our research spans from evolutionary ecology and genetics to studies of ecosystems. A number of high-profile projects address natural and sexual selection, local adaptation, speciation, molecular evolution, microbial diversity, and ecosystem processes. For more information, see ieg.uu.se. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant college town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm.

Position: The postdoc is funded by a tax-free 2-year scholarship from Carl Tryggers Foundation, amounting to 23,000 SEK per month. It is a requirement from the funding agency that you are an incoming postdoc (in other words that your Ph.D. is not from Uppsala University).

How to apply: Application deadline: February 4, 2018.

Submit an e-mail to martin.lind@ebc.uu.se with the subject heading 'POST-DOC APPLICATION', with the following documents combined into ONE pdf file:

- A cover letter describing your research interests and suitability for the position

- A detailed CV including a publication list and other achievements

- Contact details of two to three references who can be contacted by telephone or e-mail before or after the interview.

Prospective candidates will be invited for interviews in person or over Skype in February 2018.

Informal inquiries can be directed to martin.lind@ebc.uu.se

Lab home page: http:///www.martinlind.org I am looking forward to your application!

Martin Lind

Research Fellow / Assistant Professor Dept. of Animal Ecology Uppsala University Norbyvägen 18D 752 36 Uppsala Sweden

http://www.martinlind.org/ Martin Lind

<martin.lind.evolmailinglists@gmail.com>

UUppsala Speciation

UUppsala.Speciation

Postcoctoral fellow in Evolutionary Biology

A 2-year postdoc position is available in the Karrenberg group at the Dept. of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, Sweden. The project is funded by the Carl Tryggers Foundation and SciLifelab Sweden.

Title of project: How genomic divergence during speciation arises: experimental assessment of allele transmission distortion

Processes that govern speciation and divergence are of vital importance for most other areas of biology, yet our understanding of organismal and genomic processes generating divergence is still limited. While many extrinsic reproductive barriers and the evolutionary forces generating them have been identified, the evolution of intrinsic barriers is not well-understood.

This project aims at experimentally assessing allele transmission between two hybridizing sister species of the non-model plant genus Silene, S. latifolia and S. dioica using ddRADseq data. The two species exhibit a complex array of reproductive barriers, including asymmetric conspecific pollen precedence. We also know that massive transmission distortion occurs in second-generation hybrids between these species. Candidate processes generating such transmission distortion include pollen competition, segregation distortion during female meiosis (meiotic drive) and hybrid breakdown. The project will disentangle these processes by comparing transmission ratio distortion between reciprocal backcrosses of first-generation hybrids. We have already produced crosses and ddRADseq genotyped offspring such that the postdoc can directly start with data analysis. This project can easily be extended to investigate the evolutionary history of loci the lead to high segregation distortion (ddRAD seq data from range-wide sampling of each species is available) and/or a coincidence of these loci with chromosomal re-arrangements between the two species. Other extensions, for example regarding phenotypic effects of distorter loci, can be developed depending on the interest of the postdoc.

You will join the group of Sophie Karrenberg at Plant ecology and Evolution, Institute of Ecology and Genetics, Uppsala University. In this research group, we mainly study reproductive isolation and speciation in Silene, including QTL mapping of traits related reproductive isolation, and genome-wide divergence patterns. We currently also focus on the role of the sex chromosomes for divergence and on the evolution of sexually dimorphic traits within S. latifolia.

Qualifications:

The successful candidate will have a Ph.D. in evolutionary biology, ecology, genetics, or a related field. A background in or experience of some of the following areas is desirable: speciation and reproductive isolation, QTL analysis, construction of linkage maps, ideally also analysis of transmission ratio distortion, population genomics, general statistics with R and R programming, basic bioinformatics skills. Further, teamwork and communication skills are highly valued.

The environment:

EBC hosts one of the largest aggregations of evolutionary biologists in the world and Uppsala University was recently ranked 7^th in the world in evolutionary biology (CWUR 2017). The Department of Ecology and Genetics is a highly international working environment and our research spans the scope from evolutionary ecology and genetics to studies of ecosystems. A number of high-profile projects address natural and sexual selection, local adaptation, speciation, molecular evolution, microbial diversity, and ecosystem processes. For more information, see ieg.uu.se. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant college town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm.

Position:

The postdoc is funded by a tax-free 2-year scholarship from the Carl Tryggers Foundation, amounting to 23,000 SEK per month. It is a requirement from the funding agency that you are an incoming postdoc (in other words that your Ph.D. is not from Uppsala University).

How to apply:

Application deadline: February 15, 2018.

Submit an e-mail sophie.karrenberg@ebc.uu.se with the subject heading Ã’âÂÂ¬ÂÂ$POST - DOCAPPLICATION', withthefollowingdocumentscombinedintoO$

- A cover letter describing your research interests and suitability for the position

- A detailed CV including a publication list and other achievements

- Contact details of two to three references 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 late February/early March 2018. The position can be started in late spring/summer 2018 or shortly thereafter.

Please feel free to contact me with questions at sophie.karrenberg@ebc.uu.se.

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UWisconsinMadison ReproductiveIsolationGenomics

The research group of John Pool at the University of Wisconsin-Madison invites applications for a postdoctoral research position. This scientist will lead our efforts to establish a premier system for uncovering the genetic basis of early-stage reproductive isolation.

Drosophila melanogaster originated in tropical Africa before expanding worldwide as a human commensal within the past ~10,000 years. From past work, we know that partial prezygotic and postzygotic isolation exists between African and European populations, and that crosses between them result in frequent F2 lethality and sterility. We also know that American populations result from admixture between these same gene pools. Recently, I used the 205 genomes of the Drosophila Genetic Reference Panel (DGRP) to show that natural selection has powerfully influenced this admixture process, and specifically that many unlinked pairs of genes show “ancestry disequilibrium”, suggesting that many pairs of African and European alleles are unfavorable when combined (Pool 2015 MBE). Based on these recent and prior results, we expect that a significant number of incompatibilities exist between these recently isolated but adaptively differentiated populations.

We consider this a uniquely appealing study system for understanding the genetic and evolutionary determinants of the earliest stages of reproductive isolation. First, the relevant interactors are demonstrably contributing to reduced genetic exchange in nature, and have clear relevance to the evolutionary trajectories of these adaptively distinct populations. Second, the study of populations that remain partially compatible opens the door to large-scale QTL mapping of lethality and sterility. Third, the recent time-scale of divergence means that population genetics can still help us find causative loci (and even interacting pairs of loci, as hinted above). And fourth, the unparalleled functional tool kit of D. melanogaster presents an ideal opportunity to confirm and characterize incompatibilities. There are still very few clear examples of Bateson-Dobzhansky-Muller incompatibilities, and this system could lengthen the list significantly.

The successful applicant will deploy a novel QTL mapping framework to identify pairs of loci that result in lethality and sterility. They will also leverage existing population genomic data from our Drosophila Genome Nexus to detect specific candidate genes within these QTL pairs. Depending on individual interests, they may also estimate quantitative evolutionary models compatible with our genomic data. I also encourage lab members to develop their own project ideas, and I am open to letting postdocs take important portions of our lab's research program with them when they found new research groups.

Our research group was founded 6+ years ago and currently consists of the PI, one postdoc, four PhD students, and six undergraduate researchers. I have also advised four former postdocs, and the publication records of Amir Yassin and Justin Lack show what a productive environment our lab can be for postdocs. For more details on our lab's research, its current membership, and its published track record, please visit: http://www.johnpool.net UW-Madison offers a superb scientific environment with a supportive, collaborative, and egalitarian culture. There are a substantial number of labs in population genetics, evolutionary genomics, and Drosophila research: https://genetics.wisc.edu/evolutionary-and-population-genetics/ http://www.evolution.wisc.edu/view_faculty https://genetics.wisc.edu/drosophila-and-other-insects/ Madison offers an exceptional quality of life in a beautiful natural setting. Downtown and campus are bordered by lakes, and the area includes a number of long distance bike trails. Madison features diverse art, music, and cultural offerings. A great farmers market and a focus on local food are complemented by a wide range of international restaurants. Madison has been ranked as the best city in America for young adults, and has appeared on a slew of 'top cities' lists, including lists for: families, dogs, biking, walking, nature, green-ness, safety, public schools and educated population, health and fitness, friendliness, farmers markets, arts, vegetarians, biotech, careers, quality of life, and so on... http://www.visitmadison.com/media/rankings/ Applicants should send a CV and contact information for three references to jpool@wisc.edu. In addition, applicants should send a statement of research interests/background, addressing: * Their own long term scientific interests and specific overlap with the

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UZurich EvolutionHeterostyly

*Two Post-Doctoral positions at the University of Zurich *

POSITIONS DESCRIPTION*. Two post-doctoral positions in 1) evolutionary biology/genomics and 2) bioinformatics are available in Elena Conti's lab at the University of Zurich*. The main research focus is on evolutionary pathways in heterostyly and the evolution of supergenes. Current projects include: phylogenomics and evolution of breeding systems in Primulaceae; morphological, ecological and biogeographic evolution in Primulaceae; comparative genomics of selected taxa in Primulaceae aimed at clarifying the evolution of floral morphology and the heterostyly supergene; evolution of heterostyly in flowering plants; reproductive barriers in /Primula/. The successful applicants will benefit from resources and collaborations on the above-mentioned topics developed by Elena Conti's lab over several years and from concurrent projects on the genomics of heterostyly and introgression in Primulaceae funded by the European Union and the Swiss National Science Foundation. Opportunities to gain experience in teaching and grant writing are available and encouraged. The Department of Systematic and Evolutionary Botany and the University of Zurich provide state-of-the art infrastructure, excellent scientific milieu, and an international, English-speaking working environment. With a world-class airport located in the center of Europe, Zurich offers unmatched opportunities for easy travel to conferences and workshops anywhere in the world. Proximity to the Alps offers easy access to multiple outdoor activities and the species-rich Alpine flora.

REQUIREMENTS: The successful applicants will have a Ph.D. degree with evidence of publication in peer-reviewed scientific journals. *Required skills*- _Demonstrated ability to_: frame questions, hypotheses, and goals towards publication in peer-reviewed journals; utilize and analyze data from multiple Next Generation Sequencing platforms; develop novel pipelines and perform cutting-edge population genomic and phylogenomic analyses; write scientific manuscripts. Expertise in comparative genomics, bioinformatics, experimental design, and statistical analyses is necessary. Ability to collaborate, independence, and excellent writing skills are required. One of the two positions will be focused especially on _bioinformatics_and the development of new analytical methods, in collaboration also with Dr. Peter Szövenyi's lab at the University of Zurich.

APPLICATION PROCEDURE*. Applications* will be reviewed starting on *_February 20, 2018_ and will continue to be evaluated until suitable candidates are identified*. Please, *clearly indicate which position you are applying for in your application*. Send your application as a SINGLE PDF FILE titled *Primula-postdoc_yourfamilyname *to ContiElena@access.uzh.ch. Your application will contain the following documents: *1)* cv; *2)* publication record; *3)* Copy of obtained Ph.D. diploma and courses taken, with grades; *4)* letter of motivation explaining your interest in and suitability for the position (2 pages max.); *5)* names, institutional affiliations, email addresses and phone numbers of 3 referees. Applications that fail to meet the guidelines specified above will _not_ be further considered.

STARTING DATE: *May 1, 2018*(with possibility of negotiation). The positions are available for 2 to 3 years, contingent upon successful performance review after the first year. Opportunities for prolongation are available upon successful grant writing and application.

For further information, see:

http://www.systbot.uzh.ch/de/Personen/ProfessorenundDozenten/ElenaConti.html https://scholar.google.ch/citations?user=PFOsKdIAAAAJ&hl=en Dr. Barbara Keller

Department of Systematic and Evolutionary Botany University of Zurich Zollikerstrasse 107 8008 Zurich Switzerland

Tel. + 41(0)44 634 84 18 Mobile + 41(0)79 794 15 82

Monday, Tuesday, Wednesday, and Thursday at Department

Office: O 19 Lab: P1 38 barbara.keller@systbot.uzh.ch

http://www.systbot.uzh.ch/Personen/WissenschaftlicheMitarbeiterInnen/BarbaraKeller.html Barbara Keller <barbara.keller@systbot.uzh.ch>

VanderbiltU InsectMicrobeSymbiosis

Postdoctoral position in functional genetics of insect-microbe symbioses A postdoctoral position is available in the Bordenstein laboratory (bordensteinlab.vanderbilt.edu) to functionally characterize host-microbe interactions in Drosophila. This project will dissect the number and types of Drosophila genes and pathways that are altered by the endosymbiotic bacteria Wolbachia. The candidate will develop methods and apply multiple technologies to dissect how the bacteria modify host embryonic development at the molecular, genetic, and biochemical levels. As Wolbachia are increasingly relevant to vector control efforts to curb arbovirus transmission, translational aspects of this work include development of transgenic strategies for vector and pest control.

Applicants soon to acquire their Ph.D. or with previous postgraduate experience are welcome. Applicants should have a demonstrated ability to work both independently and collaboratively, possess excellent oral and written communication skills, and have a record of productivity as evidenced by publication history. Successful candidates will have some of the following skills: proteomics, transcriptomics, functional genetics, computational biology, Drosophila and Wolbachia rearing, fluorescent microscopy, molecular evolution, and molecular biology of phages.

Vanderbilt University campus is a National Arboretum located in the heart of Nashville, the capital of Tennessee. Known internationally as Music City USA, Nashville is also the home to professional sports teams, the Nashville Symphony, the Frist Center for the Visual Arts, and numerous activities for outdoor enthusiasts. Nashville, Tennessee is a wonderful place to live, work, and raise a family and has been named one of the 15 best U.S. cities for work and family and one of the 25 cities most likely to have the country's highest job growth over the coming five years. Major industries include tourism, printing and publishing, technology manufacturing, music production, higher education, finance, insurance, automobile production and health care management.

To apply, please send a single pdf including a cover letter stating career interests, research strengths, areas to develop, earliest start date, curriculum vitae, an example publication, and contact information for three or more references to s.bordenstein@vanderbilt.edu. The position is available now and renewable up to two years contingent upon satisfactory performance. Salary is commensurate with experience and includes a comprehensive benefits package. Review of applications will begin immediately and continue until the position is filled.

Contact: Seth Bordenstein: s.bordenstein@vanderbilt.edu Lab: http://bordensteinlab.vanderbilt.edu

"s.bordenstein@Vanderbilt.Edu" <s.bordenstein@Vanderbilt.Edu>

VirginiaTech ComparativeMethods

Position summary: A postdoctoral position is available in the Uyeda lab at Virginia Tech to work on novel phylogenetic comparative methods that integrate phenotypic ontologies with models of trait evolution. The Uyeda lab develops and applies phylogenetic comparative methods in a variety of empirical systems with the goal of connecting analysis of macroevolutionary patterns with a process-based understanding of evolution. Candidates will have opportunity to develop their own research projects and interests so long as they have overlap with the goals of the project. Experience with phylogenetics, comparative methods, programming, computational biology, Bayesian statistical modeling, and phenotypic ontologies are highly desirable. Applications will be considered starting on February 1, 2018. For questions and informal inquiries, send email to juyeda@vt.edu.

Virginia Tech does not discriminate against employees, students, or applicants on the basis of age, color, disability, gender, gender identity, gender expression, national origin, political affiliation, race, religion, sexual orientation, genetic information, or veteran status; or otherwise discriminate against employees or applicants who inquire about, discuss, or disclose their compensation or the compensation of other employees, or applicants; or any other basis protected by law.

For inquiries regarding non-discrimination policies, contact the executive director for Equity and Accessibility at 540-231-2010 or Virginia Tech, North End Center, Suite 2300 (0318), 300 Turner St. NW, Blacksburg, VA 24061.

Required qualifications: PhD in relevant field (evolution, organismal biology, statistics, computational biology, etc.)

Preferred qualifications: Experience in the development of phylogenetic comparative methods and comparative methods Experience with phenotypic ontologies Programming experience Experience with Bayesian statistical modeling

How To Apply: Qualified applicants must electronically submit online application, cover letter, resume/curriculum vitae, and list of references to jobs.vt.edu, posting #SR0180003. http://listings.jobs.vt.edu/postings/83217 "juyeda@vt.edu" <juyeda@vt.edu>

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Barcelona IntroGeometricMorphometrics Apr30-May5

Dear colleagues,

Registration is now open for the course "INTRODUCTION TO GEOMETRIC MORPHOMETRICS - 10th edition".

INSTRUCTORS: Dr. Chris Klingenberg (University of Manchester, UK) and Dr. JesÃºs Marugán (UAM, Spain).

Dates: April 30th-May 5th, 2018.

More information and registration: http://www.transmittingscience.org/courses/geometric-morphometrics/introduction-geometric-morphometrics/ This course is entitled to teach the main concepts of shape analysis based on landmark coordinates and its multivariate procedures, and how they can be put into practice across any biological discipline in which the phenotype (form) and its variation are the principal sources of information.

Program (this includes topics related to evolution):

1. Introduction: Shape, size and biological morphology. 2. Morphometric data: Equipment, landmarks, outlines and surfaces. 3. Visualizing shapes and shape changes. 4. Looking at variation: PCA. 5. Distinguishing groups: CVA and discriminant analysis. 6. Symmetry and asymmetry. 7. Morphometrics in a messy world: outliers and measurement error. 8. Regression and allometry. 9. Covariation between things: PLS. 10. Morphological integration. 11. Modularity. 12. Phylogeny and comparative methods. 13. Putting things together: Combining analyses to solve biological questions. 14. Presentation of group work by participants.

Software that will be used during the course: TPS, ImageJ (FIJI) and MorphoJ

With best regards

Soledad De Esteban-Trivigno,PhD. Scientific Director Transmitting Science http://www.transmittingscience.org/ Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.org>

Barcelona MappingTraitEvolution Jun4-8

Dear colleagues,

Registration is open for the second edition of the course $B!H(BMapping Trait Evolution$B!I(B, June 4th-8th, 2018.

Instructor: Dr. Jeroen Smaers (Stony Brook University, USA).

Registration: https://www.transmittingscience.org/courses/evolution/mapping-trait-evolution/ PROGRAM:

Monday. (R packages: ape, Geiger).

Morning: Phylogenetic data.

* What is the basic structure of phylogenetic data? * How to visualize and manipulate phylogenetic data?

Afternoon: Models of evolution.

* What are models of evolution? * What are the assumptions of the different models of evolution? * How are models of evolution utilized?

Tuesday. (R packages: ape, nlme, caper, evomap).

Morning: Phylogenetic regression.

* Assumptions, properties, and applications of the phylogenetic regression.

Afternoon: Phylogenetic ancova.

* Testing for grade shifts using the phylogenetic regression.

Wednesday. (R packages: phytools, motmot, geiger, ape, evomap, BayesTraits).

Morning: Ancestral estimation.

* Using models of evolution to estimate values of ancestral nodes.

Afternoon: Analysis of rates of evolution.

* Estimation of rates of evolution. * Testing hypothesis about rates of evolution.

Thursday. (R packages: bayou, phylolm, surface, OUwie, mvMORPH).

Morning: Inferring the structure of a macroevolutionary landscape.

* Using Ornstein-Uhlenbeck models to map macroevolutionary patterns.

Afternoon: Testing the structure of a macroevolutionary landscape.

* Applications and assumptions of OU models. * Using OU models to test macroevolutionary hypotheses.

Friday. (R packages: geomorph).

Morning: Modularity and integration.

* What is $B!F(Bphylogenetic$B!G(B modularity and integration? * Applications and assumptions.

Afternoon: Case study.

With best regards

Sole

Soledad De Esteban-Trivigno,PhD. Scientific Director Transmitting Science http://www.transmittingscience.org/ Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.org>

Barcelona NGSdata May14-17

Dear colleagues,

This course might be of interest to the members of this list: MANIPULATION OF NGS DATA FOR GENOMIC AND POPULATION GENETICS ANALYSES.

Date: May 14th-17th, 2018, Barcelona (Spain).

PLACE: Capellades, Barcelona.

INSTRUCTORS: Dr. François Sabot (Institute of Research for Development, France) and Dr. Christine Tranchant-Dubreuil (Institute of Research for Development, France)

PROGRAM:

- Monday, May 14th, 2018.

Introduction to NGS sequencing platforms. Introduction to basic command lines. Basic raw data manipulations (counting sequences, listing files).

- Tuesday, May 15th, 2018. Raw data QC & Cleaning. Introduction to TOGGLe, a NGS pipeline framework. Mapping: principle, tools, execution. Mapping: cleaning, data control, realigning, duplicates marking.

- Wednesday, May 16th, 2018. SNP calling: raw calling, cleaning calling, filtering. VCF manipulations: filtering on MAF, heterozygosity Impact of SNPs on genes. Population genomics using sNMF.

- Thursday, May 17th, 2018. Context-based analyses. Piping large-scale analyses for multiple samples using TOGGLe. Testing new tools and different conditions to answer different biological questions.

Questions.

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD. Scientific—Director Transmitting Science http://www.transmittingscience.org soledad.esteban@transmittingscience.org

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Berlin AdvancedRProgrammingJun25-29

Advanced R Programming (https://www.physalia-courses.org/courses-workshops/course26/)

WHEN

25-29 June 2018

WHERE Botanisches Museum, Königin-Luise-Straße 6-8, Berlin (Germany)

Instructors:

VP Nagraj (University of Virginia (USA)).

Overview R is a popular open-source statistical computing language. This course will introduce techniques for programming in R, including how to work with a variety of data structures, write functions and package code for distribution. Each lesson will be interactive with hands-on activities to solidify concepts covered in lectures. The week will conclude with a package development practicum, during which attendees will have the opportunity to implement methods covered in class for a project of their own design.

Target Audience The goal of this course is to provide training on how to start using R as a programming language: to write new functions, develop new tools or, at the very least, interact with data programmatically. While some examples may be drawn from bioinformatics, statistics and / or epidemiology, the material will not focus on data analysis techniques. As such, the course will generally be domain-agnostic. Researchers from a variety of disciplines are welcome. Those interested should have basic familiarity with R or another programming language.

STRUCTURE The course material will be delivered over 5 days, in 10 half-day sessions. These lessons will build off of one another, and feature a mix of lecture and in-class exercises.

Session content

Monday 25th. 09:30-17:30

Session 1: Data Structures

In the first session we will survey data structures in R. We'll cover assignment, indexing and programmatic interaction with a number of types of objects, including vectors, matrices, lists and data frames.

Session 2: Conditionals and Iteration

Building on the data structures overview, we'll explore approaches for implementing logic, testing conditions and iterating over R objects. The material will include comparisons via operators, looping, vectorization, "apply" functions and control flow.

Tuesday 26th. 09:30-17:30

Session 3: Functions

This session will introduce essentials of writing functions in R. We will discuss methods for passing arguments, establishing return values and handling errors. We'll also spend time covering R environments, as well as the system of searching for objects from within a function and beyond.

Session 4: Debugging, Performance and Optimization

Writing a function is one thing ... fixing semantic and syntactic errors is another altogether. We'll dive into this topic by way of looking at tools that are built into R and RStudio for debugging code. This lesson will also cover methods for diagnosing performance roadblocks and profiling code.

Wednesday 27th. 09:30-17:30

Session 5: Object Oriented Approaches

In the context of data analysis, R is most commonly used as a functional programming language. This session will introduce methodology for object oriented programming (OOP) in R. The material will include how to define S3 and S4 classes, as well as how to establish methods for generic functions.

Session 6: Version Control with Git and Github

Git is a powerful program for version control and collaboration. This session will introduce workflows for using Git and Github, which is a popular platform for managing projects and distributing code. We'll pay particular attention to how these tools are implemented in the context of R programming and package development.

Thursday 28th. 09:30-17:30

Session 7: Package Development Tools (Part 1)

In this session, we'll survey tools, techniques and use-cases for R package development. In addition to version control tools (i.e. Git), there are a quite a few packages, frameworks and convenient integrations with the RStudio IDE that can facilitate the package development workflow. We will focus on package structure, documentation, building and checking, handling dependencies and unit testing.

Session 8: Package Development Tools (Part 2)

We'll continue to explore tools for package development in this lesson. In particular, we'll discuss how to implement more robust checks, continuous integration methods, vignettes, protocols for releasing a package and best practices for including data.

Friday 29th. 09:30-17:30

Session 9: Package Development in Practice

With a baseline understanding of tools for package development, we'll explore several case studies that further enumerate the motivations and practical applications of developing your own package. This session will also feature time allocated for individualized research and development on a project of your choosing.

Session 10: Next Steps

R is a dynamic resource, with new features being added and new trends in how it is used as a programming language. We'll conclude with an

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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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Berlin EpigenomicDataAnalysis May28-Jun1

Dear all,

registration is now open for the course "Epigenomic Data Analysis"

[https://www.physalia-courses.org/courses-workshops/course31/)

28th May - 01st June 2018, Berlin (Germany)

WHERE Botanisches Museum, Königin-Luise-Straße 6-8, Berlin

Instructors:

Dr. Federico Comoglio (Cambridge Institute for Medical Research (UK))

Dr. Iros Barozzi (Imperial College London (UK))

Overview This course will introduce researchers and technical workers to the bioinformatic analysis of large epigenomic data sets obtained using Next-Generation Sequencing (NGS) technologies, with a focus on ChIP-seq, RNA-seq and DNase-seq / ATAC-seq. The course will cover the theoretical foundations of the most widely adopted algorithms and analysis pipelines, a targeted introduction to scripting in bash and R/BioConductor, and extensive hands-on tutorials using publicly available NGS data sets. At the end of this course, the students should be able to efficiently analyze their own data and identify common pitfalls of genomics data analyses.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at researchers moving the first steps in epigenomic data analysis and / or interested in learning more about this subject. The course will offer a balanced mixture of lectures and hands-on practical tutorials using popular tools and R/BioConductor packages. Previous knowledge of genomics data formats from Illumina sequencers and exposure to bioinformatics is beneficial but not a necessary prerequisite.

Assumed Background

The participants should have some basic background in biology and understand the central role of DNA for biodiversity studies. No programming or scripting expertise is required and some basic introduction to UNIX-based command line applications will be provided on the first day. However, some basic experience with using command line and/or R is clearly an advantage as not all the basics can be thoroughly covered in that short amount of time. All hands-on exercises will be run in UNIX-environments (Linux, Mac) on remote servers. Statistical analyses will be run in R using RStudio.

Session content

Monday 28th - Classes from 09:30 to 17:30 - “The basics”

Session 1: Motivation and introduction to the biological system_(morning)

We will start with an introductory lecture presenting several examples of integrative epigenomic data analyses from recent literature. We will then focus on the biological system that will be used throughout this 5-days course, where we will study dynamic chromatin changes induced by Lipopolysaccharide (LPS) stimulation of mouse bone marrow-derived macrophages.

Session 2: Introduction to Linux and bash (morning)

In this session, we will provide a targeted introduction to Linux and bash scripting, with a focus on the tools required for the rest of the course. No previous exposure to scripting is strictly required. Also, we will not attempt to provide a catalogue of functions and command syntax. Rather, we will focus on the principles and logic of scripting.

Session 3: R programming_(afternoon)

In the afternoon, we will cover the basics of R programming. This session will alternate short talks covering the basics with extensive hands-on tutorials to allow students without prior exposure to R to familiarize themselves with this language in the most natural way. This session aims at building a solid foundation of R programming, and will also cover good coding practices for reproducible research.

Tuesday 29th - Classes from 09:30 to 17:30 - “ChIP-seq data analysis”

Session 4: ChIP-seq data analysis - theory (morning)

This module covers the building blocks of a ChIP-seq data analysis workflow. We will discuss quality control metrics and common pitfalls, and the theoretical foundations of commonly used aligners and peak callers.

Session 5: ChIP-seq data analysis lab (afternoon)

In the afternoon, we will transition from theory to practice. We will run a complete ChIP-seq data analysis workflow. We will also learn how to generate and visualize tracks in formats widely adopted by genome browsers. During this hands-on session, we will randomly assign a topic for a lightning talk (3 minutes = 3 slides) on common pitfalls of ChIP-seq algorithms and/or results interpretation.

Wednesday 30th - Classes from 09:30 to 17:30 - “RNA-seq data analysis”

Session 6: Lightning talks_(morning)

In this session, the students will present their lightning talks on the topic assigned in Session 5. This will be followed by a 30’ round table open discussion.

Session 7: RNA-seq data analysis - theory (morning)

We will then move on to RNA-seq data analysis. We will first cover the theoretical basis of commonly adopted algorithms for RNA-seq data processing. We will then discuss the statistical foundation of algorithms

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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

Berlin GeometricMorphometrics 5-9March deadline

Dear all,

registration deadline is soon approaching (10.02.18) and we still have a few spots available for our course "Geometric Morphometrics" (https://www.physalia-courses.org/courses-workshops/course22/)

Where: Berlin (Germany)

When: 5th-9th March 2018

Instructor: Dr. Carmelo Fruciano (ENS, Paris (France)) http://bit.ly/2rxQVFC Overview

Geometric morphometrics has become a standard in biological research because it combines statistical rigour and ease of interpretation. Through geometric morphometrics, biological form is quantified, analysed and the results are expressed as easily interpretable and visually impactful shape changes. This course covers the main common practices of modern geometric morphometrics, including: acquiring data, analysing it, visualizing and interpreting the results.

Format

The course will be delivered over five days and will comprise both lectures and hands-on sessions. The lectures will cover both basic theoretical aspects and their practical implementation in research practice and software. During the hands-on sessions, the attendees will have the chance of both using example datasets and applying the knowledge acquired to their own data. The course will be focused mainly on 2D data and on easy-to-use software with graphical user interface to maximize the ability to understand concepts and apply them. However, some information on 3D data and on R implementations will be provided, as appropriate.

Assumed Background

This course is aimed at beginners and intermediate users. In other words, it is aimed at researchers who intend to use geometric morphometrics or who have started performing geometric morphometric analyses but feel they need a more structured background.

Requirements

Attendees should have a background in biology and a basic understanding of statistical concepts.

Session content

Monday 5th - Classes from 09:30 to 17:30

Geometric morphometrics: overview and potential applications: - Traditional and geometric morphometrics - An overview of common analyses - Examples of geometric morphometrics applied to biological problems

>From biological objects to numerical representation: - Overview of typical devices used to digitalise biological objects

- Landmarks, semilandmarks, outlines and surfaces - different types of geometric morphometric data

- Most commonly used geometric morphometric software
- Data quality, most common pitfalls in study design and data acquisition

Tuesday 6th - Classes from 09:30 to 17:30

Generalized Procrustes analysis (GPA) - the core of most geometric morphometrics:

Principal component analysis (PCA) Comparing groups:
- Between-group PCA - Canonical variate analysis (CVA)
- Tests of difference in means

Wednesday 7th - Classes from 09:30 to 17:30

Co-variation between size and shape: - Allometry, regression and general linear models

Co-variation between shapes: - Partial least squares analysis (PLS) - Modularity and integration

Thursday 8th - Classes from 09:30 to 17:30

Combining analyses in a basic workflow: - Preliminary assessment of data quality - Typical basic workflow

Expanding the basic workflow: variation in geographic space Expanding the basic workflow: association between shape and environmental variables

Friday 9th - Classes from 09:30 to 17:30

Expanding the basic workflow: elements of phylogenetic comparative analyses Review and open discussion Presentation of attendees' analyses on their own data

For more information about the course, please visit our website: https://www.physalia-courses.org/courses-workshops/course22/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/-courses-workshops/ Best regards,

Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

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https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin RStatistics Jun18-22

Getting started with R [https://www.physalia-courses.org/courses-workshops/course13/) 18-22 June 2018, Berlin (Germany) Application deadline is: May 20th, 2018.

Instructor: Dr. Alexandre Courtiol (Leibniz Institute for Zoo and Wildlife Research, Berlin (Germany)) https://www.physalia-courses.org/instructors/t40/) Overview: R is the statistical software the most used in the world. It is extremely powerful, free of charge and open source. Despite these benefits, many avoid R, or struggle with it, as writing computer code to do any operation – a requirement in R – is at first both difficult and intimidating.

This course aims at overcoming those challenges by providing solid basics in R. At the end of the course, participants should feel much more at ease writing a computer script in the R language which covers the entire spectrum of a statistical analysis: reading data, editing them, plotting them, and analysing them. Because linear models are the dominant statistical tool in many fields, the part of the course focussing on analyses per se (see schedule) will focus on those, but principles seen during the class should greatly help those interested in other kind of analyses as well. The course will be presented over five days and will mix explanations and guided exercises. Students are free to practice with their own datasets during the course.

Intended Audience & Assumed Background: This course is aimed at scientists from quantitative sciences (e.g. biology, epidemiology, psychology...). It has been created with biologists in mind but it should accommodate scientists from other disciplines. No previous experience with R is required. Participants should have a basic familiarity with statistical terms and concepts.

Session content Monday 18th 'V Classes from 09:30 to 17:30 Monday is DATA day This first day will be dedicated to the data. R is software dedicated to data analysis, so mastering the basics of data manipulation in R is essential for further steps. It will be explained how to import data into R and how to manipulate them (e.g. from adding or removing rows or columns, to merging tables and using pivot tables). This will be good practice for students to learn the basics of the R language. We will illustrate how to do everything using R base (that is R out of the box), but we will also introduce that allow users to perform some operations on large datasets a little faster.

Tuesday 19th 'V Classes from 09:30 to 17:30 Tuesday is PLOTTING day Plotting is a crucial part of any data analysis no matter how advanced you are in statistics. It is important to visualise the data before the analysis (e.g. to visually check the presence of potential errors and for getting a sense of the distribution of the data), during the analysis (e.g. to check the distribution of model residuals), and after the analysis (to communicate findings in the most efficient way). Therefore, knowing how to plot various kind of data matters a lot. We will thus show how to plot different types of data in R (points, distributions, rasters...) using different graphic environments (e.g graphics, lattice, ggplot2).

Wednesday 20th 'V Classes from 09:30 to 17:30 Wednesday is FUNCTIONS day As John Chambers – the grandfather of R – put it Everything that happens in R is a function call. That R allows for so-called functional programming is one of its great benefits: it allows the implementation of any workflow of statistical analysis as the succession of simple clearly identified steps. Each step is described by a function that takes an input and generates an output. The output of one function is often the input of the next. On this third day we will show that creating one's own function is very very easy (yes, even YOU can program!) and can be very very useful. As a first application we will create our own functions to implement a randomisation test. As a second application we will show how to create functions to perform a power analysis (the estimation of the probability of getting true positives when applying a test) for any statistical test.

Thursday 21st 'V Classes from 09:30 to 17:30 Thursday is LM day Many widely used statistical methods (t-tests, anova, ancova, linear regressions...) are just different type of Linear Models (LM), which is why LM represent the most useful statistical toolbox to be familiar with if you are in natural or social sciences. Fitting a LM in R is easy – but building models, checking model assumptions, interpreting the outputs, and plotting predictions correctly requires some know how. After refreshing the most important concepts surrounding LM, we will go through each of these steps in detail, working on real datasets. It is important to understand LM quite well before jumping into the more complex methods which we will see on the next day.

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ColoradoStateU WildlifeDiseaseGenomics Jun8-9

Where: Colorado State University, Fort Collins, Colorado, USA What: The 2nd Genomics of Disease in Wildlife Workshop When: June 3-9, 2018

Website for more information and application instructions: https://www.gdwworkshop.colostate.edu/ Application Deadline: February 15, 2018

Email inquiries: CSU_gdw@colostate.edu

Overview:

Title: Genomics of Disease in Wildlife: A Workshop

Location: Lory Conference Student Center, Colorado State University, Fort Collins, CO

Dates: June 3-9, 2018

Website: https://www.gdwworkshop.colostate.edu/ Application deadline: February 15, 2018.

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 day 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 day's 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: The workshop begins in the evening of Sunday

June 3, 2018 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: 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, assessment of sequence data quality, long and short reads, scaffolds, contigs, and genome assembly algorithms and de novo assembly.

Day 3: Lectures and computer labs will outline the critical steps

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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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Europe MEME EvolutionaryBiology

Erasmus Mundus Master Program in Evolutionary Biology (MEME)

MEME is a two-year research oriented master program for talented and motivated students who are interested in understanding evolution in all its facets. It intends to provide an optimal preparation for subsequent doctoral studies and eventually a career in academic research.

The MEME program addresses the driving forces of evolution at all levels of organismal organization (from cells and individuals to populations and ecosystems), and allows students to study all kinds of organisms (microorganisms, plants, animals) in all kinds of habitats (marine as well as terrestrial) with a diversity of approaches (field, lab, theory). The focus of the program is not only on how evolution shaped life on our planet in the past, but also on how understanding the principles underlying evolution can provide new insights and help to cope with present-day challenges in a variety of fields, including ecology, epidemiology, physiology, immunology, genetics/genomics, bioinformatics, economics and the social sciences.

To offer a program of such broad scope, four European universities (University of Groningen, Netherlands; University of Montpellier, France; Ludwig Maximilians University of Munich, Germany; Uppsala University, Sweden), have joined forces with Harvard University (USA). Together, this consortium has put together an attractive multidisciplinary program that meets highest standards. All students have to study at (at least) two partner universities, and they will receive a double degree from two partner universities they have attended.

A limited number of full scholarships is available for European and non-European students and these will be awarded in a selective procedure. Details on the program and the selection procedure can be found on www.evobio.eu . Starting date: 1 September 2018

Application deadline: 1 February 2018

Please alert your students to this great opportunity!

More information and how to apply - please see www.evobio.eu Questions about the contents of the program:

Franjo Weissing (f.j.weissing@rug.nl)

Questions about the requirements and the application procedure:

Maartje Giesbers <m.c.w.g.giesbers@rug.nl>

Finland MathematicalEvolution Aug

THE HELSINKI SUMMER SCHOOL ON MATHEMATICAL ECOLOGY AND EVOLUTION 2018

Application deadline extended to 15 February

Dear Colleagues,

We are glad to invite applications to the 2018 edition of The Helsinki Summer School on Mathematical Ecology and Evolution, an EMS-ESMTB School in Applied Mathematics. The school will be held between 19 and 26 August 2018 in Turku, Finland, and will be part of the EMS Year of Mathematical Biology < http://euro-math-soc.eu/year-mathematical-biology-2018 >.

The core program consists of five series of lectures:

Karl Sigmund (University of Vienna): Evolutionary game theory Odo Diekmann (Utrecht University): Renewal equations in population biology Sebastian Schreiber (University of California, Davis): Coexistence in variable environments Ellen Baake (University of Bielefeld): Probabilistic models and ancestral processes in population genetics Mick Roberts (Massey University of New Zealand): Ecology of infectious diseases

All young researchers working in mathematical ecology can apply from all countries, especially from Europe and the Mediterranean. The school is aimed at graduate students of mathematics, but we also welcome students of biology with sufficient background in mathematics, as well as advanced undergraduates and postdocs.

For more information and details of the application procedure, please visit the school's webpage https://wiki.helsinki.fi/display/BioMath/-The+Helsinki+Summer+School+on+Mathematical+Ecology+and+Evolution+2018 With best regards, Eva Kisdi (eva.kisdi@helsinki.fi)

"Kisdi, Eva" <eva.kisdi@helsinki.fi>

FridayHarborLabs EvolQuantGenetics Jun4-8

Evolutionary Quantitative Genetics Workshop

Friday Harbor Laboratories, University of Washington, 3-9 June 2018

Non-credit workshop. Participants arrive at Friday Harbor Labs on Sunday, June 3, lectures and exercises occur June 4-8, and participants depart on Saturday, June 9, 2018.

Application deadline March 1, 2018. Details and links to the application forms will be found here: http://-tinyurl.com/EQG2018 The blog web pages for the workshop will be found at http://blogs.uw.edu/fhleqg/ They currently include a 2017 workshop schedule which has links to the materials for that year's workshop.

Instructors: Dr. Joe Felsenstein, Dept. of Genome Sciences and Dept. of Biology, University of Washington Dr. Stevan J. Arnold, Department of Integrative Biology, Oregon State University

This workshop has been given yearly since 2011. Since 2017 it has been given at the Friday Harbor Laboratories of the University of Washington, on San Juan Island.

The workshop will review the basics of theory in the field of evolutionary quantitative genetics and its connections to evolution observed at various time scales. The aim of the workshop is to build a bridge between the traditionally separate disciplines of quantitative genetics and comparative methods.

Quantitative genetic theory for natural populations was developed considerably in the period from 1970 to 1990 and up to the present, and it has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements.

Phylogenetic approaches to comparative biology were developed in the 1980s and 1990s, including inferring how traits covary in evolution and how optimum values of traits vary between species.

Textbooks have not kept pace with these developments, and currently few universities offer courses on these subjects aimed at evolutionary biologists.

Evolutionary biologists need to understand this field because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics. This workshop aims to fill this need by reviewing basic aspects of theory and illustrating how that theory can be tested with data, both from single species and from multiple-species phylogenies.

Participants will use R, an open-source statistical programming language, to build and test evolutionary models.

The workshop involves lectures and in-class computer exercises. You can consult the 2017 workshop website for examples, using the links found at the 2017 schedule mentioned above.

The intended participants for this workshop are graduate students, postdoctoral fellows, and junior faculty members in evolutionary biology. The workshop can accommodate up to 30 participants. Guest instructors are:

* Adam Jones, Biology, Texas A&M University, College Station * Patrick Phillips, Biology, University of Oregon * Patrick Carter, Evolutionary Physiology, Washington State University, Pullman * Emilia Martins, Biology, Arizona State University * Marguerite Butler, Biology, Univ. Hawai'i, Manoa * Brian O'Meara, Ecology & Evolutionary Biology, Univ. of Tennessee, Knoxville * Josef Uyeda, Biological Sciences, Virginia Tech, Blacksburg

Cost: $1000, to be paid to Friday Harbor Laboratories. This fee will cover housing and meals at FHL and all other workshop expenses, except travel. Participants who have been admitted to attend will make their payment prior to arrival at FHL. Details of payment by credit card or check will be provided once the applicant has been admitted to attend.

This workshop is also sponsored by the American Society of Naturalists and the Society for the Study of Evolution.

Participants who are already members or join one of these societies are eligible for a $200 compensation award that reduces the net cost of the workshop to $800.

—- Joe Felsenstein joe@gs.washington.edu Department of Genome Sciences and Department of Biology, University of Washington, Box 355065, Seattle, WA 98195-5065 USA

"felsenst@uw.edu" <felsenst@uw.edu>

FridayHarborLabs MarineInvertebrateEvol Jun11-Jul13

Friday Harbor Laboratories Marine Invertebrate Zoology Summer 2018

Instructors: Dr. Kevin Kocot (University of Alabama) & Dr. Johanna Cannon (U. C. Santa Barbara)

Dates: Monday, June 11 - Friday, July 13, 2018 (5 weeks)

Credits: 9

Marine Invertebrate Zoology is designed to provide advanced undergraduates, post-baccalaureates and graduate students with comprehensive exposure to the subject of invertebrate zoology. Students will learn about the diversity, taxonomy, ecology, evolution, structure, and function of invertebrates. We will cover all animal phyla from Annelida to Xenacoelomorpha and explore diversity within phyla based on the rich marine biota of the San Juan Islands. Students will learn about the field of invertebrate zoology in light of information gained through the use of traditional tools like electron microscopy and histology as well as new tools like genomics and evolutionary developmental biology ("evo-devo"). If you like going to zoos and aquariums, you should like this course! Most of the time of the course will be spent focusing on the study of living animals in the laboratory and field. Prior coursework in invertebrate biology or animal diversity is preferred but not required; if in doubt, please contact one of the instructors. Enrollment is limited to 20 students.

For more information, visit: https://fhl.uw.edu/courses/ Applications due February 1, 2018!

Kevin M. Kocot Assistant Professor, Department of Biological Sciences Curator of Invertebrates, Alabama Museum of Natural History The University of Alabama < https://www.ua.edu/ > 307 Mary Harmon Bryant Hall, Tuscaloosa, AL 35487 office 205-348-4052 <tel:205-348-4052> fax 205-348-4039 kmkocot@ua.edu | http://bsc.ua.edu/ [The University of Alabama] < https://www.ua.edu/ > [Facebook] < https://www.facebook.com/kmkocot > [Twitter] < https://twitter.com/kmkocot >

"Kocot, Kevin" <kmkocot@ua.edu>

Glasgow ViralBioinformaticsGenomics Aug20-24

Training course on Viral Bioinformatics and Genomics MRC - University of Glasgow Centre for Virus Research, United Kingdom

Monday 20th - Friday 24th August 2018 Application deadline 20th April 2018 Cost pounds 500

The MRC-University of Glasgow Centre for Virus Research (CVR) has been running a successful training course on Viral Bioinformatics and Genomics annually since 2015 and applications are now open for the 2018 course. The full details and how to apply can be found at: https://www.gla.ac.uk/researchinstitutes/iii/cvr/events/OIEtraining The 5-day course consists of a series of lectures and practical exercises that directly address bioinformatics challenges posed by the current surge of sequence data, with a focus on viral data sets and analyses. We will enable participants to understand and deal with high-throughput sequence datasets and encourage the exchange of ideas among diagnosticians, virologists, bioinformaticians and evolutionary biologists.

The 2018 course will introduce participants to the power of the UNIX command- line and bash scripts, as well as a suite of bioinformatics tools covering the following topics: - HTS sequencing technologies: overview of the different HTS platforms and sample preparations. - The power of Unix: essential bash scripting. - Reference assembly: aligning sequence reads to a known reference and visualizing the alignment (e.g. bowtie2, BWA, Tanoti, Tablet, UGENE). - Variant calling: consensus sequence generation, low frequency variant calling and error correction (e.g. samtools, LoFreq, DiversiTools). - De-novo assembly: overlap layout and de Bruijn graphs approaches for sequence assembly, quality assessment and merging contigs (e.g. ABySS, SPAdes, MIRA, IDBA-UD, QUAST, Mauve). - Metagenomic analyses: sanitizing sequence datasets, assembling, annotating, visualizing (e.g. MetAMOS, Krona, DIAMOND, Kraken). - Genomics: scaffolding, improving and finishing the assembly, gene annotation (e.g. ICORN, Artemis, RATT). - Phylogenetic analysis: introduction to multiple sequence alignment and phylogenetic reconstruction (e.g. Muscle, PhyML, FigTree).

The course will be held at the CVR, Garscube Campus, University of Glasgow, UK. The CVR has been designated an World Organisation for Animal Health (OIE) Collaborating Centre for Viral Genomics and Bioinformatics at the 82nd OIE General Session.

To apply, please fill in the online application form before 20th April 2018: https://goo.gl/forms/-QXhSO0IuEkEHILko2 Please could you circulate this email to people or institutions you think maybe interested in the course.

Cheers

Quan

Dr. Quan Gu MRC - University of Glasgow Centre for Virus Research 117 Sir Michael Stoker Building 464 Bearsden Road Glasgow G61 1QH United Kingdom Tel: (+44) 01413304019 www.bioinformatics.cvr.ac.uk [University of Glasgow: The Times Scottish University of the Year 2018]

Quan Gu <quan.gu@glasgow.ac.uk>

Guarda SummerSchoolEvol Jun16-23

Guarda summer school in evolutionary biology 2018

It is my pleasure to announce the 2018 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 16. - 23. June in the Swiss mountain village Guarda. Faculty includes Hopi Hoekstra (Harvard University, USA), Janis Antonovics (University of Virginia), Sebastian Bonhoeffer (ETH-Zurich, Switzerland) and Dieter Ebert (Basel University, Switzerland; organizer).

The course is intended for master students and early PhD students with a keen interest in evolutionary biology.

The web page with all details can be found: http://-www.evolution.unibas.ch/teaching/guarda/index.htm

Application is open now. Deadline is 1. February 2018

Please communicate this information to interested students.

With best wishes, dieter ebert

– Dieter Ebert University of Basel, Zoology, 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>

Kyoto EvolutionInCognition Jul15-19

3rd Evolution in Cognition Workshop

to be held as part of the

2018 Genetic and Evolutionary Computation Conference (GECCO-2018)

July 15-19, Kyoto, Japan

Organized by ACM SIGEVO

http://gecco-2018.sigevo.org Webpage: https://-sites.google.com/champlain.edu/eic2018/ Submission Deadline: March 27th, 2018

=== Topic =Evolution by natural selection has shaped life over billions of years leading to the emergence of complex organism capable of exceptional cognitive abilities. These natural evolutionary processes have inspired the development of Evolutionary Algorithms (EAs), which are optimization algorithms widely popular due to their efficiency and robustness. Beyond their ability to optimize, EAs have also proven to be creative and efficient at generating innovative solutions to novel problems. The combination of these two abilities makes them a tool of choice for the resolution of complex problems.

There is evidence that the principle of selection on variation is at play in the human brain, as proposed in Changeux???s and Edelman???s models of Neuronal Darwinism, and more recently properly reformulated in the theory of the Neuronal Replicators. Consequently, the idea of an interaction between evolutionary processes and cognition over physiological time scales has been gaining some traction. Since the development of human cognition requires years of maturation, it can be expected that artificial cognitive agents will also require months if not years of learning and adaptation. It is in this context that the optimizing and creative abilities of EAs could become an ideal framework that complement, aid in understanding, and facilitate the implementation of cognitive processes. Additionally, a better understanding of how evolution can be implemented as part of an artificial cognitive architecture can lead to new insights into cognition in humans and other animals.

The goals of the workshop are to depict the current state of the art of evolution in cognition and to sketch the main challenges and future directions. In particular, we aim at bringing together the different theoretical and empirical approaches that can potentially contribute to the understanding of how evolution and cognition can act together in an algorithmic way in order to solve complex problems. In this workshop we welcome approaches that contribute to an improved understanding of evolution in cognition using robotic agents, in silico computation as well as mathematical models.

Keywords: Evolutionary Computation, Evolution, Cognition,Cultural Evolution, Darwinian Neurodynamics, Neuronal Darwinism, Robotics.

=== Invited speakers = * Prof. Kenji Doya * Additional invited speakers will be announced in the near future.

=== Organizers = * Prof. St??phane Doncieux, University Pierre and Marie Curie, Paris, France * Dr. Joshua Auerbach, Champlain College, VT, USA * Prof. Richard Duro, Universidade da Coru??a, A Coru??a, Spain * Dr. Harold P. de Vladar, KLI ??? Konrad Lorenz Institute for Evolution and Cognition Research, Vienna, Austria

=== Submissions and deadlines submissions: * Original: experimental work, position papers as well as overviews of author's recent work are all welcome. These submissions will be included in the proceedings and be presented during the workshop

* Abstracts submitted as poster to GECCO 2018: the authors of selected abstracts will be given a talk. The abstract won???t be included in the proceedings. * Hot-of-the-press: authors can submit a recently published work. Selected articles will be given a talk.

Submission: extended abstracts (2-4 pages) and long papers (8 pages) are accepted. They should follow ACM template. The submission process will use the GECCO submission system. Please ask any question you may have to eic_ws@isir.upmc.fr:

* March, 27th, 2018: Papers Submission Deadline * April, 10th, 2018: Notification of Acceptance * April, 24th, 2018: Camera-Ready Paper Submission * July 15 or 16th, 2018: Workshop

GECCO is sponsored by the Association for Computing Machinery Special

Interest Group on Genetic and Evolutionary Computation (SIGEVO). SIG

Services: 2 Penn Plaza, Suite 701, New York, NY, 10121, USA,

1-800-342-6626 (USA and Canada) or +212-626-0500 (Global).

St??phane Doncieux, Josh Auerbach, Richard Duro and Harold P. de Vladar

Dr. Harold P. de Vladar Senior Fellow KLI Martinstrasse 12 3400 Klosterneuburg, Austria

harold.devladar@kli.ac.at

http://hpvladar.wordpress.com http://kli.ac.at Harold de Vladar <harold.devladar@kli.ac.at>

Montpellier Evol2018 Aug18 TeachingEvolution

Workshop on Teaching Evolution at the Joint Congress

Looking for ways to share your excitement about evolution with your students? Save the date! Higher education faculty and future faculty are invited to a workshop on teaching evolution before the Joint Congress in Montpellier. Learn about effective resources and methods for teaching evolution. This workshop is offered by the SSE Education Committee (www.evolutionsociety.org/), EvoKE (https://evokeproject.org/), and ESEB (eseb.org/). Watch for more details in early Spring, 2018. You may also submit your email to receive updates (https://tinyurl.com/evoPD2018).

Date: Saturday, August 18, 2018 Location: Montpellier, France

"awarwick@msu.edu" <awarwick@msu.edu>

Naples ELIXIRPopulationGenomics Apr21-27

Deadline on 05.02.2018 - only one week to go!

ELIXIR-IIB, in collaboration with the National Research Council Italy, is pleased to announce the upcoming training course on "Population Genomics: background and tools".

IMPORTANT DATES

Deadline for applications: 5 February 2018

Chosen participants will be notified by: 28 February 2018

Payment deadline: 10 March 2018

Course date: 21-27 April 2018

A maximum of 28 candidates will be accepted in the course. Priority will be given to candidates from ELIXIR-IIB member institutions and ELIXIR nodes.

REGISTRATION FEE: 500 euro

Registration fee includes course material, coffee breaks and lunches.

VENUE

Biblioteca - Consiglio Nazionale delle Ricerche - Istituto di Genetica e Biofisica "Adriano Buzzati-Traverso" - via Pietro Castellino 111 - 80131 Napoli - IT

Full details at: https://elixir-iib-training.github.io/-website/2018/04/21/PopGen-Napoli.html 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 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 include 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 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.

COURSE SPEAKERS

§Aida Andrés, Max Planck Institute for Evolutionary Anthropology, Germany, balancing selection in humans and primates

§Andrew Clark, Cornell University, USA, population genetics

§Mathias Currat, Université de Genève, Switzerland, coalescent simulations in European populations

§Olivier Delaneau, Université de Genève, Switzerland, statistical genomics

§Pascale Gerbault, University of Westminster, United Kingdom, positive selection in humans

§Garrett Hellenthal, University College London, United kingdom, population structure and demography

§Andrea Manica, University of Cambridge, United Kingdom, population genetics, natural selection

§Ida Moltke, University of Copenhagen, Denmark, human evolution evolutionary medicine

§Martin Sikora, Natural History Museum of Denmark

Tweet #popgenELIXIR

Should you have any question, do not hesitate to contact the ELIXIR-IIB Training Team (elixir.popgen.2018@gmail.com)

Thank you for your interest,

The Organisers and the ELIXIR-IIB Training Team

Chiara Batini (University of Leicester, UK), Vincenza Colonna (CNR, Napoli, IT) and Allegra Via (CNR, Bari, IT)

"Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

NHM London IntroductoryMolecPylogenetics May14-18

Dear Colleagues,

The Natural History Museum, London and BBSRC are offering a one-week introductory course 'Integrating molecules with taxonomy and systematics: an introductory molecular phylogenetics course for species identification and evolutionary analysis', to run from 14-18th May 2018. The course will be taught by NHM scientists and will benefit anyone wishing to gain expertise in molecular diagnostics and phylogenetic analysis for systematic, taxonomic and ecological studies. Note that this course assumes no prior experience with DNA sequence analyses and is an introductory course. As such, it is not appropriate for more advanced students.

More information can be found here: http://www.nhm.ac.uk/our-science/courses-and-students/integrating-molecules-with-taxonomy-and-systematics.html Summary: A phylogeny is essential for defining species boundaries, species identifications, recognition of cryptic species, testing systematic hypotheses, identifying evolutionary and biogeographic patterns and understanding the evolution of traits. As such, knowing how to produce a robust tree is an indispensable tool for modern taxonomists, systematists and evolutionary biologists.

This one-week introductory-level course will teach participants the steps involved to produce molecular phylogenies from raw Sanger and next-generation sequence data (i.e. Illumina paired-end). By the time the participants have completed the course, they will have had theoretical and practical experience enabling them to i) edit raw Sanger and NGS sequence data, ii) carry out multiple sequence alignments, iii) choose appropriate models of sequence evolution, iv) carry out phylogenetic analyses (including Bayesian inference, maximum likelihood), v) interpret tree topology and nodal support, vi) produce publication ready trees, vii) work with public sequence repositories, vii) assemble and annotate next generation sequence data, and viii) recognise cryptic species.

Venue and duration: The Natural History Museum, London, UK. The course will run for one week, 9.30am-6.00pm, 14-18th May 2018.

Eligibility and how to apply: The course is available to anyone but please note that priority will be given to applicants supported by BBSRC, working on a BBSRC grant or based at a BBSRC institute. There are a maximum of 12 places available. The course is sponsored by BBSRC and the NHM and we are charging only a nominal fee of 'Ã300, which includes all course costs as well as accommodation in London and some travel costs within the UK. Lunch and light refreshments will be provided each day. To apply please use the application form provided and return by the closing date: 31 March 2017. Applications will be accepted up to the deadline and places will be decided based on merit and suitability.

Email applications to: molec_NHMBBSRC@nhm.ac.uk (Note that this is an automated email account do not send queries. Your application will receive a bounce back message so you know it has arrived safely). Application forms can be found here: http://www.nhm.ac.uk/our-science/courses-and-students/integrating-molecules-with-taxonomy-and-systematics.html Dr Suzanne Williams Dept of Life Sciences Natural History Museum Cromwell Rd London SW7 5BD United Kingdom Tel: + 44 (0) 207 942 5351

http://www.nhm.ac.uk/research-curation/staff-directory/zoology/s-williams/index.html
s.williams@nhm.ac.uk

Norwich GenomicsOfMeiosis Mar5

Workshop "Meisosis and beyond: understanding the genomics before, during and after"

One-day workshop on 5th of March 2018 at the Earlham Institute in Norwich, UK. Link to workshop website: http://www.earlham.ac.uk/meiosis-and-beyond . About:

Meiosis is the necessary consequence of sexual reproduction in eukaryotes. Despite its ubiquity we know relatively little about the genomics of meiosis and what happens before, during and after.

In this workshop, we aim to summarise the state-of-the-art genomics view on the processes leading to, and resulting from, meiosis across different taxa and identify open questions. We will discuss how the most recent sequencing technologies, including single-cell sequencing technology or long-read, can help us to decipher the unknowns of meiosis.

The workshop will be composed of oral presentations by a combination of invited speakers and delegates and will provide ample space for discussions. The outcome of the workshop will be written up and published as a review or perspective paper with participants as co-authors.

Target Audience:

Researchers using any model system with an interest in processes linked with meiosis, interest in applying recently developed genomic tools and Single-Cell sequencing in particular. Open to everybody.

Abstracts:

We welcome abstract submissions from all delegates, both early career researchers and experienced. Abstracts should include a title, list of authors with presenting author in bold, affiliations for authors and the main body of the abstract must be no longer than 250 words. Abstracts must be submitted in one of the following file formats: .doc .docx .pdf to training@earlham.ac.uk

Deadline for abstract submission is: Monday 5th February at 17:00 GMT.

Abstracts will be reviewed and successful authors will be contacted within 10 days of submission closing. Abstracts will be selected based on scientific merit and complementarity to the symposium themes. Successful authors will be given a 15 minute slot comprising of 12 minute presentation and 3 minutes for questions. Speakers will be asked to send their presentation in advance, plus to bring a backup copy of the presentation in an appropriate format (either USB or accessible from a download site).

Prerequisites:

None though more beneficial if you already have a project in mind in experimental planning stages.

Questions:

If you have any questions feel free to contact me: s.immler@uea.ac.uk –

Dr Simone Immler School of Biological Sciences University of East Anglia Norwich Research Park NR4 7TJ UK

Tel: +44 (0)1603 59 1241 Email: s.immler@uea.ac.uk Homepage: https://simoneimmler.com/ Simone Immler <S.Immler@uea.ac.uk>

OrfordMusique Quebec MixedModels May14-18

Introduction to Mixed (Hierarchical) models for biologists using R (IMBR01)

https://www.prstatistics.com/course/introduction-to-mixed-hierarchical-models-for-biologists-using-r-imbr01/ Delivered by Prof. Subhash Lele from the 14th - 18th May 2018 at Orford Musique, Quebec, Canada

Course overview: Mixed models, also known as hierarchical models and multilevel models, is a useful class of models for many applied sciences, including biology, ecology and evolution. The goal of this course is to give a thorough introduction to the logic, theory and most importantly implementation of these models to solve practical problems in ecology. Participants are not expected to know mathematics beyond the basic algebra and calculus. Participants are expected to know some R programming and to be familiar with the linear and generalized linear regression. We will be using JAGS (Just Another Gibbs Sampler) for Markov Chain Monte Carlo (MCMC) simulations for analyzing mixed models. The course will be conducted so that participants have substantial hands-on experience.

Full details can be found at www.prstatistics.com or

https://www.prstatistics.com/course/introduction-to-mixed-hierarchical-models-for-biologists-using-r-imbr01/ Other up-coming courses - email oliverhooker@prstatistics.com for details

1. January 29t 'V February 2nd 2018 INTRODUCTION TO BAYESIAN HIERARCHICAL MODELLING (IBHM02) SCENE, Scotland, Dr. Andrew Parnell http://www.prstatistics.com/course/-introduction-to-bayesian-hierarchical-modelling-using-r-ibhm02/ 2. January 29th 'V February 2nd 2018 PHYLOGENETIC DATA ANALYSIS USING R (PHYL02) SCENE, Scotland, Dr. Emmanuel Paradis https://www.prstatistics.com/course/introduction-to-phylogenetic-analysis-with-r-phyg-phyl02/ —–

3. February 19th 'V 23rd 2018 MOVEMENT ECOLOGY (MOVE01) Margam Discovery Centre, Wales, Dr Luca Borger, Dr Ronny Wilson, Dr Jonathan Potts https://www.prstatistics.com/course/movement-ecology-move01/ 4. February 19th 'V 23rd 2018 GEOMETRIC MORPHOMETRICS USING R (GMMR01) Margam Discovery Centre, Wales, Prof. Dean Adams, Prof. Michael Collyer, Dr. Antigoni Kaliontzopoulou http://www.prstatistics.com/course/-geometric-morphometrics-using-r-gmmr01/ —–

5. March 5th - 9th 2018 SPATIAL PRIORITIZATION USING MARXAN (MRXN01) Margam Discovery Centre, Wales, Jennifer McGowan https://www.prstatistics.com/course/introduction-to-marxan-mrxn01/ 6. March 12th - 16th 2018 ECOLOGICAL NICHE MODELLING USING R (ENMR02) Glasgow, Scotland, Dr. Neftali Sillero http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr02/ 7. March 19th 'V 23rd 2018 BEHAVIOURAL DATA ANALYSIS USING MAXIMUM LIKLIHOOD IN R (BDML01) Glasgow, Scotland, Dr William Hoppitt http://www.psstatistics.com/-course/behavioural-data-analysis-using-maximum-likelihood-bdml01/ —–

8. April 9th 'V 13th 2018 NETWORK ANAYLSIS FOR ECOLOGISTS USING R (NTWA02 Glasgow, Scotland, Dr. Marco Scotti https://www.prstatistics.com/course/-network-analysis-ecologists-ntwa02/ 9. April 16th 'V 20th 2018 INTRODUCTION TO STATISTICAL MODELLING FOR PSYCHOLOGISTS USING R (IPSY01) Glasgow, Scotland, Dr. Dale Barr, Dr Luc Bussierre http://www.psstatistics.com/course/introduction-to-statistics-using-r-for-psychologists-ipsy01/ 10. April 23rd 'V 27th 2018 MULTIVARIATE ANALYSIS OF ECOLOGICAL COMMUNITIES USING THE

VEGAN PACKAGE (VGNR01) Glasgow, Scotland, Dr. Peter Solymos, Dr. Guillaume Blanchet https://www.prstatistics.com/course/multivariate-analysis-of-ecological-communities-in-r-with-the-vegan-package-vgnr01/ 11. April 30th 'V 4th May 2018 QUANTITATIVE GEOGRAPHIC ECOLOGY: MODELING GENOMES, NICHES, AND

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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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Panama PolychaeteSystematics Jul1-14

Systematics and Ecology of Caribbean Polychaete

Dates: 1 July - 14 July 2018

Location: Bocas Research Station, Bocas del Toro, Panama

Instructors:

Leslie Harris, Natural History Museum of Los Angeles, California

Sergio I. Salazar-Vallejo, El Colegio de la Frontera Sur, Mexico

Luis Carrera-Parra, El Colegio de la Frontera Sur, Mexico

Organizer: Dr. Rachel Collin

Registration Fee: $850 (includes room and board, STRI registration fee, etc.). Some need-based fellowships are available

Course Description

Polychaetes are under appreciated but highly important components in marine ecosystems. The course is aimed at graduate students, post-docs, or professionals who work or plan to work on taxonomic and or ecological studies with polychaetes in general and Caribbean species in particular. The participants in this course will:

Learn to collect, identify, and preserve the most common polychaetes in different substrates of the Bocas del Toro region, such as mangrove roots, soft sediments, and hard bottoms in coral reefs.

Learn general biological and ecological characteristics of the group.

Improve their taxonomic experience with tropical polychaetes.

Improve their photographic skills to record pigmentation patterns of living worms.

Learn the basics of taxonomic description and publication.

Learn museum standards for long-term care of wet-preserved biological specimens.

Although polychaetes are largely unknown to most people our understanding of the impacts of human activities on the oceans can be monitored accurately only through the careful study of these fascinating animals. Polychaetes comprise a major animal lineage with well over 16,000 recognized species that occupy a wide range of marine environments. They form a major component of benthic communities from the intertidal to abyssal depths, in soft sediments, coral reefs and other hard substrates. Many members of this ancient group are ecologically and economically important as ecosystem engineers, as food sources for other organisms, as the basis of commercial enterprises, as indicators of environmental health, and as invasive or pest species. The over 80 families of polychaetes show an amazing array of body forms and sizes. As one of the few segmented phyla, annelids are key to understanding the evolution of bilaterian body plans.

Bocas del Toro has a rich polychaete fauna. To date approximately 400 species have been found in the area, about half of them described and half of them provisional species in need of further identification. The course will be most useful for students from the greater Caribbean as most species are wide-spread through-out the region but anyone wishing to gain experience with the group will benefit.

This course will last 13 day, split between field collecting and lab work. After the 2013 Bocas polychaete workshop the students were asked to evaluate the course. Overall they preferred to spend as much time as possible learning the characters & techniques that would enable them to proceed on their own after returning home. Accordingly, the main focus here will be on basic systematics & ecology with a minor emphasis on phylogeny. A pdf library of 1600+ publications on or relevant to Caribbean polychaetes will be provided.

Daily activities will include 2 to 3 lectures, discussion, and laboratory practice. Field trips will be arranged with the station staff to visit at least once each of the different types of environments (soft sediments, mangrove, coral rocks, sandy beaches) near the Bocas Research station to collect baseline data for conservation and for future studies. Snorkeling will be part of the field work but not SCUBA. Those who want to dive can arrange to do so through one of the local dive shops on their day off.

During the second half of the course students will each prepare descriptive species pages using specimen they collect & photograph live. The pages will be incorporated into a photo ID guide for the use of station visitors, students, outreach programs, and others.

Application: Please e-mail your CV, 1 letter of recommendation, and a 1-2 page statement explaining your background and reasons for taking the course, to bocasresearchstation@gmail.com before January 30th, 2018. Limit 12 students. To be considered for a need-based fellowship, applicants should send a description of their need, their efforts to obtain funding from other available sources, and a travel budget. For more information see http://www.stri.si.edu/sites/-taxonomy_training/ Thank you very much, Maycol

“Madrid, Maycol” <MadridM@si.edu>

Prague BeetleSystematics Jul8-21

Systematics of Beetles

Basic Information

Systematics of Beetles is a summer course (6 ECTS) open to advanced MSc. and Ph.D. students interested in beetle systematics, natural history and evolution.

The course will focus on systematics of extant beetles (Coleoptera), with lectures and laboratories treating the classification, morphology of adults and larvae, and classification of all families.

The course is limited to 25 students. Why apply? The course is a unique opportunity for students to engage with leading world beetle systematists, appreciate the full spectrum of the world’s beetle diversity, and interact with other students keen on beetle research. A seminar session for students will be held at the beginning of the course, to allow students to introduce their research. Where: Prague, Czech Republic Faculty of Environmental Sciences, Czech University of Life Sciences Prague When: July 8-21, 2018 Application deadline: March 15, 2018 Details: http://beetles.fzp.czu.cz/ Hermes Escalona Humboldt Postdoctoral Fellow Zoologisches Forschungsmuseum Alexander Koenig Centre for Molecular Biodiversity Research (ZMB) Adenauerallee 160, 53113 Bonn, Germany mob. +49 17674884354 https:/-/hermesescalonaweb.wordpress.com Hermes Escalona <hermesescalona@gmail.com>

Sweden ParentalCareSexualSelection Feb26-Mar03

WORKSHOP INVITATION

INTERPLAY BETWEEN PARENTAL CARE AND SEXUAL SELECTION

Dear Colleagues,

We are glad to invite you to our Workshop that will take place between th February and 3rd March 2018 in Fiskebäckskil, Sweden.

The main goal of this workshop is to provide a relaxed atmosphere where searchers interested in different aspects of the interplay between rental care and sexual selection will exchange ideas, discuss the recent velopments in the field, and propose in details future directions. We brace diversity as a way to enrich scientific discussions and we will ioritize attendees with diverse backgrounds, at different career stages, d that use different organisms and methodological approaches to address eir questions. Besides, the workshop will provide the perfect forum for searchers (especially young scientists) to network with other specialists the field.

The event will start with a reception on Monday 26th February, will clude 3 full days of talks from invited speakers and attendees, 1 night poster exhibition, and a last full day of general discussion of relevant b-themes in the field, conducted in small groups self-organized by the rticipants. We ask participants to present results or ideas from on-going search instead of already published papers, given that the main focus of e workshop is the discussion of fresh perspectives and initiatives.

Confirmed invited speakers include:

Professor Suzanne H. Alonzo

University of California - Santa Cruz, USA

Dr Lutz Fromhage

University of Jyväskylä, Finland

Professor Wolfgang Goymann

Max Planck Institute for Ornithology, Germany

Dr. Irja Ida Ratikainen

Norwegian University of Science and Technology, Norway

Dr. Nick Royle

University of Exeter, UK

There are no registration fees. Accommodation and meals for 40 rticipants will be covered by the financial support of the Gothenburg ntre for Advanced Studies in Science & Technology (GoCAS) and the Royal edish Academy of Sciences (KVA). Participants will only be charged for e costs of their social events and the transportation to the event venue.

For more details, access: tps://parentalcaresexualselection.wordpress.com/

Application deadline: Monday, 08th January 2018.

We look forward to hearing from you.

Best regards,

Gustavo S. Requena

Postdoctoral Fellow

Universidade de Sāo Paulo

http://campuspress.yale.edu/gsrequena/ Charlotta Kvarnemo

Professor

University of Gothenburg

https://sites.google.com/site/kvarnemolab/home Gustavo Requena <gs.requena@gmail.com>

Sweden ParentalCareSexualSelection Feb26-Mar03 DeadlineExt

DEADELINE EXTENDED!

WORKSHOP INVITATION

INTERPLAY BETWEEN PARENTAL CARE AND SEXUAL SELECTION

Dear Colleagues,

We are glad to invite you to our Workshop that will take place between 26th February and 3rd March 2018 in Fiskebäckskil, Sweden.

The main goal of this workshop is to provide a relaxed atmosphere where researchers interested in different aspects of the interplay between parental care and sexual selection will exchange ideas, discuss the recent developments in the field, and propose in details future directions. We embrace diversity as a way to enrich scientific discussions and we will prioritize attendees with diverse backgrounds, at different career stages, and that use different organisms and methodological approaches to address their questions. Besides, the workshop will provide the perfect forum for researchers (especially young scientists) to network with other specialists in the field.

The event will start with a reception on Monday 26th February, will include 3 full days of talks from invited speakers and attendees, 1 night of poster exhibition, and a last full day of general discussion of relevant sub-themes in the field, conducted in small groups self-organized by the participants. We ask participants to present results or ideas from on-going research instead of already published papers, given that the main focus of the workshop is the discussion of fresh perspectives and initiatives.

Confirmed invited speakers include:

Professor Suzanne H. Alonzo

University of California - Santa Cruz, USA

Dr Lutz Fromhage

University of Jyväskylä, Finland

Professor Wolfgang Goymann

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Dr. Irja Ida Ratikainen

Norwegian University of Science and Technology, Norway

Dr. Nick Royle

University of Exeter, UK

There are no registration fees. Accommodation and meals for 40 participants will be covered by the financial support of the Gothenburg Centre for Advanced Studies in Science & Technology *(GoCAS)* and the Royal Swedish Academy of Sciences (*KVA).* Participants will only be charged for the costs of their social events and the transportation to the event venue.

For more details, access: https://parentalcaresexualselection.wordpress.com/ Please, share this message with your students, collaborators, and colleagues that may be interested in attending our event!

Application deadline: Friday, 12th January 2018.

We look forward to hearing from you.

Best regards,

Gustavo S. Requena

Postdoctoral Fellow

Universidade de Sao Paulo

http://campuspress.yale.edu/gsrequena/ *Charlotta Kvarnemo*

Professor

University of Gothenburg

https://sites.google.com/site/kvarnemolab/home gs.requena@gmail.com

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UCalifornia LosAngeles ConservationGenomics Mar24-28

UCLA/La Kretz Workshop in Conservation Genomics, 24 - 28 March, 2018

Conservation biology, genetics, and evolutionary biology have had a long and intimate relationship, and conservation constitutes one of the key applications of evolutionary analysis to real-world biological problems. The impacts of population and landscape genetics and gene expression studies have been particularly striking, and are helping to solve some of the most pressing problems in biological conservation.As the field of conservation genetics continues to grow and mature, the availability of genome-scale data stand to make profound new contributions to our ability to identify and protect at-risk populations and recover those that are most endangered. However, genomic analyses also carry a computational burdendata sets are enormous, often require diverse skills and approaches for assembly, quality control and analysis.

The La Kretz annual workshop provides a comfortable, rigorous, and informal training environment for a small group of motivated graduate students to explore how conservation problems can best be addressed with genomic-level data. Our goal is to provide hands-on experience in the efficient collection, troubleshooting, and analysis of large data sets for conservation-relevant problems. One of the highlights of our workshop is active participation from members of several governmental agencies who are at the forefront of endangered species protection and management, providing a forum for exploring the most relevant aspects of conservation genomics to managers. The UCLA/La Kretz workshop is held at the La Kretz Field Station (https://www.ioes.ucla.edu/santa-monica-mountains-research/) and Stunt Ranch Reserve (http://stuntranch.ucnrs.org/) in the heart of the Santa Monica Mountains. Only 30 miles from UCLA and the LAX airport, but nestled in the relatively undeveloped 160,000 acre Santa Monica Mountains National Recreation Area, the Field Station/Stunt Reserve provides an ideal location to explore new developments in genomic science and pressing needs in conservation and management together in a single setting.

Our current instructor list, drawn from UCLA faculty and several other partner institutions, includes: Ben Fitzpatrick (U. Tennessee Knoxville), Kirk Lohmueller (UCLA), Evan McCartney-Melstad (UCLA), Ian Wang (UC Berkeley), Brad Shaffer (UCLA), Victoria Sork (UCLA), Bob Wayne (UCLA), Ying Zhen (UCLA), Erin Toffelmier (UCLA), Alice Mouton (UCLA), Devaughn Fraser (UCLA), Emily Curd (UCLA), Zach Gold (UCLA).

Agency partners represented include: US Geological Survey, Bureau of Land Management, US Fish and Wildlife Service, and the California Dept. of Fish and Wildlife.

Topics covered include:

Overview of traditional conservation genetics

Next generation platforms: the best tool for the job

Data management pipelines:

Quality Control

Data storage

Data organization

Data types and analyses:

SNPs

Sequences

Exploring very large data sets

Functional genomic data

RNA-seq

RADseq pipelines, from raw reads to analyzing data

Genomic data and GIS

Visualizing geographic structure and demographic history

Admixture, clines, and hybridization

Detecting adaptive variation

RNAseq in a conservation context

eDNA: promise and reality

PREREQUISITES

Available housing limits course enrollment to ~20 students. Preference will be given to masters and doctoral candidates who are in the early to middle stages of their thesis research, and who have some familiarity with using a command line interface or programming languages (i.e. Perl, python etc.). We also welcome applications from postdocs, faculty, and government researchers, although our top priority is graduate student applicants. We encourage applications from women, minorities, and individuals from under-represented demographics in the sciences.

ADMISSION AND FEES Applicants will be admitted based on academic qualifications and appropriateness of research interests. The course fee is $425 USD. This includes food and lodging at the La Kretz Field Station, as well as all incidental fees, for the duration of the course (arriving Saturday March 24, departing Thursday March 29). Like last year, the workshop is co-sponsored by a UC Catalyst program grant, which will provide some student support and staffing. University of California students from any campus may apply for partial support (up to $225) from the Conservation Genomics Consortium (https://ucconservationgenomics.eeb.ucla.edu/) funded under the UC Catalyst program. To do so, simply note in your application that you would like to apply for this partial support. UCLA students

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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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UK AnalysingBehaviouralData Mar19-23

PS statistics are running a course aimed specifically at analysing behavioural data and is therefor highly relevant to those studying the evolution of behaviour (both human and animal)

“Behavioural data analysis using maximum likelihood in R (BDML01)”

https://www.psstatistics.com/course/behavioural-data-analysis-using-maximum-likelihood-bdml01/ This course is being devilled by Dr Will Hoppitt and will run from 19th - 23rd March 2018 in Glasgow

Course Overview: This 5-day course will involve a combination of lectures and practical sessions. Students will learn to build and fit custom models for analysing behavioural data using maximum likelihood techniques in R. This flexible approach allows a researcher to a) use a statistical model that directly represents their hypothesis, in cases where standard models are not appropriate and b) better understand how standard statistical models (e.g. GLMs) are fitted, many of which are fitted by maximum likelihood. Students will learn how to deal with binary, count and continuous data, including time-to-event data which is commonly encountered in behavioural analysis.

1) After successfully completing this course students should be able to: 2) fit a multi-parameter maximum likelihood model in R 3) derive likelihood functions for binary, count and continuous data 4) deal with time-to-event data 5) build custom models to test specific behavioural hypotheses 6) conduct hypothesis tests and construct confidence intervals 7) use Akaike’s information criterion (AIC) and model averaging 8) understand how maximum likelihood relates to Bayesian techniques

Full details and time table can be found at

https://www.psstatistics.com/course/behavioural-data-analysis-using-maximum-likelihood-bdml01/ We offer accommodation packages as well to make travel cheaper, easier and stress free.

Please email any questions to oliverhooker@PSstatistics.com

Also check out our sister sites, www.PRstatistics.com (ecology courses) and wwwPRinformatics.com (data science courses)

Other up-coming PS stats courses

Oliver Hooker PhD. PS statistics

Introduction to Bayesian hierarchical modelling using R (IBHM02) https://www.psstatistics.com/course/introduction-to-bayesian-hierarchical-modelling-using-r-ibhm02/ Behavioural data analysis using maximum likelihood in R (BDML01) https://www.psstatistics.com/course/behavioural-data-analysis-using-maximum-likelihood-bdml01/ Introduction to statistical modelling for psychologists in R (IPSY01) https://www.psstatistics.com/course/introduction-to-statistics-using-r-for-psychologists-ipsy01/ Social Network Analysis for Behavioural Scientists using R (SNAR01) https://www.psstatistics.com/course/social-network-analysis-for-behavioral-scientists-snar01/ PSstatistics.com facebook.com/PSstatistics/ twitter.com/PSstatistics

6 Hope Park Crescent Edinburgh EH8 9NA +44 (0) 7966500340

– Oliver Hooker PhD. PR statistics

2017 publications -

Ecosystem size predicts eco-morphological variability in post-glacial diversification. Ecology and Evolution. In press.

The physiological costs of prey switching reinforce foraging specialization. Journal of animal ecology.

prstatistics.com facebook.com/prstatistics/ twitter.com/PRstatistics groups.google.com/d/forum/prstatistics-post-course-forum prstatistics.com/organiser/oliver-hooker/

6 Hope Park Crescent Edinburgh EH8 9NA

+44 (0) 7966500340

Oliver Hooker <oliverhooker@prstatistics.com>

UK GeometricMorphometricsUsingR Feb19-23

PARTFUNDED SCHOLARHPS for the course "Geometric Morphometrics Using R (GMMR01)"

PR STATISTICS ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE "Geometric Morphometrics Using R (GMMR01)"

SCHOLARSHIPS CONTRIBUTE TOWARDS COURSE FEES WITH 5 PLACES AVAILABLE AT 250.00 (Fees have been subsidised by 45% from 450.00).

This course is being delivered by Prof. Dean Adams, Prof. Michael Collyer and Dr. Antigoni Kaliontzopoulou

Applications should be sent to oliverhooker@prstatistics.com and contain the following. 1. Full name 2. Institute name 3. PhD subject title or Post doc research questions 4. Do you hold a funded position 5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Wednesday 7th February 2018 and decisions will be made by Thursday 8th February 2018

We still have 'normal' places available for anyone else interested.

Full course details are given below

Geometric Morphometrics Using R (GMMR01)

https://www.prstatistics.com/course/geometric-morphometrics-using-r-gmmr01/ This course is being delivered by Prof. Dean Adams, Prof. Michael Collyer and Dr. Antigoni Kaliontzopoulou — This course will run from 19th - 23rd February 2018 at Margam Discovery Centre, Wales, UK. — The field of geometric morphometrics (GM) is concerned with the quantification and analysis of patterns of shape variation, and its covariation with other variables. Over the past several decades these approaches have become a mainstay in the field of ecology, evolutionary biology, and anthropology, and a panoply of analytical tools for addressing specific biological hypotheses concerning shape have been developed. The goal of this is to provide participants with a working knowledge of the theory of geometric morphometrics, as well as practical training in the application of these methods. — The course is organized in both theoretical and practical sessions. The theoretical sessions will provide a comprehensive introduction to the methods of landmark-based geometric morphometrics, which aims at providing the participants with a solid theoretical background for understanding the procedures used in shape data analysis. Practical sessions will include worked examples, giving the participants the opportunity to gain hands-on experience in the treatment of shape data using the R package geomorph. These sessions focus on the generation of shape variables from primary landmark data, the statistical treatment of shape variation with respect to biological hypotheses, and the visualization of patterns of shape variation and of the shapes themselves for interpretation of statistical findings, using the R language for statistical programming. While practice datasets will be available, it is strongly recommended that participants come with their own datasets. — Note: Because this is a geometric morphometrics workshop in R, it is required that participants have some working knowledge in R. The practical sessions of the course will focus on GM-based analyses, and not basic R user-interfacing. It is therefore strongly recommended that participants refresh their R skills prior to attending the workshop. — — Course Programme — Sunday 5th Meet at Millport field centre at approximately 18:30. — Monday 6th - Classes from 09:00 to 17:30 1: Morphometrics: History, Introduction and Data Types 2: Review of matrix algebra and multivariate statistics 3: Superimposition 4: Software demonstration and lab practicum — Tuesday 7th - Classes from 09:00 to 17:30 1: Shape spaces, shape variables, PCA 2: GPA with semi-landmarks 3: Shape covariation 4: Software demonstration and lab practicum — Wednesday 8th - Classes from 09:00 to 17:30 1: Phylogenetic shape variation 2: Group Differences & Trajectory Analysis 3: Allometry 4: Software demonstration and lab practicum — Thursday 9th - Classes from 09:00 to 17:30 1: Assymetry 2: Missing Data 3: Integration and Modularity 4: Disparity 5: Software demonstration and lab practicum — Friday 10th - Classes from 09:00 to 16:00 1: Future Directions 2: Lab Pacticum 3: Student Presentations — Please send inquiries to oliverhooker@prstatistics.com or visit the website www.prstatistics.com — Please feel free to distribute this information anywhere you think suitable — Upcoming courses - email for details oliverhooker@prstatistics.com — — 1. January 29t - February 2nd 2018 INTRODUCTION TO BAYESIAN HIERARCHICAL MODELLING (IBHM02) SCENE, Scotland, Dr. Andrew Parnell

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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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UParisSud Coevolution Apr22-25

We are pleased to announce our first ESEB-STN Workshop 2018 “Experimental approaches to test for coevolution”

WHO? Organizers: Amandine Cornille Eva Stukenbrock Peter Tiffin Dieter Ebert Daniel Croll Ricardo Rodriguez de la Vega

Invited speakers Anna-Liisa Laine (Univ. Helsinki, Finland) Kayla King (Univ. Oxford, UK) Stineke van Houte (Univ. Of Exeter, UK) Lutz Beck (Max Plank Institute, Germany)

WHERE? Univ. Paris Sud, France

WHEN? 22-25th April 2018

Info: Fee (all inclusive: tuition, accommodation and food) : 350 euros Application deadline : 28th February - 30 participants max. More info and application at http://workshop.inra.fr/ecol-genome-coevol #WorkshopEcolGenomCoevol, contact: workshop-ecol-genom-coevol1@inra.fr

Amandine Cornille

Chargee de Recherche CNRS Genetique Quantitative et ??volution - Le Moulon INRA - Universite Paris-Sud - CNRS - AgroParisTech Ferme du Moulon 91190 Gif-sur-Yvette France

Amandine Cornille <amandine.cornille@gmail.com>

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.